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(54) Title: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST CANCER

(57) Abstract: The invention relates to compositions, kits, and methods for detecting, characterizing, preventing, and treating human breast cancers. A variety of novel markers are provided, wherein changes in the levels of expression of one or more of the markers is correlated with the presence of breast cancer.

NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST CANCER

RELATED APPLICATIONS

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The present application claims priority to U.S. provisional application serial no. 60/176,077, filed January 14, 2000, U.S. provisional application serial no. 60/189,167, filed March 14, 2000, U.S. provisional application serial no. 60/192,099, filed March 24, 2000, U.S. provisional application serial no. 60/193,480, filed March 29, 2000, U.S. provisional application serial no. 60/205,230, filed May 15, 2000, U.S. provisional application serial no. 60/211,315, filed June 9, 2000, U.S. provisional application serial no. 60/220,534, filed July 25, 2000, all of which are expressly incorporated by reference.

FIELD OF THE INVENTION

The field of the invention is breast cancer, including diagnosis, characterization, management, and therapy of breast cancer.

BACKGROUND OF THE INVENTION

The increased number of cancer cases reported in the United States, and, indeed, around the world, is a major concern. Currently there are only a handful of treatments available for specific types of cancer, and these provide no absolute guarantee of success. In order to be most effective, these treatments require not only an early detection of the malignancy, but a reliable assessment of the severity of the malignancy.

The incidence of breast cancer, a leading cause of death in women, has been gradually increasing in the United States over the last thirty years. In 1997, it was estimated that 181,000 new cases were reported in the U.S., and that 44,000 people would die of breast cancer (Parker et al, 1997, CA Cancer J. Clin. 47:5-27; Chu et al, 1996, J. Nat. Cancer Inst. 88:1571-1579). While the pathogenesis of breast cancer is unclear, transformation of normal breast epithelium to a malignant phenotype may be the result of genetic factors, especially in women under 30 (Miki et al., 1994, Science, 266:66-71). The discovery and characterization of BRCA1 and BRCA2 has recently expanded our knowledge of genetic factors which can contribute to familial breast

cancer. Germ-line mutations within these two loci are associated with a 50 to 85% lifetime risk of breast and/or ovarian cancer (Casey, 1997, Curr. Opin. Oncol. 9:88-93; Marcus et al, 1996, Cancer 77:697-709). However, it is likely that other, non-genetic factors also have a significant effect on the etiology of the disease. Regardless of its origin, breast cancer morbidity and mortality increases significantly if it is not detected early in its progression. Thus, considerable effort has focused on the early detection of cellular transformation and tumor formation in breast tissue.

Currently, the principal manner of identifying breast cancer is through detection of the presence of dense tumorous tissue. This may be accomplished to varying degrees of effectiveness by direct examination of the outside of the breast, or through mammography or other X-ray imaging methods (Jatoi, 1999, Am. J. Surg. 177:518-524). The latter approach is not without considerable cost, however. Every time a mammogram is taken, the patient incurs a small risk of having a breast tumor induced by the ionizing properties of the radiation used during the test. In addition, the process is expensive and the subjective interpretations of a technician can lead to imprecision, e.g., one study showed major clinical disagreements for about one-third of a set of mammograms that were interpreted individually by a surveyed group of radiologists. Moreover, many women find that undergoing a mammogram is a painful experience. Accordingly, the National Cancer Institute has not recommended mammograms for women under fifty years of age, since this group is not as likely to develop breast cancers as are older women. It is compelling to note, however, that while only about 22% of breast cancers occur in women under fifty, data suggests that breast cancer is more aggressive in pre-menopausal women.

It would therefore be beneficial to provide specific methods and reagents for the diagnosis, staging, prognosis, monitoring, and treatment of diseases associated with breast cancer, or to indicate a predisposition to such for preventative measures.

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SUMMARY OF THE INVENTION

The invention relates to novel genes associated with breast cancer as well as

methods of assessing whether a patient is afflicted with breast cancer. The methods of
the present invention comprise the step of comparing the level of expression of a marker
in a patient sample, wherein the marker is listed in Tables 1-6 and the normal level of

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expression of the marker in a control, e.g., a sample from a patient without breast cancer. A significant difference between the level of expression of the marker in the patient sample and the normal level is an indication that the patient is afflicted with breast cancer. Preferably, a protein corresponding to the marker is a secreted protein or is predicted to correspond to a secreted protein. Alternatively, the marker can correspond to a protein having an extracellular portion, to one which is normally expressed in breast tissue at a detectable level, or both.

In one method, the marker(s) are preferably selected such that the positive predictive value of the method is at least about 10%. Also preferred are embodiments of the method wherein the marker is over- or under-expressed by at least two-fold in at least about 20% of stage 0 breast cancer patients, stage I breast cancer patients, stage IIA breast cancer patients, stage IIIB breast cancer patients, stage IV breast cancer patients, grade I breast cancer patients, grade II breast cancer patients, grade III breast cancer patients, malignant breast cancer patients, ductal carcinoma breast cancer patients, and lobular carcinoma breast cancer patients.

In one embodiment of the methods of the present invention, the patient sample is a breast tissue-associated body fluid. Such fluids include, for example, blood fluids, lymph and cystic fluids, as well as nipple aspirates. In another embodiment, the sample comprises cells obtained from the patient. In another embodiment, the patient sample is *in vivo*.

In accordance with the methods of the present invention, the level of expression of the marker in a sample can be assessed, for example, by detecting the presence in the sample of:

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• a protein or a fragment of the protein corresponding to the marker (e.g. using a reagent, such as an antibody, an antibody derivative, or an antibody fragment, which binds specifically with the protein or a fragment of the protein)

• a metabolite which is produced directly (i.e., catalyzed) or indirectly by a protein corresponding to the marker

• a transcribed polynucleotide (e.g. an mRNA or a cDNA), or fragment thereof, having at least a portion with which the marker is substantially

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homologous (e.g. by contacting a mixture of transcribed polynucleotides obtained from the sample with a substrate having one or more of the markers listed in Tables 1-6 fixed thereto at selected positions)

 a transcribed polynucleotide or fragment thereof, wherein the polynucleotide anneals with the marker under stringent hybridization conditions.

The methods of the present invention are particularly useful for patients with an identified breast mass or symptoms associated with breast cancer. The methods of the present invention can also be of particular use with patients having an enhanced risk of developing breast cancer (e.g., patients having a familial history of breast cancer, patients identified as having a mutant oncogene, and patients at least about 50 years of age). The methods of the present invention may further be of particular use in monitoring the efficacy of treatment of a breast cancer patient (e.g. the efficacy of chemotherapy).

The methods of the present invention may be performed using a plurality (e.g. 2, 3, 5, or 10 or more) of markers. According to a method involving a plurality of markers, the level of expression in the sample of each of a plurality of markers independently selected from the markers listed in Tables 1-6 is compared with the normal level of expression of each of the plurality of markers in samples of the same type obtained from control humans not afflicted with breast cancer. A significantly enhanced level of expression of one or more of the markers listed in Tables 1-6 in the sample, relative to the corresponding normal levels, is an indication that the patient is afflicted with breast cancer. The markers of Tables 1-6 may also be used in combination with known breast cancer markers in the methods of the present invention.

In a preferred method of assessing whether a patient is afflicted with breast cancer (e.g., new detection ("screening"), detection of recurrence, reflex testing), the method comprises comparing:

- a) the level of expression of a marker in a patient sample, wherein at least one marker is selected from the markers of Tables 1-6, and
- b) the normal level of expression of the marker in a control non-breast cancer sample.

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A significant difference between the level of expression of the marker in the patient sample and the normal level is an indication that the patient is afflicted with breast cancer.

The methods of the present invention further include a method of assessing the efficacy of a test compound for inhibiting breast cancer in a patient. This method comprises comparing:

a) expression of a marker in a first sample obtained from the patient and maintained in the presence of the test compound, wherein the marker is selected from the group consisting of the markers listed in Tables 1-6, and

b) expression of the marker in a second sample obtained from the patient and maintained in the absence of the test compound.

A significantly lower level of expression of the marker in the first sample, relative to the second sample, is an indication that the test compound is efficacious for inhibiting breast cancer in the patient. For example, the first and second samples can be portions of a single sample obtained from the patient or portions of pooled samples obtained from the patient.

The invention further relates to a method of assessing the efficacy of a therapy for inhibiting breast cancer in a patient. This method comprises comparing:

a) expression of a marker in a first sample obtained from the patient prior to providing at least a portion of the therapy to the patient, wherein the marker is selected from the group consisting of the markers listed in Tables 1-6, and

b) expression of the marker in a second sample obtained from the patient following provision of the portion of the therapy.

A significantly lower level of expression of the marker in the second sample, relative to the first sample, is an indication that the therapy is efficacious for inhibiting breast cancer in the patient.

It will be appreciated that in these methods the "therapy" may be any therapy for treating breast cancer including, but not limited to, chemotherapy, radiation therapy and surgical removal of tissue, e.g., a breast tumor. Thus, the methods of the invention may

be used to evaluate a patient before, during and after therapy, for example, to evaluate the reduction in tumor burden.

The present invention therefore further comprises a method for monitoring the progression of breast cancer in a patient, the method comprising:

- a) detecting in a patient sample at a first time point, the expression of a marker, wherein the marker is selected from the group consisting of the markers listed in Tables 1-6;
 - b) repeating step a) at a subsequent time point; and

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c) comparing the level of expression detected in steps a) and b), and therefrom monitoring the progression of breast cancer in the patient. 10

The invention also includes a method of selecting a composition for inhibiting breast cancer in a patient. This method comprises the steps of:

- a) obtaining a sample comprising cancer cells from the patient;
- b) separately maintaining aliquots of the sample in the presence of a plurality of test compositions;
- c) comparing expression of a marker listed in Tables 1-6 in each of the aliquots; and
- d) selecting one of the test compositions which induces a lower level of expression of the marker in the aliquot containing that test composition, relative to other test compositions.

In addition, the invention includes a method of inhibiting breast cancer in a patient. This method comprises the steps of:

- a) obtaining a sample comprising cancer cells from the patient;
- b) separately maintaining aliquots of the sample in the presence of a plurality of test compositions;
- c) comparing expression of a marker listed in Tables 1-6 in each of the aliquots; and
- d) administering to the patient at least one of the test compositions which induces a lower level of expression of the marker in the aliquot containing that test composition, relative to other test compositions.

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The invention also includes a kit for assessing whether a patient is afflicted with breast cancer. This kit comprises reagents for assessing expression of a marker listed in Tables 1-6.

In another aspect, the invention relates to a kit for assessing the suitability of each of a plurality of compounds for inhibiting breast cancer in a patient. The kit comprises a reagent for assessing expression of a marker listed in Tables 1-6, and may also comprise a plurality of compounds.

In another aspect, the invention relates to a kit for assessing the presence of breast cancer cells. This kit comprises an antibody, wherein the antibody binds specifically with a protein corresponding to a marker listed in Tables 1-6. The kit may also comprise a plurality of antibodies, wherein the plurality binds specifically with a protein corresponding to a different marker which is also listed in Tables 1-6.

The invention also includes a kit for assessing the presence of breast cancer cells, wherein the kit comprises a nucleic acid probe. The probe binds specifically with a transcribed polynucleotide corresponding to a marker listed in Tables 1-6. The kit may also comprise a plurality of probes, wherein each of the probes binds specifically with a transcribed polynucleotide corresponding to a different marker listed in Tables 1-6.

The invention further relates to a method of making an isolated hybridoma which produces an antibody useful for assessing whether a patient is afflicted with breast cancer. The method comprises isolating a protein or protein fragment corresponding to a marker listed in Tables 1-6, immunizing a mammal using the isolated protein or protein fragment, isolating splenocytes from the immunized mammal, fusing the isolated splenocytes with an immortalized cell line to form hybridomas, and screening individual hybridomas for production of an antibody which specifically binds with the protein or protein fragment to isolate the hybridoma. The invention also includes an antibody produced by this method.

The invention further includes a method of assessing the breast carcinogenic or irregular growth promoting potential of a test compound. This method comprises the steps of:

a) maintaining separate aliquots of breast cells in the presence and absence of the test compound; and

b) comparing expression of a marker in each of the aliquots.

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The marker is selected from those listed in Tables 1-6. A significantly enhanced level of expression of the marker in the aliquot maintained in the presence of (or exposed to) the test compound, relative to the aliquot maintained in the absence of the test compound, is an indication that the test compound possesses breast carcinogenic or irregular growth promoting potential.

Additionally, the invention includes a kit for assessing the breast carcinogenic potential of a test compound. The kit comprises breast cells and a reagent for assessing expression of a marker in each of the aliquots. The marker is selected from those listed in Tables 1-6.

The invention further includes a method of treating a patient afflicted with breast cancer, comprising providing to cells of the patient an antisense oligonucleotide complementary to a polynucleotide corresponding to a marker listed in Tables 1-6.

The invention includes a method of inhibiting breast cancer in a patient at risk for developing breast cancer. This method comprises inhibiting expression or overexpression of a gene corresponding to a marker listed in Tables 1-6.

It will be appreciated that the methods and kits of the present invention may also include known cancer markers including known breast cancer markers. It will further be appreciated that the methods and kits may be used to identify cancers other than breast cancer.

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DETAILED DESCRIPTION OF THE INVENTION

The invention relates to newly discovered correlations between expression of certain markers and the cancerous state of breast cells. It has been discovered that the level of expression of individual markers and combinations of markers described herein correlates with the presence of breast cancer in a patient. Methods are provided for detecting the presence of breast cancer in a sample, the absence of breast cancer in a sample, the stage of breast cancer, and other characteristics of breast cancer that are relevant to prevention, diagnosis, characterization, and therapy of breast cancer in a patient.

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Definitions

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As used herein, each of the following terms has the meaning associated with it in this section.

The articles "a" and "an" are used herein to refer to one or to more than one (i.e. to at least one) of the grammatical object of the article. By way of example, "an element" means one element or more than one element.

A "marker" is a naturally-occurring polymer corresponding to at least one of the novel nucleic acids listed in Tables 1-6. For example, markers include, without limitation, sense and anti-sense strands of genomic DNA (*i.e.* including any introns occurring therein), RNA generated by transcription of genomic DNA (*i.e.* prior to splicing), RNA generated by splicing of RNA transcribed from genomic DNA, and proteins generated by translation of spliced RNA (*e.g.* including proteins both before and after cleavage of normally cleaved regions such as transmembrane signal sequences). As used herein, "marker" may also include a cDNA made by reverse transcription of an RNA generated by transcription of genomic DNA (including spliced RNA).

As used herein a "polynucleotide corresponds to" another (a first) polynucleotide if it is related to the first polynucleotide by any of the following relationships: 1) The second polynucleotide comprises the first polynucleotide and the second polynucleotide encodes a gene product. 2) The second polynucleotide is 5' or 3' to the first polynucleotide in cDNA, RNA, genomic DNA, or fragment of any of these polynucleotides. For example, a second polynucleotide may be fragment of a gene that includes the first and second polynucleotides. The first and second polynucleotides are related in that they are components of the gene coding for a gene product, such as a protein or antibody. However, it is not necessary that the second polynucleotide comprises or overlaps with the first polynucleotide to be encompassed within the definition of "corresponding to" as used herein. For example, the first polynucleotide may be a fragment of a 3' untranslated region of the second polynucleotide. The first and second polynucleotide may be fragments of a gene coding for a gene product. The second polynucleotide may be an exon of the gene while the first polynucleotide may be an intron of the gene. 3) The second polynucleotide is the complement of the first polynucleotide.

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The term "probe" refers to any molecule which is capable of selectively binding to a specifically intended target molecule, for example a marker of the invention. Probes can be either synthesized by one skilled in the art, or derived from appropriate biological preparations. For purposes of detection of the target molecule, probes may be specifically designed to be labeled, as described herein. Examples of molecules that can be utilized as probes include, but are not limited to, RNA, DNA, proteins, antibodies, and organic monomers.

A "breast-associated" body fluid is a fluid which, when in the body of a patient, contacts or passes through breast cells or into which cells, nucleic acids or proteins shed from breast cells are capable of passing. Exemplary breast-associated body fluids include blood fluids, lymph, cystic fluid, urine and nipple aspirates.

The "normal" level of expression of a marker is the level of expression of the marker in breast cells of a patient, e.g. a human, not afflicted with breast cancer.

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"Over-expression" and "under-expression" of a marker refer to expression of the marker of a patient at a greater or lesser level, respectively, than normal level of expression of the marker (e.g. at least two-fold greater or lesser level).

As used herein, the term "promoter/regulatory sequence" means a nucleic acid sequence which is required for expression of a gene product operably linked to the promoter/regulatory sequence. In some instances, this sequence may be the core promoter sequence and in other instances, this sequence may also include an enhancer sequence and other regulatory elements which are required for expression of the gene product. The promoter/regulatory sequence may, for example, be one which expresses the gene product in a tissue-specific manner.

A "constitutive" promoter is a nucleotide sequence which, when operably linked with a polynucleotide which encodes or specifies a gene product, causes the gene product to be produced in a living human cell under most or all physiological conditions of the cell.

An "inducible" promoter is a nucleotide sequence which, when operably linked with a polynucleotide which encodes or specifies a gene product, causes the gene product to be produced in a living human cell substantially only when an inducer which corresponds to the promoter is present in the cell.

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A "tissue-specific" promoter is a nucleotide sequence which, when operably linked with a polynucleotide which encodes or specifies a gene product, causes the gene product to be produced in a living human cell substantially only if the cell is a cell of the tissue type corresponding to the promoter.

A "transcribed polynucleotide" is a polynucleotide (e.g. an RNA, a cDNA, or an analog of one of an RNA or cDNA) which is complementary to or homologous with all or a portion of a mature RNA made by transcription of a genomic DNA corresponding to a marker of the invention and normal post-transcriptional processing (e.g. splicing), if any, of the transcript.

"Complementary" refers to the broad concept of sequence complementarity between regions of two nucleic acid strands or between two regions of the same nucleic acid strand. It is known that an adenine residue of a first nucleic acid region is capable of forming specific hydrogen bonds ("base pairing") with a residue of a second nucleic acid region which is antiparallel to the first region if the residue is thymine or uracil. Similarly, it is known that a cytosine residue of a first nucleic acid strand is capable of base pairing with a residue of a second nucleic acid strand which is antiparallel to the first strand if the residue is guanine. A first region of a nucleic acid is complementary to a second region of the same or a different nucleic acid if, when the two regions are arranged in an antiparallel fashion, at least one nucleotide residue of the first region is capable of base pairing with a residue of the second region. Preferably, the first region comprises a first portion and the second region comprises a second portion, whereby, when the first and second portions are arranged in an antiparallel fashion, at least about 50%, and preferably at least about 75%, at least about 90%, or at least about 95% of the nucleotide residues of the first portion are capable of base pairing with nucleotide residues in the second portion. More preferably, all nucleotide residues of the first portion are capable of base pairing with nucleotide residues in the second portion.

"Homologous" as used herein, refers to nucleotide sequence similarity between two regions of the same nucleic acid strand or between regions of two different nucleic acid strands. When a nucleotide residue position in both regions is occupied by the same nucleotide residue, then the regions are homologous at that position. A first region is homologous to a second region if at least one nucleotide residue position of each region is occupied by the same residue. Homology between two regions is expressed in

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terms of the proportion of nucleotide residue positions of the two regions that are occupied by the same nucleotide residue. By way of example, a region having the nucleotide sequence 5'-ATTGCC-3' and a region having the nucleotide sequence 5'-TATGGC-3' share 50% homology. Preferably, the first region comprises a first portion and the second region comprises a second portion, whereby, at least about 50%, and preferably at least about 75%, at least about 90%, or at least about 95% of the nucleotide residue positions of each of the portions are occupied by the same nucleotide residue. More preferably, all nucleotide residue positions of each of the portions are occupied by the same nucleotide residue.

A marker is "fixed" to a substrate if it is covalently or non-covalently associated with the substrate such the substrate can be rinsed with a fluid (e.g. standard saline citrate, pH 7.4) without a substantial fraction of the marker dissociating from the substrate.

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As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (e.g. encodes a natural protein).

Expression of a marker in a patient is "significantly" higher or lower than the normal level of expression of a marker if the level of expression of the marker is greater or less, respectively, than the normal level by an amount greater than the standard error of the assay employed to assess expression, and preferably at least twice, and more preferably three, four, five or ten times that amount. Alternately, expression of the marker in the patient can be considered "significantly" higher or lower than the normal level of expression if the level of expression is at least about two, and preferably at least about three, four, or five times, higher or lower, respectively, than the normal level of expression of the marker.

Breast cancer is "inhibited" if at least one symptom of the cancer is alleviated, terminated, slowed, or prevented. As used herein, breast cancer is also "inhibited" if recurrence or metastasis of the cancer is reduced, slowed, delayed, or prevented.

A kit is any manufacture (e.g. a package or container) comprising at least one reagent, e.g. a probe, for specifically detecting a marker of the invention, the manufacture being promoted, distributed, or sold as a unit for performing the methods of the present invention.

Description

The present invention is based, in part, on identification of novel markers which are expressed at a different level in breast cancer cells than they are in normal (*i.e.* non-cancerous) breast cells. The markers of the invention correspond to nucleic acid and polypeptide molecules which can be detected in one or both of normal and cancerous breast cells. The presence, absence, or level of expression of one or more of these markers in breast cells is herein correlated with the cancerous state of the tissue. The invention thus includes compositions, kits, and methods for assessing the cancerous state of breast cells (*e.g.* cells obtained from a human, cultured human cells, archived or preserved human cells and *in vivo* cells).

The compositions, kits, and methods of the invention have the following uses, among others:

- 1) assessing whether a patient is afflicted with breast cancer; 15 2) assessing the stage of breast cancer in a human patient; 3) assessing the grade of breast cancer in a patient; 4) assessing the benign or malignant nature of breast cancer in a patient; 5) assessing the histological type of neoplasm (e.g. ductal, lobular, etc.) associated with breast cancer in a patient; 20 making an isolated hybridoma which produces an antibody useful for 6) assessing whether a patient is afflicted with breast cancer; 7) assessing the presence of breast cancer cells; 8) assessing the efficacy of one or more test compounds for inhibiting breast cancer in a patient; 25 9) assessing the efficacy of a therapy for inhibiting breast cancer in a patient; 10) monitoring the progression of breast cancer in a patient; selecting a composition or therapy for inhibiting breast cancer in a 11) patient: 30 treating a patient afflicted with breast cancer; 12)
 - 12) Boaring a parient armeted with breast eathers,
 - 13) inhibiting breast cancer in a patient;
 - 14) assessing the carcinogenic potential of a test compound; and

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15) inhibiting breast cancer in a patient at risk for developing breast cancer.

The invention thus includes a method of assessing whether a patient is afflicted with breast cancer. This method comprises comparing the level of expression of a marker in a patient sample and the normal level of expression of the marker in a control, e.g., a non-breast cancer sample. A significant difference between the level of expression of the marker in the patient sample and the normal level is an indication that the patient is afflicted with breast cancer. The marker is selected from the group consisting of the markers listed in Tables 1-6.

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The polynucleotides set forth in Tables 1-6 represent previously unidentified nucleotide sequences. These nucleotide sequences were identified through subtracted library experiments described herein. In Tables 1 and 3, SEQ ID NOS 316-470, 793-890, 1255-1363, 2125-2454 and 3352-3626 are preferred and SEQ ID NOS 1-315, 676-792, 1056-1254, 1645-2124 and 2942-3351 are most preferred. In Tables 2 and 4, SEQ ID NOS: 1879-1959 are preferred and SEQ ID NOS: 1-1878 are most preferred. Also provided by this invention are polynucleotides that correspond to the polynucleotides of Tables 1-6. In one embodiment, these polynucleotides are obtained by identification of a larger fragment or full-length coding sequence of these polynucleotides. Gene delivery vehicles, host cells, compositions and databases (all describe herein) containing these polynucleotides are also provided by this invention.

The invention also encompasses polynucleotides which differ from that of the polynucleotides described above, but which produce the same phenotypic effect, e.g. allelic variants. These altered, but phenotypically equivalent polynucleotides are referred to "equivalent nucleic acids." This invention also encompasses polynucleotides characterized by changes in non-coding regions that do not alter the polypeptide produced therefrom when compared to the polynucleotide herein. This invention further encompasses polynucleotides, which hybridize to the polynucleotides of the subject invention under conditions of moderate or high stringency. Alternatively, the polynucleotides are at least 85%, or at least 90%, or more preferably, greater or equal to 95% identical as determined by a sequence alignment program when run under default parameters.

Any marker or combination of markers listed in Tables 1-6, as well as any known markers in combination with the markers set forth in Tables 1-6, may be used in the compositions, kits, and methods of the present invention. In general, it is preferable to use markers for which the difference between the level of expression of the marker in breast cancer cells and the level of expression of the same marker in normal breast cells is as great as possible. Although this difference can be as small as the limit of detection of the method for assessing expression of the marker, it is preferred that the difference be at least greater than the standard error of the assessment method, and preferably a difference of at least 2-, 3-, 4-, 5-, 6-, 7-, 8-, 9-, 10-, 15-, 20-, 25-, 100-, 500-, 1000-fold or greater.

It is recognized that certain markers correspond to proteins which are secreted from breast cells (*i.e.* one or both of normal and cancerous cells) to the extracellular space surrounding the cells. These markers are preferably used in certain embodiments of the compositions, kits, and methods of the invention, owing to the fact that the protein corresponding to each of these markers can be detected in an breast-associated body fluid sample, which may be more easily collected from a human patient than a tissue biopsy sample. In addition, preferred *in vivo* techniques for detection of a protein corresponding to a marker of the invention include introducing into a subject a labeled antibody directed against the protein. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

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Although not every marker corresponding to a secreted protein is indicated as such herein, it is a simple matter for the skilled artisan to determine whether any particular marker corresponds to a secreted protein. In order to make this determination, the protein corresponding to a marker is expressed in a test cell (e.g. a cell of a breast cell line), extracellular fluid is collected, and the presence or absence of the protein in the extracellular fluid is assessed (e.g. using a labeled antibody which binds specifically with the protein).

The following is an example of a method which can be used to detect secretion of a protein corresponding to a marker of the invention. About 8 x 10⁵ 293T cells are incubated at 37°C in wells containing growth medium (Dulbecco's modified Eagle's medium {DMEM} supplemented with 10% fetal bovine serum) under a 5% (v/v) CO₂,

95% air atmosphere to about 60-70% confluence. The cells are then transfected using a standard transfection mixture comprising 2 micrograms of DNA comprising an expression vector encoding the protein and 10 microliters of LipofectAMINETM (GIBCO/BRL Catalog no. 18342-012) per well. The transfection mixture is maintained for about 5 hours, and then replaced with fresh growth medium and maintained in an air atmosphere. Each well is gently rinsed twice with DMEM which does not contain methionine or cysteine (DMEM-MC; ICN Catalog no. 16-424-54). About 1 milliliter of DMEM-MC and about 50 microcuries of Trans-³⁵STM reagent (ICN Catalog no. 51006) are added to each well. The wells are maintained under the 5% CO₂ atmosphere described above and incubated at 37°C for a selected period. Following incubation, 150 microliters of conditioned medium is removed and centrifuged to remove floating cells and debris. The presence of the protein in the supernatant is an indication that the protein is secreted.

Examples of breast-associated body fluids include blood fluids (e.g. whole blood, blood serum, blood having platelets removed therefrom, etc.), lymph, ascitic fluid, cystic fluid, urine and nipple aspirates. In these embodiments, the level of expression of the marker can be assessed by assessing the amount (e.g. absolute amount or concentration) of the marker in a breast-associated body fluid obtained from a patient. The fluid can, of course, be subjected to a variety of well-known post-collection preparative and storage techniques (e.g. storage, freezing, ultrafiltration, concentration, evaporation, centrifugation, etc.) prior to assessing the amount of the marker in the fluid.

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Many breast-associated body fluids (*i.e.* usually excluding urine) can have breast cells therein, particularly when the breast cells are cancerous, and, more particularly, when the breast cancer is metastasizing. Thus, the compositions, kits, and methods of the invention can be used to detect expression of markers corresponding to proteins having at least one portion which is displayed on the surface of cells which express it. It is a simple matter for the skilled artisan to determine whether the protein corresponding to any particular marker comprises a cell-surface protein. For example, immunological methods may be used to detect such proteins on whole cells, or well known computer-based sequence analysis methods (*e.g.* the SIGNALP program; Nielsen *et al.*, 1997, *Protein Engineering* 10:1-6) may be used to predict the presence of at least one extracellular domain (*i.e.* including both secreted proteins and proteins having at

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least one cell-surface domain). Expression of a marker corresponding to a protein having at least one portion which is displayed on the surface of a cell which expresses it may be detected without necessarily lysing the cell (e.g. using a labeled antibody which binds specifically with a cell-surface domain of the protein).

Expression of a marker of the invention may be assessed by any of a wide variety of well known methods for detecting expression of a transcribed molecule or protein. Non-limiting examples of such methods include immunological methods for detection of secreted, cell-surface, cytoplasmic, or nuclear proteins, protein purification methods, protein function or activity assays, nucleic acid hybridization methods, nucleic acid reverse transcription methods, and nucleic acid amplification methods.

In a preferred embodiment, expression of a marker is assessed using an antibody (e.g. a radio-labeled, chromophore-labeled, fluorophore-labeled, or enzyme-labeled antibody), an antibody derivative (e.g. an antibody conjugated with a substrate or with the protein or ligand of a protein-ligand pair {e.g. biotin-streptavidin}), or an antibody fragment (e.g. a single-chain antibody, an isolated antibody hypervariable domain, etc.) which binds specifically with a protein or a fragment thereof, corresponding to the marker, such as the protein encoded by the open reading frame corresponding to the marker or such a protein which has undergone all or a portion of its normal post-translational modification.

In another preferred embodiment, expression of a marker is assessed by preparing mRNA/cDNA (*i.e.* a transcribed polynucleotide) from cells in a patient sample, and by hybridizing the mRNA/cDNA with a reference polynucleotide which is a complement of a polynucleotide comprising the marker, and fragments thereof. cDNA can, optionally, be amplified using any of a variety of polymerase chain reaction methods prior to hybridization with the reference polynucleotide; preferably, it is not amplified. Expression of one or more markers can likewise be detected using quantitative PCR to assess the level of expression of the marker(s). Alternatively, any of the many known methods of detecting mutations or variants (*e.g.* single nucleotide polymorphisms, deletions, etc.) of a marker of the invention may be used to detect occurrence of a marker in a patient.

In a related embodiment, a mixture of transcribed polynucleotides obtained from the sample is contacted with a substrate having fixed thereto a polynucleotide complementary to or homologous with at least a portion (e.g. at least 7, 10, 15, 20, 25, 30, 40, 50, 100, 500, or more nucleotide residues) of a marker of the invention. If polynucleotides complementary to or homologous with are differentially detectable on the substrate (e.g. detectable using different chromophores or fluorophores, or fixed to different selected positions), then the levels of expression of a plurality of markers can be assessed simultaneously using a single substrate (e.g. a "gene chip" microarray of polynucleotides fixed at selected positions). When a method of assessing marker expression is used which involves hybridization of one nucleic acid with another, it is preferred that the hybridization be performed under stringent hybridization conditions.

Because the compositions, kits, and methods of the invention rely on detection of a difference in expression levels of one or more markers of the invention, it is preferable that the level of expression of the marker is significantly greater than the minimum detection limit of the method used to assess expression in at least one of normal breast cells and cancerous breast cells.

It is understood that by routine screening of additional patient samples using one or more of the markers of the invention, it will be realized that certain of the markers are over- or under-expressed in cancers of various types, including specific breast cancers, as well as other cancers such as ovarian cancer, cervical cancer, etc. For example, it will be confirmed that some of the markers of the invention are over- or under-expressed in most (i.e. 50% or more) or substantially all (i.e. 80% or more) of breast cancer. Furthermore, it will be confirmed that certain of the markers of the invention are associated with breast cancer of various stages (i.e. stage 0, I, II, II, and IV breast cancers, as well as subclassifications IIA, IIB, IIIA, and IIIB, using the FIGO Stage Grouping system for primary carcinoma of the breast; (see Breast, In: American Joint Committee on Cancer: AJCC Cancer Staging Manual. Lippincott-Raven Publishers, 5th ed., 1997, pp. 171-180), of various histologic subtypes (e.g. serous, mucinous, endometroid, and clear cell subtypes, as well as subclassifications and alternate classifications adenocarcinoma, papillary adenocarcinoma, papillary cystadenocarcinoma, surface papillary carcinoma, malignant adenofibroma, cystadenofibroma, adenocarcinoma, cystadenocarcinoma, adenoacanthoma,

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endometrioid stromal sarcoma, mesodermal (Müllerian) mixed tumor, mesonephroid tumor, malignant carcinoma, Brenner tumor, mixed epithelial tumor, and undifferentiated carcinoma, using the WHO/FIGO system for classification of malignant breast tumors; Scully, *Atlas of Tumor Pathology*, 3d series, Washington DC), and various grades (*i.e.* grade I {well differentiated}, grade II {moderately well differentiated}, and grade III {poorly differentiated from surrounding normal tissue})). In addition, as a greater number of patient samples are assessed for expression of the markers of the invention and the outcomes of the individual patients from whom the samples were obtained are correlated, it will also be confirmed that altered expression of certain of the markers of the invention are strongly correlated with malignant cancers and that altered expression of other markers of the invention are strongly correlated with benign tumors. The compositions, kits, and methods of the invention are thus useful for characterizing one or more of the stage, grade, histological type, and benign/malignant nature of breast cancer in patients. In addition, these compositions, kits, and methods can be used to detect and differentiate lobular and ductal carcinoma breast cancers.

When the compositions, kits, and methods of the invention are used for characterizing one or more of the stage, grade, histological type, and benign/malignant nature of breast cancer in a patient, it is preferred that the marker or panel of markers of the invention is selected such that a positive result is obtained in at least about 20%, and preferably at least about 40%, 60%, or 80%, and more preferably in substantially all patients afflicted with an breast cancer of the corresponding stage, grade, histological type, or benign/malignant nature. Preferably, the marker or panel of markers of the invention is selected such that a PPV of greater than about 10% is obtained for the general population (more preferably coupled with an assay specificity greater than 99.5%).

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When a plurality of markers of the invention are used in the compositions, kits, and methods of the invention, the level of expression of each marker in a patient sample can be compared with the normal level of expression of each of the plurality of markers in non-cancerous samples of the same type, either in a single reaction mixture (*i.e.* using reagents, such as different fluorescent probes, for each marker) or in individual reaction mixtures corresponding to one or more of the markers. In one embodiment, a significantly enhanced level of expression of more than one of the plurality of markers

in the sample, relative to the corresponding normal levels, is an indication that the patient is afflicted with breast cancer. In another embodiment, a significantly lower level of expression in the sample of each of the plurality of markers, relative to the corresponding normal levels, is an indication that the patient is afflicted with breast cancer. In yet another embodiment, a significantly enhanced level of expression of one or more markers and a significantly lower level of expression of one or more markers in a sample relative to the corresponding normal levels, is an indication that the patient is afflicted with breast cancer. When a plurality of markers is used, it is preferred that 2, 3, 4, 5, 8, 10, 12, 15, 20, 30, or 50 or more individual markers be used, wherein fewer markers are preferred.

In order to maximize the sensitivity of the compositions, kits, and methods of the invention (i.e. by interference attributable to cells of non-breast origin in a patient sample), it is preferable that the marker of the invention used therein be a marker which has a restricted tissue distribution, e.g., normally not expressed in a non-breast tissue.

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Only a small number of markers are known to be associated with breast cancers (e.g. BRCA1 and BRCA2). These markers are not, of course, included among the markers of the invention, although they may be used together with one or more markers of the invention in a panel of markers, for example. It is well known that certain types of genes, such as oncogenes, tumor suppressor genes, growth factor-like genes, protease-like genes, and protein kinase-like genes are often involved with development of cancers of various types. Thus, among the markers of the invention, use of those which correspond to proteins which resemble known proteins encoded by known oncogenes and tumor suppressor genes, and those which correspond to proteins which resemble growth factors, proteases, and protein kinases are preferred.

Known oncogenes and tumor suppressor genes include, for example, abl, abr, akt2, apc, bcl2α, bcl2β, bcl3, bcr, brca1, brca2, cbl, ccnd1, cdc42, cdk4, crk- II, csf1r/fms, dbl, dcc, dpc4/smad4, e-cad, e2f1/rbap, egfr/erbb-1, elk1, elk3, eph, erg, ets1, ets2, fer, fgr/src2, fli1/ergb2, fos, fps/fes, fra1, fra2, fyn, hck, hek, her2/erbb- 2/neu, her3/erbb-3, her4/erbb-4, hras1, hst2, hstf1, igfbp2, ink4a, ink4b, int2/fgf3, jun, junb, jund, kip2, kit, kras2a, kras2b, lck, lyn, mas, max, mcc, mdm2, met, mlh1, mmp10, mos, msh2, msh3, msh6, myb, myba, mybb, myc, mycl1, mycn, nf1, nf2, nme2, nras, p53, pdgfb, phb, pim1, pms1, pms2, ptc, pten, raf1, rap1a, rb1, rel, ret, ros1, ski, src1, tal1,

tgfbr2, tgfb3, tgfbr3, thra1, thrb, tiam1, timp3, tjp1, tp53, trk, vav, vhl, vil2, waf1, wnt1, wnt2, wt1, and yes1 (Hesketh, 1997, In: The Oncogene and Tumour Suppressor Gene Facts Book, 2nd Ed., Academic Press; Fishel et al., 1994, Science 266:1403-1405).

Known growth factors include platelet-derived growth factor alpha, plateletderived growth factor beta (simian sarcoma viral {v-sis} oncogene homolog), thrombopoietin (myeloproliferative leukemia virus oncogene ligand, megakaryocyte growth and development factor), erythropoietin, B cell growth factor, macrophage stimulating factor 1 (hepatocyte growth factor-like protein), hepatocyte growth factor (hepapoietin A), insulin-like growth factor 1 (somatomedia C), hepatoma-derived growth factor, amphiregulin (schwannoma-derived growth factor), bone morphogenetic proteins 1, 2, 3, 3 beta, and 4, bone morphogenetic protein 7 (osteogenic protein 1), bone morphogenetic protein 8 (osteogenic protein 2), connective tissue growth factor, connective tissue activation peptide 3, epidermal growth factor (EGF), teratocarcinomaderived growth factor 1, endothelin, endothelin 2, endothelin 3, stromal cell-derived factor 1, vascular endothelial growth factor (VEGF), VEGF-B, VEGF-C, placental growth factor (vascular endothelial growth factor-related protein), transforming growth factor alpha, transforming growth factor beta 1 and its precursors, transforming growth factor beta 2 and its precursors, fibroblast growth factor 1 (acidic), fibroblast growth factor 2 (basic), fibroblast growth factor 5 and its precursors, fibroblast growth factor 6 and its precursors, fibroblast growth factor 7 (keratinocyte growth factor), fibroblast growth factor 8 (androgen-induced), fibroblast growth factor 9 (glia-activating factor), pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1), brain-derived neurotrophic factor, and recombinant glial growth factor 2.

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Known proteases include interleukin-1 beta convertase and its precursors, Mch6
and its precursors, Mch2 isoform alpha, Mch4, Cpp32 isoform alpha, Lice2 gamma
cysteine protease, Ich-1S, Ich-1L, Ich-2 and its precursors, TY protease, matrix
metalloproteinase 1 (interstitial collagenase), matrix metalloproteinase 2 (gelatinase A,
72kD gelatinase, 72kD type IV collagenase), matrix metalloproteinase 7 (matrilysin),
matrix metalloproteinase 8 (neutrophil collagenase), matrix metalloproteinase 12
(macrophage elastase), matrix metalloproteinase 13 (collagenase 3), metallopeptidase 1,
cysteine-rich metalloprotease (disintegrin) and its precursors, subtilisin-like protease Pc8
and its precursors, chymotrypsin, snake venom-like protease, cathepsin l, cathepsin D

(lysosomal aspartyl protease), stromelysin, aminopeptidase N, plasminogen, tissue plasminogen activator, plasminogen activator inhibitor type II, and urokinase-type plasminogen activator.

Known protein kinases include DAP kinase, serine/threonine protein kinases NIK, PK428, Krs-2, SAK, and EMK, interferon-inducible double stranded RNA dependent protein kinase, FAST kinase, AIM1, IPL1-like midbody-associated protein kinase-1, NIMA-like protein kinase 1 (NLK1), the cyclin-dependent kinases (cdk1-10), checkpoint kinase Chk1, Nek3 protein kinase, BMK1 beta kinase, Clk1, Clk2, Clk3, extracellular signal-regulated kinases 1, 3, and 6, cdc28 protein kinase 1, cdc28 protein kinase 2, pLK, Myt1, c-Jun N-terminal kinase 2, Cam kinase 1, the MAP kinases, insulin-stimulated protein kinase 1, beta-adrenergic receptor kinase 2, ribosomal protein S6 kinase, kinase suppressor of ras-1 (KSR1), putative serine/threonine protein kinase Prk, PkB kinase, cAMP-dependent protein kinase, cGMP-dependent protein kinase, type II cGMP-dependent protein kinase, protein kinases Dyrk2, Dyrk3, and Dyrk4, Rhoassociated coiled-coil containing protein kinase p160ROCK, protein tyrosine kinase t-Ror1, Ste20-related kinases, cell adhesion kinase beta, protein kinase 3, stress-activated protein kinase 4, protein kinase Zpk, serine kinase hPAK65, dual specificity mitogenactivated protein kinases 1 and 2, casein kinase I gamma 2, p21-activated protein kinase Pak1, lipid-activated protein kinase PRK2, focal adhesion kinase, dual-specificity tyrosine-phosphorylation regulated kinase, myosin light chain kinase, serine kinases 20 SRPK2, TESK1, and VRK2, B lymphocyte serine/threonine protein kinase, stressactivated protein kinases JNK1 and JNK2, phosphorylase kinase, protein tyrosine kinase Tec, Jak2 kinase, protein kinase Ndr, MEK kinase 3, SHB adaptor protein (a Src homology 2 protein), agammaglobulinaemia protein-tyrosine kinase (Atk), protein kinase ATR, guanylate kinase 1, thrombopoeitin receptor and its precursors, DAG kinase epsilon, and kinases encoded by oncogenes or viral oncogenes such as v-fgr (Gardner-Rasheed), v-abl (Abelson murine leukemia viral oncogene homolog 1), v-arg (Abelson murine leukemia viral oncogene homolog, Abelson-related gene), v-fes and vfps (feline sarcoma viral oncogene and Fujinami avian sarcoma viral oncogene homologs), proto-oncogene c-cot, oncogene pim-1, and oncogene mas1.

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It is recognized that the compositions, kits, and methods of the invention will be of particular utility to patients having an enhanced risk of developing breast cancer and their medical advisors. Patients recognized as having an enhanced risk of developing breast cancer include, for example, patients having a familial history of breast cancer, patients identified as having a mutant oncogene (*i.e.* at least one allele), and patients of advancing age (*i.e.* women older than about 50 or 60 years).

The level of expression of a marker in normal (i.e. non-cancerous) human breast tissue can be assessed in a variety of ways. In one embodiment, this normal level of expression is assessed by assessing the level of expression of the marker in a portion of breast cells which appears to be non-cancerous and by comparing this normal level of expression with the level of expression in a portion of the breast cells which is suspected of being cancerous. For example, when mammogrophy or other medical procedure, reveals the presence of a lump in a patient's breast, the normal level of expression of a marker may be assessed using the non-affected breast tissue, and this normal level of expression may be compared with the level of expression of the same marker in an affected portion (i.e. the lump) of the affected breast. Alternately, and particularly as further information becomes available as a result of routine performance of the methods described herein, population-average values for normal expression of the markers of the invention may be used. In other embodiments, the 'normal' level of expression of a marker may be determined by assessing expression of the marker in a patient sample obtained from a non-cancer-afflicted patient, from a patient sample obtained from a patient before the suspected onset of breast cancer in the patient, from archived patient samples, and the like.

The invention includes compositions, kits, and methods for assessing the presence of breast cancer cells in a sample (e.g. an archived tissue sample or a sample obtained from a patient). These compositions, kits, and methods are substantially the same as those described above, except that, where necessary, the compositions, kits, and methods are adapted for use with samples other than patient samples. For example, when the sample to be used is a parafinized, archived human tissue sample, it can be necessary to adjust the ratio of compounds in the compositions of the invention, in the kits of the invention, or the methods used to assess levels of marker expression in the

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sample. Such methods are well known in the art and within the skill of the ordinary artisan.

The invention includes a kit for assessing the presence of breast cancer cells (e.g. in a sample such as a patient sample). The kit comprises a plurality of reagents, each of which is capable of binding specifically with a nucleic acid or polypeptide corresponding to a marker of the invention. Suitable reagents for binding with a polypeptide corresponding to a marker of the invention include antibodies, antibody derivatives, antibody fragments, and the like. Suitable reagents for binding with a nucleic acid (e.g. a genomic DNA, an mRNA, a spliced mRNA, a cDNA, or the like) include complementary nucleic acids. For example, the nucleic acid reagents may include oligonucleotides (labeled or non-labeled) fixed to a substrate, labeled oligonucleotides not bound with a substrate, pairs of PCR primers, molecular beacon probes, and the like.

The kit of the invention may optionally comprise additional components useful for performing the methods of the invention. By way of example, the kit may comprise fluids (e.g. SSC buffer) suitable for annealing complementary nucleic acids or for binding an antibody with a protein with which it specifically binds, one or more sample compartments, an instructional material which describes performance of a method of the invention, a sample of normal breast cells, a sample of breast cancer cells, and the like.

The invention also includes a method of making an isolated hybridoma which produces an antibody useful for assessing whether patient is afflicted with breast cancer. In this method, a protein corresponding to a marker of the invention is isolated (e.g. by purification from a cell in which it is expressed or by transcription and translation of a nucleic acid encoding the protein in vivo or in vitro using known methods). A vertebrate, preferably a mammal such as a mouse, rat, rabbit, or sheep, is immunized using the isolated protein or protein fragment. The vertebrate may optionally (and preferably) be immunized at least one additional time with the isolated protein or protein fragment, so that the vertebrate exhibits a robust immune response to the protein or protein fragment. Splenocytes are isolated from the immunized vertebrate and fused with an immortalized cell line to form hybridomas, using any of a variety of methods well known in the art. Hybridomas formed in this manner are then screened using standard methods to identify one or more hybridomas which produce an antibody which

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specifically binds with the protein or protein fragment. The invention also includes hybridomas made by this method and antibodies made using such hybridomas.

The invention also includes a method of assessing the efficacy of a test compound for inhibiting breast cancer cells. As described above, differences in the level of expression of the markers of the invention correlate with the cancerous state of breast cells. Although it is recognized that changes in the levels of expression of certain of the markers of the invention likely result from the cancerous state of breast cells, it is likewise recognized that changes in the levels of expression of other of the markers of the invention induce, maintain, and promote the cancerous state of those cells. Thus, compounds which inhibit breast cancer in a patient will cause the level of expression of one or more of the markers of the invention to change to a level nearer the normal level of expression for that marker (*i.e.* the level of expression for the marker in non-cancerous breast cells).

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This method thus comprises comparing expression of a marker in a first breast cell sample and maintained in the presence of the test compound and expression of the marker in a second breast cell sample and maintained in the absence of the test compound. A significant alteration in the level of expression of a marker listed in Tables 1-6, may be is an indication that the test compound inhibits breast cancer (e.g., decreases in expression in those markers that are over-expressed in breast cancer cells or more aggressive breast cancer cells and breast cancer cells from patients with poor clinical outcome or increases expression in those markers that are under-expressed in breast cancer cells or in more aggressive breast cancer cells or breast cancer cells from patients with poor clinical outcome. The breast cell samples may, for example, be aliquots of a single sample of normal breast cells obtained from a patient, pooled samples of normal breast cells obtained from a patient, cells of a normal breast cell line, aliquots of a single sample of breast cancer cells obtained from a patient, pooled samples of breast cancer cells obtained from a patient, cells of a breast cancer cell line, or the like. In one embodiment, the samples are breast cancer cells obtained from a patient and a plurality of compounds known to be effective for inhibiting various breast cancers are tested in order to identify the compound which is likely to best inhibit the breast cancer in the patient.

This method may likewise be used to assess the efficacy of a therapy for inhibiting breast cancer in a patient. In this method, the level of expression of one or more markers of the invention in a pair of samples (one subjected to the therapy, the other not subjected to the therapy) is assessed. As with the method of assessing the efficacy of test compounds, if the therapy induces a significant alteration in the level of expression of a marker listed in Tables 1-6, or blocks induction of a marker listed in Tables 1-6, then the therapy may be efficacious for inhibiting breast cancer. As above, if samples from a selected patient are used in this method, then alternative therapies can be assessed *in vitro* in order to select a therapy most likely to be efficacious for inhibiting breast cancer in the patient.

As described herein, breast cancer in patients is associated with levels of expression of one or more markers listed in Tables 1-6. While, as discussed above, some of these changes in expression level result from occurrence of the breast cancer, others of these changes induce, maintain, and promote the cancerous state of breast cancer cells. Thus, breast cancer characterized by an alteration in the level of expression of one or more markers listed in Tables 1-6 can be inhibited by hampering or increasing expression of those markers.

Expression of a marker listed in Tables 1-6 can be inhibited in a number of ways generally known in the art. For example, an antisense oligonucleotide can be provided to the breast cancer cells in order to inhibit transcription, translation, or both, of the marker(s). Alternately, a polynucleotide encoding an antibody, an antibody derivative, or an antibody fragment, and operably linked with an appropriate promoter/regulator region, can be provided to the cell in order to generate intracellular antibodies which will inhibit the function or activity of the protein corresponding to the marker(s). Using the methods described herein, a variety of molecules, particularly including molecules sufficiently small that they are able to cross the cell membrane, can be screened in order to identify molecules which inhibit expression of the marker(s). The compound so identified can be provided to the patient in order to inhibit expression of the marker(s) in the breast cancer cells of the patient.

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Expression of a marker listed within Tables 1-6 can be enhanced in number of ways generally known in the art. For example, a polynucleotide encoding the marker and operably linked with an appropriate promoter/regulator region can be provided to

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breast cancer cells of the patient in order to induce enhanced expression of the protein (and mRNA) corresponding to the marker therein. Alternatively, if the protein is capable of crossing the cell membrane, inserting itself in the cell membrane, or is normally a secreted protein, then expression of the protein can be enhanced by providing the protein (e.g. directly or by way of the bloodstream or another breast-associated fluid) to breast cancer cells in the patient.

As described above, the cancerous state of human breast cells is correlated with changes in the levels of expression of the markers of the invention. The invention thus includes a method for assessing the human breast cell carcinogenic potential of a test compound. This method comprises maintaining separate aliquots of human breast cells in the presence and absence of the test compound. Expression of a marker of the invention in each of the aliquots is compared. A significant alteration in the level of expression of a marker listed in Tables 1-6 in the aliquot maintained in the presence of the test compound (relative to the aliquot maintained in the absence of the test compound) may be an indication that the test compound possesses human breast cell carcinogenic potential. The relative carcinogenic potentials of various test compounds can be assessed by comparing the degree of enhancement or inhibition of the level of expression of the relevant markers, by comparing the number of markers for which the level of expression is enhanced or inhibited, or by comparing both.

Various aspects of the invention are described in further detail in the following subsections.

I. Isolated Nucleic Acid Molecules

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One aspect of the invention pertains to novel isolated nucleic acid molecules that correspond to a marker of the invention, including nucleic acids which encode a polypeptide corresponding to a marker of the invention or a portion of such a polypeptide. Isolated nucleic acids of the invention also include nucleic acid molecules sufficient for use as hybridization probes to identify nucleic acid molecules that correspond to a marker of the invention, including nucleic acids which encode a polypeptide corresponding to a marker of the invention, and fragments of such nucleic acid molecules, e.g., those suitable for use as PCR primers for the amplification or mutation of nucleic acid molecules. As used herein, the term "nucleic acid molecule" is

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intended to include DNA molecules (e.g., cDNA or genomic DNA) and RNA molecules (e.g., mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA.

An "isolated" nucleic acid molecule is one which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid molecule. Preferably, an "isolated" nucleic acid molecule is free of sequences (preferably protein-encoding sequences) which naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated nucleic acid molecule can contain less than about 5 kB, 4 kB, 3 kB, 2 kB, 1 kB, 0.5 kB or 0.1 kB of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the present invention, e.g., a nucleic acid encoding a protein corresponding to a marker listed in Tables 1-6, can be isolated using standard molecular biology techniques and the sequence information in the database records described herein. Using all or a portion of such nucleic acid sequences, nucleic acid molecules of the invention can be isolated using standard hybridization and cloning techniques (e.g., as described in Sambrook et al., ed., Molecular Cloning: A Laboratory Manual, 2nd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989).

A process for identifying a larger fragment or the full-length coding sequence of a marker of the present invention is thus also provided. Any conventional recombinant DNA techniques applicable for isolating polynucleotides may also be employed. One such method involves the 5'-RACE-PCR technique, in which the poly-A mRNA that contains the coding sequence of particular interest is first reverse transcribed with a 3'-primer comprising a sequence disclosed herein. The newly synthesized cDNA strand is then tagged with an anchor primer with a known sequence, which preferably contains a convenient cloning restriction site attached at the 5'end. The tagged cDNA is then

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amplified with the 3'-primer (or a nested primer sharing sequence homology to the internal sequences of the coding region) and the 5'-anchor primer. The amplification may be conducted under conditions of various levels of stringency to optimize the amplification specificity. 5'-RACE-PCR can be readily performed using commercial kits (available from, e.g., BRL Life Technologies Inc., Clontech) according to the manufacturer's instructions.

Isolating the complete coding sequence of a gene can also be carried out in a hybridization assay using a suitable probe. The probe preferably comprises at least 10 nucleotides, and more preferably exhibits sequence homology to the polynucleotides of the markers of the present invention. Other high throughput screens for cDNAs, such as those involving gene chip technology, can also be employed in obtaining the complete cDNA sequence.

In addition, databases exist that reduce the complexity of ESTs by assembling contiguous EST sequences into tentative genes. For example, TIGR has assembled human ESTs into a datable called THC for tentative human consensus sequences. The THC database allows for a more definitive assignment compared to ESTs alone. Software programs exist (TIGR assembler and TIGEM EST assembly machine and contig assembly program (see Huang, X., 1996, Genomes 33:21-23)) that allow for assembling ESTs into contiguous sequences from any organism.

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Alternatively, mRNA from a sample preparation is used to construct cDNA library in the ZAP Express vector following the procedure described in Velculescu *et al.*, 1997, *Science* 270:484. The ZAP Express cDNA synthesis kit (Stratagene) is used accordingly to the manufacturer's protocol. Plates containing 250 to 2000 plaques are hybridized as described in Rupert *et al.*, 1988, *Mol. Cell. Bio.* 8:3104 to oligonucleotide probes with the same conditions previously described for standard probes except that the hybridization temperature is reduced to a room temperature. Washes are performed in 6X standard-saline-citrate 0.1% SDS for 30 minutes at room temperature. The probes are labeled with ³²P-ATP trough use of T4 polynucleotide kinase.

A partial cDNA (3' fragment) can be isolated by 3' directed PCR reaction. This procedure is a modification of the protocol described in Polyak *et al.*, 1997, *Nature* 389:300. Briefly, the procedure uses SAGE tags in PCR reaction such that the resultant PCR product contains the SAGE tag of interest as well as additional cDNA, the length

of which is defined by the position of the tag with respect to the 3' end of the cDNA. The cDNA product derived from such a transcript driven PCR reaction can be used for many applications.

RNA from a source to express the cDNA corresponding to a given tag is first converted to double-stranded cDNA using any standard cDNA protocol. Similar conditions used to generate cDNA for SAGE library construction can be employed except that a modified oligo-dT primer is used to derive the first strand synthesis. For example, the oligonucleotide of composition 5'-B-TCC GGC GCG CCG TTT TCC CAG TCA CGA(30)- 3', contains a poly-T stretch at the 3' end for hybridization and priming from poly-A tails, an M13 priming site for use in subsequent PCR steps, a 5' Biotin label (B) for capture to strepavidin-coated magnetic beads, and an AscI restriction endonuclease site for releasing the cDNA from the strepavidin-coated magnetic beads. Theoretically, any sufficiently-sized DNA region capable of hybridizing to a PCR primer can be used as well as any other 8 base pair recognizing endonuclease.

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cDNA constructed utilizing this or similar modified oligo-dT primer is then processed exactly as described in U.S. Patent No. 5,695,937 up until adapter ligation where only one adapter is ligated to the cDNA pool. After Adapter ligation, the cDNA is released from the streptavidin-coated magnetic beads and is then used as a template for cDNA amplification.

Various PCR protocols can be employed using PCR priming sites within the 3' modified oligo-dT primer and the SAGE tag. The SAGE tag-derived PCR primer employed can be of varying length dictated by 5' extension of the tag into the adaptor sequence. cDNA products are now available for a variety of applications.

This technique can be further modified by: (1) altering the length and/or content of the modified oligo-dT primer; (2) ligating adaptors other than that previously employed within the SAGE protocol; (3) performing PCR from template retained on the streptavidin-coated magnetic beads; and (4) priming first strand cDNA synthesis with non-oligo-dT based primers.

Gene trapper technology can also be used. The reagents and manufacturer's instructions for this technology are commercially available from Life Technologies, Inc., Gaithsburg, Maryland. Briefly, a complex population of single-stranded phagemid DNA containing directional cDNA inserts is enriched for the target sequence by

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hybridization in solution to a biotinylated oligonucleotide probe complementary to the target sequence. The hybrids are captured on streptavidin-coated paramagnetic beads. A magnet retrieves the paramagnetic beads from the solution, leaving nonhybridized single-stranded DNAs behind. Subsequently, the captured single-stranded DNA target is released from the biotinylated oligonucleotide. After release, the cDNA clone is further enriched by using a nonbiotinylated target oligonucleotide to specifically prime conversion of the single-stranded DNA. Following transformation and plating, typically 20% to 100% of the colonies represent the cDNA clone of interest. To identify the desired cDNA clone, the colonies may be screened by colony hybridization using the ³²P-labeled oligonucleotide as described above for solution hybridization, or alternatively by DNA sequencing and alignment of all sequences obtained from numerous clones to determine a consensus sequence.

A nucleic acid molecule of the invention can be amplified using cDNA, mRNA, or genomic DNA as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to all or a portion of a nucleic acid molecule of the invention can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

In another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule which has a nucleotide sequence complementary to the nucleotide sequence of a nucleic acid corresponding to a marker of the invention or to the nucleotide sequence of a nucleic acid encoding a protein which corresponds to a marker of the invention. A nucleic acid molecule which is complementary to a given nucleotide sequence is one which is sufficiently complementary to the given nucleotide sequence that it can hybridize to the given nucleotide sequence thereby forming a stable duplex.

Moreover, a nucleic acid molecule of the invention can comprise only a portion of a nucleic acid sequence, wherein the full length nucleic acid sequence comprises a marker of the invention or which encodes a polypeptide corresponding to a marker of the invention. Such nucleic acids can be used, for example, as a probe or primer. The probe/primer typically is used as one or more substantially purified oligonucleotides.

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The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 7, preferably about 15, more preferably about 25, 50, 75, 100, 125, 150, 175, 200, 250, 300, 350, or 400 or more consecutive nucleotides of a nucleic acid of the invention.

Probes based on the sequence of a nucleic acid molecule of the invention can be used to detect transcripts or genomic sequences corresponding to one or more markers of the invention. The probe comprises a label group attached thereto, e.g., a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as part of a diagnostic test kit for identifying cells or tissues which misexpress the protein, such as by measuring levels of a nucleic acid molecule encoding the protein in a sample of cells from a subject, e.g., detecting mRNA levels or determining whether a gene encoding the protein has been mutated or deleted.

The invention further encompasses nucleic acid molecules that differ, due to degeneracy of the genetic code, from the nucleotide sequence of nucleic acids encoding a protein which corresponds to a marker of the invention, and thus encode the same protein.

In addition to the nucleotide sequences described herein, it will be appreciated by those skilled in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequence can exist within a population (e.g., the human population). Such genetic polymorphisms can exist among individuals within a population due to natural allelic variation. An allele is one of a group of genes which occur alternatively at a given genetic locus. In addition, it will be appreciated that DNA polymorphisms that affect RNA expression levels can also exist that may affect the overall expression level of that gene (e.g., by affecting regulation or degradation).

As used herein, the phrase "allelic variant" refers to a nucleotide sequence which occurs at a given locus or to a polypeptide encoded by the nucleotide sequence.

As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding a polypeptide corresponding to a marker of the invention. Such natural allelic variations can typically result in 1-5% variance in the nucleotide sequence of a given gene. Alternative alleles can be identified by sequencing the gene of interest in a number of different individuals. This can be readily carried out by using hybridization probes to identify the same genetic locus in a

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variety of individuals. Any and all such nucleotide variations and resulting amino acid polymorphisms or variations that are the result of natural allelic variation and that do not alter the functional activity are intended to be within the scope of the invention.

In another embodiment, an isolated nucleic acid molecule of the invention is at least 7, 15, 20, 25, 30, 40, 60, 80, 100, 150, 200, 250, 300, 350, 400, 450, 550, 650, 700, 800, 900, 1000, 1200, 1400, 1600, 1800, 2000, 2200, 2400, 2600, 2800, 3000, 3500, 4000, 4500, or more nucleotides in length and hybridizes under stringent conditions to a nucleic acid corresponding to a marker of the invention or to a nucleic acid encoding a protein corresponding to a marker of the invention. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 75% (80%, 85%, preferably 90%) identical to each other typically remain hybridized to each other. Such stringent conditions are known to those skilled in the art and can be found in sections 6.3.1-6.3.6 of Current Protocols in Molecular Biology, John Wiley & Sons, N.Y. (1989). A preferred, non-limiting example of stringent hybridization conditions for annealing two single-stranded DNA each of which is at least about 100 bases in length and/or for annealing a single-stranded DNA and a single-stranded RNA each of which is at least about 100 bases in length, are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 50-65°C. Further preferred hybridization conditions are taught in Lockhart, et al., Nature Biotechnology, Volume 14, 1996 August: 1675-1680; Breslauer, et al., Proc. Natl. Acad. Sci. USA, Volume 83, 1986 June: 3746-3750; Van Ness, et al., Nucleic Acids Research, Volume 19, No. 19, 1991 September: 5143-5151; McGraw, et al., BioTechniques,

In addition to naturally-occurring allelic variants of a nucleic acid molecule of the invention that can exist in the population, the skilled artisan will further appreciate that sequence changes can be introduced by mutation thereby leading to changes in the amino acid sequence of the encoded protein, without altering the biological activity of the protein encoded thereby. For example, one can make nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues. A "non-essential" amino acid residue is a residue that can be altered from the wild-type

Volume 8, No. 6 1990: 674-678; and Milner, et al., Nature Biotechnology, Volume 15,

1997 June: 537-541, all expressly incorporated by reference.

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sequence without altering the biological activity, whereas an "essential" amino acid residue is required for biological activity. For example, amino acid residues that are not conserved or only semi-conserved among homologs of various species may be non-essential for activity and thus would be likely targets for alteration. Alternatively, amino acid residues that are conserved among the homologs of various species (e.g., murine and human) may be essential for activity and thus would not be likely targets for alteration.

Accordingly, another aspect of the invention pertains to nucleic acid molecules encoding a polypeptide of the invention that contain changes in amino acid residues that are not essential for activity. Such polypeptides differ in amino acid sequence from the naturally-occurring proteins which correspond to the markers of the invention, yet retain biological activity. In one embodiment, such a protein has an amino acid sequence that is at least about 40% identical, 50%, 60%, 70%, 80%, 90%, 95%, or 98% identical to the amino acid sequence of one of the proteins which correspond to the markers of the invention.

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An isolated nucleic acid molecule encoding a variant protein can be created by introducing one or more nucleotide substitutions, additions or deletions into the nucleotide sequence of nucleic acids of the invention, such that one or more amino acid residue substitutions, additions, or deletions are introduced into the encoded protein. Mutations can be introduced by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), non-polar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine). Alternatively, mutations can be introduced randomly along all or part of the coding sequence, such as by saturation mutagenesis,

and the resultant mutants can be screened for biological activity to identify mutants that retain activity. Following mutagenesis, the encoded protein can be expressed recombinantly and the activity of the protein can be determined.

The present invention encompasses antisense nucleic acid molecules, *i.e.*, molecules which are complementary to a sense nucleic acid of the invention, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule corresponding to a marker of the invention or complementary to an mRNA sequence corresponding to a marker of the invention. Accordingly, an antisense nucleic acid of the invention can hydrogen bond to (*i.e.* anneal with) a sense nucleic acid of the invention. The antisense nucleic acid can be complementary to an entire coding strand, or to only a portion thereof, *e.g.*, all or part of the protein coding region (or open reading frame). An antisense nucleic acid molecule can also be antisense to all or part of a noncoding region of the coding strand of a nucleotide sequence encoding a polypeptide of the invention. The non-coding regions ("5' and 3' untranslated regions") are the 5' and 3' sequences which flank the coding region and are not translated into amino acids.

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An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45, or 50 or more nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (e.g., an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, e.g., phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified nucleotides which can be used to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-

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N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine.

Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been sub-cloned in an antisense orientation (i.e., RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

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The antisense nucleic acid molecules of the invention are typically administered to a subject or generated in situ such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a polypeptide corresponding to a selected marker of the invention to thereby inhibit expression of the marker, e.g., by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule which binds to DNA duplexes, through specific interactions in the major groove of the double helix. Examples of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site or infusion of the antisense nucleic acid into an breast-associated body fluid. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, e.g., by linking the antisense nucleic acid molecules to peptides or antibodies which bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of the antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

An antisense nucleic acid molecule of the invention can be an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual α -units, the strands run parallel to each other (Gaultier *et al.*, 1987, *Nucleic Acids Res.* 15:6625-6641). The

antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue et al., 1987, Nucleic Acids Res. 15:6131-6148) or a chimeric RNA-DNA analogue (Inoue et al., 1987, FEBS Lett. 215:327-330).

The invention also encompasses ribozymes. Ribozymes are catalytic RNA molecules with ribonuclease activity which are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (e.g., hammerhead ribozymes as described in Haselhoff and Gerlach, 1988, Nature 334:585-591) can be used to catalytically cleave mRNA transcripts to thereby inhibit translation of the protein encoded by the mRNA. A ribozyme having specificity for a nucleic acid molecule encoding a polypeptide corresponding to a marker of the invention can be designed based upon the nucleotide sequence of a cDNA corresponding to the marker. For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved (see Cech et al. U.S. Patent No. 4,987,071; and Cech et al. U.S. Patent No. 5,116,742). Alternatively, an mRNA encoding a polypeptide of the invention can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules (see, e.g., Bartel and Szostak, 1993, Science 261:1411-1418).

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The invention also encompasses nucleic acid molecules which form triple helical structures. For example, expression of a polypeptide of the invention can be inhibited by targeting nucleotide sequences complementary to the regulatory region of the gene encoding the polypeptide (e.g., the promoter and/or enhancer) to form triple helical structures that prevent transcription of the gene in target cells. See generally Helene (1991) Anticancer Drug Des. 6(6):569-84; Helene (1992) Ann. N.Y. Acad. Sci. 660:27-36; and Maher (1992) Bioassays 14(12):807-15.

In various embodiments, the nucleic acid molecules of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, e.g., the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup et al., 1996, Bioorganic & Medicinal Chemistry 4(1): 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, e.g., DNA mimics, in which the deoxyribose phosphate backbone is replaced by a

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pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup et al. (1996), supra; Perry-O'Keefe et al. (1996) Proc. Natl. Acad. Sci. USA 93:14670-675.

PNAs can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, e.g., inducing transcription or translation arrest or inhibiting replication. PNAs can also be used, e.g., in the analysis of single base pair mutations in a gene by, e.g., PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, e.g., S1 nucleases (Hyrup (1996), supra; or as probes or primers for DNA sequence and hybridization (Hyrup, 1996, supra; Perry-O'Keefe et al., 1996, Proc. Natl. Acad. Sci. USA 93:14670-675).

In another embodiment, PNAs can be modified, e.g., to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras can be generated which can combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, e.g., RNASE H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup, 1996, supra). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996), supra, and Finn et al. (1996) Nucleic Acids Res. 24(17):3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry and modified nucleoside analogs. Compounds such as 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite can be used as a link between the PNA and the 5' end of DNA (Mag et al., 1989, Nucleic Acids Res. 17:5973-88). PNA monomers are then coupled in a step-wise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn et al., 1996,

Nucleic Acids Res. 24(17):3357-63). Alternatively, chimeric molecules can be

synthesized with a 5' DNA segment and a 3' PNA segment (Peterser et al., 1975, Bioorganic Med. Chem. Lett. 5:1119-11124).

In other embodiments, the oligonucleotide can include other appended groups such as peptides (e.g., for targeting host cell receptors in vivo), or agents facilitating transport across the cell membrane (see, e.g., Letsinger et al., 1989, Proc. Natl. Acad. Sci. USA 86:6553-6556; Lemaitre et al., 1987, Proc. Natl. Acad. Sci. USA 84:648-652; PCT Publication No. WO 88/09810) or the blood-brain barrier (see, e.g., PCT Publication No. WO 89/10134). In addition, oligonucleotides can be modified with hybridization-triggered cleavage agents (see, e.g., Krol et al., 1988, Bio/Techniques 6:958-976) or intercalating agents (see, e.g., Zon, 1988, Pharm. Res. 5:539-549). To this end, the oligonucleotide can be conjugated to another molecule, e.g., a peptide, hybridization triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent, etc.

The invention also includes molecular beacon nucleic acids having at least one region which is complementary to a nucleic acid of the invention, such that the molecular beacon is useful for quantitating the presence of the nucleic acid of the invention in a sample. A "molecular beacon" nucleic acid is a nucleic acid comprising a pair of complementary regions and having a fluorophore and a fluorescent quencher associated therewith. The fluorophore and quencher are associated with different portions of the nucleic acid in such an orientation that when the complementary regions are annealed with one another, fluorescence of the fluorophore is quenched by the quencher. When the complementary regions of the nucleic acid are not annealed with one another, fluorescence of the fluorophore is quenched to a lesser degree. Molecular beacon nucleic acids are described, for example, in U.S. Patent 5,876,930.

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II. Isolated Proteins and Antibodies

One aspect of the invention pertains to isolated proteins which correspond to individual markers of the invention, and biologically active portions thereof, as well as polypeptide fragments suitable for use as immunogens to raise antibodies directed against a polypeptide corresponding to a marker of the invention. In one embodiment, the native polypeptide corresponding to a marker can be isolated from cells or tissue sources by an appropriate purification scheme using standard protein purification

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techniques. In another embodiment, polypeptides corresponding to a marker of the invention are produced by recombinant DNA techniques. Alternative to recombinant expression, a polypeptide corresponding to a marker of the invention can be synthesized chemically using standard peptide synthesis techniques.

An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the protein is derived, or substantially free of chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of protein in which the protein is separated from cellular components of the cells from which it is isolated or recombinantly produced. Thus, protein that is substantially free of cellular material includes preparations of protein having less than about 30%, 20%, 10%, or 5% (by dry weight) of heterologous protein (also referred to herein as a "contaminating protein"). When the protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, i.e., culture medium represents less than about 20%, 10%, or 5% of the volume of the protein preparation. When the protein is produced by chemical synthesis, it is preferably substantially free of chemical precursors or other chemicals, i.e., it is separated from chemical precursors or other chemicals which are involved in the synthesis of the protein. Accordingly such preparations of the protein have less than about 30%, 20%, 10%, 5% (by dry weight) of chemical precursors or compounds other than the polypeptide of interest.

Biologically active portions of a polypeptide corresponding to a marker of the invention include polypeptides comprising amino acid sequences sufficiently identical to or derived from the amino acid sequence of the protein corresponding to the marker, which include fewer amino acids than the full length protein, and exhibit at least one activity of the corresponding full-length protein. Typically, biologically active portions comprise a domain or motif with at least one activity of the corresponding protein. A biologically active portion of a protein of the invention can be a polypeptide which is, for example, 10, 25, 50, 100 or more amino acids in length. Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the functional activities of the native form of a polypeptide of the invention.

Preferred polypeptides have amino acid sequences encoded by the nucleic acid sequences described herein. Other useful proteins are substantially identical (e.g., at least about 40%, preferably 50%, 60%, 70%, 80%, 90%, 95%, or 99%) to one of these sequences and retain the functional activity of the protein of the corresponding naturally-occurring protein yet differ in amino acid sequence due to natural allelic variation or mutagenesis.

To determine the percent identity of two amino acid sequences or of two nucleic acids, the sequences are aligned for optimal comparison purposes (e.g., gaps can be introduced in the sequence of a first amino acid or nucleic acid sequence for optimal alignment with a second amino or nucleic acid sequence). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are identical at that position. The percent identity between the two sequences is a function of the number of identical positions shared by the sequences (i.e., % identity = # of identical positions/total # of positions (e.g., overlapping positions) $\times 100$). In one embodiment the two sequences are the same length.

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The determination of percent identity between two sequences can be accomplished using a mathematical algorithm. A preferred, non-limiting example of a mathematical algorithm utilized for the comparison of two sequences is the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA* 87:2264-2268, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA* 90:5873-5877. Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-410. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to a nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to a protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.* (1997) *Nucleic Acids Res.* 25:3389-3402. Alternatively, PSI-Blast can be used to perform an iterated search which detects distant relationships between molecules. When utilizing BLAST, Gapped BLAST, and PSI-Blast programs, the

default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. See http://www.ncbi.nlm.nih.gov. Another preferred, non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller, (1988) CABIOS 4:11-17. Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Yet another useful algorithm for identifying regions of local sequence similarity and alignment is the FASTA algorithm as described in Pearson and Lipman (1988) Proc. Natl. Acad. Sci. USA 85:2444-2448. When using the FASTA algorithm for comparing nucleotide or amino acid sequences, a PAM120 weight residue table can, for example, be used with a k-tuple value of 2.

The percent identity between two sequences can be determined using techniques similar to those described above, with or without allowing gaps. In calculating percent identity, only exact matches are counted.

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The invention also provides chimeric or fusion proteins corresponding to a marker of the invention. As used herein, a "chimeric protein" or "fusion protein" comprises all or part (preferably a biologically active part) of a polypeptide corresponding to a marker of the invention operably linked to a heterologous polypeptide (*i.e.*, a polypeptide other than the polypeptide corresponding to the marker). Within the fusion protein, the term "operably linked" is intended to indicate that the polypeptide of the invention and the heterologous polypeptide are fused in-frame to each other. The heterologous polypeptide can be fused to the amino-terminus or the carboxyl-terminus of the polypeptide of the invention.

One useful fusion protein is a GST fusion protein in which a polypeptide corresponding to a marker of the invention is fused to the carboxyl terminus of GST sequences. Such fusion proteins can facilitate the purification of a recombinant polypeptide of the invention.

In another embodiment, the fusion protein contains a heterologous signal sequence at its amino terminus. For example, the native signal sequence of a polypeptide corresponding to a marker of the invention can be removed and replaced with a signal sequence from another protein. For example, the gp67 secretory sequence

of the baculovirus envelope protein can be used as a heterologous signal sequence (Ausubel et al., ed., Current Protocols in Molecular Biology, John Wiley & Sons, NY, 1992). Other examples of eukaryotic heterologous signal sequences include the secretory sequences of melittin and human placental alkaline phosphatase (Stratagene; La Jolla, California). In yet another example, useful prokaryotic heterologous signal sequences include the phoA secretory signal (Sambrook et al., supra) and the protein A secretory signal (Pharmacia Biotech; Piscataway, New Jersey).

In yet another embodiment, the fusion protein is an immunoglobulin fusion protein in which all or part of a polypeptide corresponding to a marker of the invention is fused to sequences derived from a member of the immunoglobulin protein family. The immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ligand (soluble or membrane-bound) and a protein on the surface of a cell (receptor), to thereby suppress signal transduction *in vivo*. The immunoglobulin fusion protein can be used to affect the bioavailability of a cognate ligand of a polypeptide of the invention. Inhibition of ligand/receptor interaction can be useful therapeutically, both for treating proliferative and differentiative disorders and for modulating (e.g. promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be used as immunogens to produce antibodies directed against a polypeptide of the invention in a subject, to purify ligands and in screening assays to identify molecules which inhibit the interaction of receptors with ligands.

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Chimeric and fusion proteins of the invention can be produced by standard recombinant DNA techniques. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and re-amplified to generate a chimeric gene sequence (see, e.g., Ausubel et al., supra). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). A nucleic acid encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the polypeptide of the invention.

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A signal sequence can be used to facilitate secretion and isolation of the secreted protein or other proteins of interest. Signal sequences are typically characterized by a core of hydrophobic amino acids which are generally cleaved from the mature protein during secretion in one or more cleavage events. Such signal peptides contain processing sites that allow cleavage of the signal sequence from the mature proteins as they pass through the secretory pathway. Thus, the invention pertains to the described polypeptides having a signal sequence, as well as to polypeptides from which the signal sequence has been proteolytically cleaved (i.e., the cleavage products). In one embodiment, a nucleic acid sequence encoding a signal sequence can be operably linked in an expression vector to a protein of interest, such as a protein which is ordinarily not secreted or is otherwise difficult to isolate. The signal sequence directs secretion of the protein, such as from a eukaryotic host into which the expression vector is transformed, and the signal sequence is subsequently or concurrently cleaved. The protein can then be readily purified from the extracellular medium by art recognized methods. Alternatively, the signal sequence can be linked to the protein of interest using a sequence which facilitates purification, such as with a GST domain.

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The present invention also pertains to variants of the polypeptides corresponding to individual markers of the invention. Such variants have an altered amino acid sequence which can function as either agonists (mimetics) or as antagonists. Variants can be generated by mutagenesis, e.g., discrete point mutation or truncation. An agonist can retain substantially the same, or a subset, of the biological activities of the naturally occurring form of the protein. An antagonist of a protein can inhibit one or more of the activities of the naturally occurring form of the protein by, for example, competitively binding to a downstream or upstream member of a cellular signaling cascade which includes the protein of interest. Thus, specific biological effects can be elicited by treatment with a variant of limited function. Treatment of a subject with a variant having a subset of the biological activities of the naturally occurring form of the protein can have fewer side effects in a subject relative to treatment with the naturally occurring form of the protein.

Variants of a protein of the invention which function as either agonists (mimetics) or as antagonists can be identified by screening combinatorial libraries of mutants, e.g., truncation mutants, of the protein of the invention for agonist or antagonist activity. In

one embodiment, a variegated library of variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential protein sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (e.g., for phage display). There are a variety of methods which can be used to produce libraries of potential variants of the polypeptides of the invention from a degenerate oligonucleotide sequence. Methods for synthesizing degenerate oligonucleotides are known in the art (see, e.g., Narang, 1983, Tetrahedron 39:3; Itakura et al., 1984, Annu. Rev. Biochem. 53:323; Itakura et al., 1984, Science 198:1056; Ike et al., 1983 Nucleic Acid Res. 11:477).

In addition, libraries of fragments of the coding sequence of a polypeptide corresponding to a marker of the invention can be used to generate a variegated population of polypeptides for screening and subsequent selection of variants. For example, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of the coding sequence of interest with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA which can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes amino terminal and internal fragments of various sizes of the protein of interest.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. The most widely used techniques, which are amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a technique which enhances the frequency of functional

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mutants in the libraries, can be used in combination with the screening assays to identify variants of a protein of the invention (Arkin and Yourvan, 1992, *Proc. Natl. Acad. Sci. USA* 89:7811-7815; Delgrave *et al.*, 1993, *Protein Engineering* 6(3):327-331).

An isolated polypeptide corresponding to a marker of the invention, or a fragment thereof, can be used as an immunogen to generate antibodies using standard techniques for polyclonal and monoclonal antibody preparation. The full-length polypeptide or protein can be used or, alternatively, the invention provides antigenic peptide fragments for use as immunogens. The antigenic peptide of a protein of the invention comprises at least 8 (preferably 10, 15, 20, or 30 or more) amino acid residues of the amino acid sequence of one of the polypeptides of the invention, and encompasses an epitope of the protein such that an antibody raised against the peptide forms a specific immune complex with a marker of the invention to which the protein corresponds. Preferred epitopes encompassed by the antigenic peptide are regions that are located on the surface of the protein, *e.g.*, hydrophilic regions. Hydrophobicity sequence analysis, hydrophilicity sequence analysis, or similar analyses can be used to identify hydrophilic regions.

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An immunogen typically is used to prepare antibodies by immunizing a suitable (*i.e.* immunocompetent) subject such as a rabbit, goat, mouse, or other mammal or vertebrate. An appropriate immunogenic preparation can contain, for example, recombinantly-expressed or chemically-synthesized polypeptide. The preparation can further include an adjuvant, such as Freund's complete or incomplete adjuvant, or a similar immunostimulatory agent.

Accordingly, another aspect of the invention pertains to antibodies directed against a polypeptide of the invention. The terms "antibody" and "antibody substance" as used interchangeably herein refer to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, *i.e.*, molecules that contain an antigen binding site which specifically binds an antigen, such as a polypeptide of the invention, e.g., an epitope of a polypeptide of the invention. A molecule which specifically binds to a given polypeptide of the invention is a molecule which binds the polypeptide, but does not substantially bind other molecules in a sample, e.g., a biological sample, which naturally contains the polypeptide. Examples of immunologically active portions of immunoglobulin molecules include F(ab) and F(ab')₂ fragments which can be generated

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by treating the antibody with an enzyme such as pepsin. The invention provides polyclonal and monoclonal antibodies. The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one species of an antigen binding site capable of immunoreacting with a particular epitope.

Polyclonal antibodies can be prepared as described above by immunizing a suitable subject with a polypeptide of the invention as an immunogen. Preferred polyclonal antibody compositions are ones that have been selected for antibodies directed against a polypeptide or polypeptides of the invention. Particularly preferred polyclonal antibody preparations are ones that contain only antibodies directed against a polypeptide or polypeptides of the invention. Particularly preferred immunogen compositions are those that contain no other human proteins such as, for example, immunogen compositions made using a non-human host cell for recombinant expression of a polypeptide of the invention. In such a manner, the only human epitope or epitopes recognized by the resulting antibody compositions raised against this immunogen will be present as part of a polypeptide or polypeptides of the invention.

The antibody titer in the immunized subject can be monitored over time by standard techniques, such as with an enzyme linked immunosorbent assay (ELISA) using immobilized polypeptide. If desired, the antibody molecules can be harvested or isolated from the subject (e.g., from the blood or serum of the subject) and further purified by well-known techniques, such as protein A chromatography to obtain the IgG fraction. Alternatively, antibodies specific for a protein or polypeptide of the invention can be selected or (e.g., partially purified) or purified by, e.g., affinity chromatography. For example, a recombinantly expressed and purified (or partially purified) protein of the invention is produced as described herein, and covalently or non-covalently coupled to a solid support such as, for example, a chromatography column. The column can then be used to affinity purify antibodies specific for the proteins of the invention from a sample containing antibodies directed against a large number of different epitopes, thereby generating a substantially purified antibody composition, i.e., one that is substantially free of contaminating antibodies. By a substantially purified antibody composition is meant, in this context, that the antibody sample contains at most only 30% (by dry weight) of contaminating antibodies directed against epitopes other than

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those of the desired protein or polypeptide of the invention, and preferably at most 20%, yet more preferably at most 10%, and most preferably at most 5% (by dry weight) of the sample is contaminating antibodies. A purified antibody composition means that at least 99% of the antibodies in the composition are directed against the desired protein or polypeptide of the invention.

At an appropriate time after immunization, e.g., when the specific antibody titers are highest, antibody-producing cells can be obtained from the subject and used to prepare monoclonal antibodies by standard techniques, such as the hybridoma technique originally described by Kohler and Milstein (1975) Nature 256:495-497, the human B cell hybridoma technique (see Kozbor et al., 1983, Immunol. Today 4:72), the EBV-hybridoma technique (see Cole et al., pp. 77-96 In Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc., 1985) or trioma techniques. The technology for producing hybridomas is well known (see generally Current Protocols in Immunology, Coligan et al. ed., John Wiley & Sons, New York, 1994). Hybridoma cells producing a monoclonal antibody of the invention are detected by screening the hybridoma culture supernatants for antibodies that bind the polypeptide of interest, e.g., using a standard ELISA assay.

Alternative to preparing monoclonal antibody-secreting hybridomas, a monoclonal antibody directed against a polypeptide of the invention can be identified and isolated by screening a recombinant combinatorial immunoglobulin library (e.g., an antibody phage display library) with the polypeptide of interest. Kits for generating and screening phage display libraries are commercially available (e.g., the Pharmacia Recombinant Phage Antibody System, Catalog No. 27-9400-01; and the Stratagene SurfZAP Phage Display Kit, Catalog No. 240612). Additionally, examples of methods and reagents particularly amenable for use in generating and screening antibody display library can be found in, for example, U.S. Patent No. 5,223,409; PCT Publication No. WO 92/18619; PCT Publication No. WO 91/17271; PCT Publication No. WO 92/20791; PCT Publication No. WO 92/15679; PCT Publication No. WO 93/01288; PCT Publication No. WO 92/01047; PCT Publication No. WO 92/09690; PCT Publication No. WO 90/02809; Fuchs et al. (1991) Bio/Technology 9:1370-1372; Hay et al. (1992) Hum. Antibod. Hybridomas 3:81-85; Huse et al. (1989) Science 246:1275-1281; Griffiths et al. (1993) EMBO J. 12:725-734.

Additionally, recombinant antibodies, such as chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. A chimeric antibody is a molecule in which different portions are derived from different animal species, such as those having a variable region derived from a murine mAb and a human immunoglobulin constant region. (See, e.g., Cabilly et al., U.S. Patent No. 4,816,567; and Boss et al., U.S. Patent No. 4,816,397, which are incorporated herein by reference in their entirety.) Humanized antibodies are antibody molecules from non-human species having one or more complementarily determining regions (CDRs) from the non-human species and a framework region from a human immunoglobulin molecule. (See, e.g., Queen, U.S. Patent No. 5,585,089, which is incorporated herein by reference in its entirety.) Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art, for example using methods described in PCT Publication No. WO 87/02671; European Patent Application 184,187; European Patent Application 171,496; European Patent Application 173,494; PCT Publication No. WO 86/01533; U.S. Patent No. 4,816,567; European Patent Application 125,023; Better et al. (1988) Science 240:1041-1043; Liu et al. (1987) Proc. Natl. Acad. Sci. USA 84:3439-3443; Liu et al. (1987) J. Immunol. 139:3521-3526; Sun et al. (1987) Proc. Natl. Acad. Sci. USA 84:214-218; Nishimura et al. (1987) Cancer Res. 47:999-1005; Wood et al. (1985) Nature 314:446-20 449; and Shaw et al. (1988) J. Natl. Cancer Inst. 80:1553-1559); Morrison (1985) Science 229:1202-1207; Oi et al. (1986) Bio/Techniques 4:214; U.S. Patent 5,225,539; Jones et al. (1986) Nature 321:552-525; Verhoeyan et al. (1988) Science 239:1534; and

Antibodies of the invention may be used as therapeutic agents in treating cancers. In a preferred embodiment, completely human antibodies of the invention are used for therapeutic treatment of human cancer patients, particularly those having breast cancer. Such antibodies can be produced, for example, using transgenic mice which are incapable of expressing endogenous immunoglobulin heavy and light chains genes, but which can express human heavy and light chain genes. The transgenic mice are immunized in the normal fashion with a selected antigen, *e.g.*, all or a portion of a polypeptide corresponding to a marker of the invention. Monoclonal antibodies directed

Beidler et al. (1988) J. Immunol. 141:4053-4060.

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against the antigen can be obtained using conventional hybridoma technology. The human immunoglobulin transgenes harbored by the transgenic mice rearrange during B cell differentiation, and subsequently undergo class switching and somatic mutation. Thus, using such a technique, it is possible to produce therapeutically useful IgG, IgA and IgE antibodies. For an overview of this technology for producing human antibodies, see Lonberg and Huszar (1995) *Int. Rev. Immunol.* 13:65-93). For a detailed discussion of this technology for producing human antibodies and human monoclonal antibodies and protocols for producing such antibodies, see, *e.g.*, U.S. Patent 5,625,126; U.S. Patent 5,633,425; U.S. Patent 5,569,825; U.S. Patent 5,661,016; and U.S. Patent 5,545,806. In addition, companies such as Abgenix, Inc. (Freemont, CA), can be engaged to provide human antibodies directed against a selected antigen using technology similar to that described above.

Completely human antibodies which recognize a selected epitope can be generated using a technique referred to as "guided selection." In this approach a selected non-human monoclonal antibody, e.g., a murine antibody, is used to guide the selection of a completely human antibody recognizing the same epitope (Jespers et al., 1994, Bio/technology 12:899-903).

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An antibody directed against a polypeptide corresponding to a marker of the invention (*e.g.*, a monoclonal antibody) can be used to isolate the polypeptide by standard techniques, such as affinity chromatography or immunoprecipitation. Moreover, such an antibody can be used to detect the marker (*e.g.*, in a cellular lysate or cell supernatant) in order to evaluate the level and pattern of expression of the marker. The antibodies can also be used diagnostically to monitor protein levels in tissues or body fluids (*e.g.* in an ovary-associated body fluid) as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β-galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate,

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rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ¹²⁵I, ¹³¹I, ³⁵S or ³H.

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Further, an antibody (or fragment thereof) can be conjugated to a therapeutic moiety such as a cytotoxin, a therapeutic agent or a radioactive metal ion. A cytotoxin or cytotoxic agent includes any agent that is detrimental to cells. Examples include taxol, cytochalasin B, gramicidin D, ethidium bromide, emetine, mitomycin, etoposide, tenoposide, vincristine, vinblastine, colchicin, doxorubicin, daunorubicin, 10 dihydroxy anthracin dione, mitoxantrone, mithramycin, actinomycin D, 1-dehydrotestosterone, glucocorticoids, procaine, tetracaine, lidocaine, propranolol, and puromycin and analogs or homologs thereof. Therapeutic agents include, but are not limited to, antimetabolites (e.g., methotrexate, 6-mercaptopurine, 6-thioguanine, cytarabine, 5-fluorouracil decarbazine), alkylating agents (e.g., mechlorethamine, thioepa chlorambucil, melphalan, carmustine (BSNU) and lomustine (CCNU), cyclothosphamide, busulfan, dibromomannitol, streptozotocin, mitomycin C, and cis-dichlorodiamine platinum (II) (DDP) cisplatin), anthracyclines (e.g., daunorubicin (formerly daunomycin) and doxorubicin), antibiotics (e.g., dactinomycin (formerly actinomycin), bleomycin, mithramycin, and anthramycin (AMC)), and anti-mitotic agents (e.g., vincristine and vinblastine).

The conjugates of the invention can be used for modifying a given biological response, the drug moiety is not to be construed as limited to classical chemical therapeutic agents. For example, the drug moiety may be a protein or polypeptide possessing a desired biological activity. Such proteins may include, for example, a toxin such as abrin, ricin A, pseudomonas exotoxin, or diphtheria toxin; a protein such as tumor necrosis factor, .alpha.-interferon, .beta.-interferon, nerve growth factor, platelet derived growth factor, tissue plasminogen activator; or, biological response modifiers such as, for example, lymphokines, interleukin-1 ("IL-1"), interleukin-2 ("IL-2"), interleukin-6 ("IL-6"), granulocyte macrophase colony stimulating factor ("GM-CSF"), granulocyte colony stimulating factor ("G-CSF"), or other growth factors.

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Techniques for conjugating such therapeutic moiety to antibodies are well known, see, e.g., Arnon et al., "Monoclonal Antibodies For Immunotargeting Of Drugs In Cancer Therapy", in Monoclonal Antibodies And Cancer Therapy, Reisfeld et al. (eds.), pp. 243-56 (Alan R. Liss, Inc. 1985); Hellstrom et al., "Antibodies For Drug Delivery", in Controlled Drug Delivery (2nd Ed.), Robinson et al. (eds.), pp. 623-53 (Marcel Dekker, Inc. 1987); Thorpe, "Antibody Carriers Of Cytotoxic Agents In Cancer Therapy: A Review", in Monoclonal Antibodies '84: Biological And Clinical Applications, Pinchera et al. (eds.), pp. 475-506 (1985); "Analysis, Results, And Future Prospective Of The Therapeutic Use Of Radiolabeled Antibody In Cancer Therapy", in Monoclonal Antibodies For Cancer Detection And Therapy, Baldwin et al. (eds.), pp. 303-16 (Academic Press 1985), and Thorpe et al., "The Preparation And Cytotoxic Properties Of Antibody-Toxin Conjugates", Immunol. Rev., 62:119-58 (1982).

antibody heteroconjugate as described by Segal in U.S. Patent No. 4,676,980. Accordingly, in one aspect, the invention provides substantially purified antibodies or fragments thereof, and non-human antibodies or fragments thereof, which antibodies or fragments specifically bind to a polypeptide comprising an amino acid sequence selected from the group consisting of the amino acid sequences of the present invention, an amino acid sequence encoded by the cDNA of the present invention, a fragment of at least 15 amino acid residues of an amino acid sequence of the present invention, an amino acid sequence which is at least 95% identical to the amino acid sequence of the present invention (wherein the percent identity is determined using the ALIGN program of the GCG software package with a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4) and an amino acid sequence which is encoded by a nucleic acid molecule which hybridizes to a nucleic acid molecule consisting of the nucleic acid molecules of the present invention, or a complement thereof, under conditions of hybridization of 6X SSC at 45°C and washing in 0.2 X SSC, 0.1% SDS at 65°C. In various embodiments, the substantially purified antibodies of the invention, or fragments thereof, can be human, non-human, chimeric and/or humanized antibodies.

Alternatively, an antibody can be conjugated to a second antibody to form an

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In another aspect, the invention provides non-human antibodies or fragments thereof, which antibodies or fragments specifically bind to a polypeptide comprising an amino acid sequence selected from the group consisting of: the amino acid sequence of

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the present invention, an amino acid sequence encoded by the cDNA of the present invention, a fragment of at least 15 amino acid residues of the amino acid sequence of the present invention, an amino acid sequence which is at least 95% identical to the amino acid sequence of the present invention (wherein the percent identity is determined using the ALIGN program of the GCG software package with a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4) and an amino acid sequence which is encoded by a nucleic acid molecule which hybridizes to a nucleic acid molecule consisting of the nucleic acid molecules of the present invention, or a complement thereof, under conditions of hybridization of 6X SSC at 45°C and washing in 0.2 X SSC, 0.1% SDS at 65°C. Such non-human antibodies can be goat, mouse, sheep, horse, chicken, rabbit, or rat antibodies. Alternatively, the non-human antibodies of the invention can be chimeric and/or humanized antibodies. In addition, the non-human antibodies of the invention can be polyclonal antibodies or monoclonal antibodies.

In still a further aspect, the invention provides monoclonal antibodies or fragments thereof, which antibodies or fragments specifically bind to a polypeptide comprising an amino acid sequence selected from the group consisting of the amino acid sequences of the present invention, an amino acid sequence encoded by the cDNA of the present invention, a fragment of at least 15 amino acid residues of an amino acid sequence of the present invention, an amino acid sequence which is at least 95% identical to an amino acid sequence of the present invention (wherein the percent identity is determined using the ALIGN program of the GCG software package with a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4) and an amino acid sequence which is encoded by a nucleic acid molecule which hybridizes to a nucleic acid molecule consisting of the nucleic acid molecules of the present invention, or a complement thereof, under conditions of hybridization of 6X SSC at 45°C and washing in 0.2 X SSC, 0.1% SDS at 65°C. The monoclonal antibodies can be human, humanized, chimeric and/or non-human antibodies.

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The substantially purified antibodies or fragments thereof may specifically bind to a signal peptide, a secreted sequence, an extracellular domain, a transmembrane or a cytoplasmic domain or cytoplasmic membrane of a polypeptide of the invention. In a particularly preferred embodiment, the substantially purified antibodies or fragments

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thereof, the non-human antibodies or fragments thereof, and/or the monoclonal antibodies or fragments thereof, of the invention specifically bind to a secreted sequence or an extracellular domain of the amino acid sequences of the present invention.

Any of the antibodies of the invention can be conjugated to a therapeutic moiety or to a detectable substance. Non-limiting examples of detectable substances that can be conjugated to the antibodies of the invention are an enzyme, a prosthetic group, a fluorescent material, a luminescent material, a bioluminescent material, and a radioactive material.

The invention also provides a kit containing an antibody of the invention conjugated to a detectable substance, and instructions for use. Still another aspect of the invention is a pharmaceutical composition comprising an antibody of the invention and a pharmaceutically acceptable carrier. In preferred embodiments, the pharmaceutical composition contains an antibody of the invention, a therapeutic moiety, and a pharmaceutically acceptable carrier.

Still another aspect of the invention is a method of making an antibody that specifically recognizes a polypeptide of the present invention, the method comprising immunizing a mammal with a polypeptide. The polypeptide used as an immungen comprises an amino acid sequence selected from the group consisting of the amino acid sequence of the present invention, an amino acid sequence encoded by the cDNA of the nucleic acid molecules of the present invention, a fragment of at least 15 amino acid residues of the amino acid sequence of the present invention, an amino acid sequence which is at least 95% identical to the amino acid sequence of the present invention (wherein the percent identity is determined using the ALIGN program of the GCG software package with a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4) and an amino acid sequence which is encoded by a nucleic acid molecule which hybridizes to a nucleic acid molecule consisting of the nucleic acid molecules of the present invention, or a complement thereof, under conditions of hybridization of 6X SSC at 45°C and washing in 0.2 X SSC, 0.1% SDS at 65°C.

After immunization, a sample is collected from the mammal that contains an antibody that specifically recognizes the polypeptide. Preferably, the polypeptide is recombinantly produced using a non-human host cell. Optionally, the antibodies can be further purified from the sample using techniques well known to those of skill in the art.

The method can further comprise producing a monoclonal antibody-producing cell from the cells of the mammal. Optionally, antibodies are collected from the antibody-producing cell.

5 III. Recombinant Expression Vectors and Host Cells

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding a polypeptide corresponding to a marker of the invention (or a portion of such a polypeptide). As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (e.g., bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (e.g., non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors, namely expression vectors, are capable of directing the expression of genes to which they are operably linked. In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids (vectors). However, the invention is intended to include such other forms of expression vectors, such as viral vectors (e.g., replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell. This means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operably linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (e.g., in an in vitro transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory

sequence" is intended to include promoters, enhancers and other expression control elements (e.g., polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel, *Methods in Enzymology: Gene Expression Technology* vol.185, Academic Press, San Diego, CA (1991). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells (e.g., tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, and the like. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein.

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The recombinant expression vectors of the invention can be designed for expression of a polypeptide corresponding to a marker of the invention in prokaryotic (e.g., E. coli) or eukaryotic cells (e.g., insect cells {using baculovirus expression vectors}, yeast cells or mammalian cells). Suitable host cells are discussed further in Goeddel, supra. Alternatively, the recombinant expression vector can be transcribed and translated in vitro, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out in *E. coli* with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein. Such fusion vectors typically serve three purposes: 1) to increase expression of recombinant protein; 2) to increase the solubility of the recombinant protein; and 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith and Johnson, 1988, *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, MA) and

pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann *et al.*, 1988, *Gene* 69:301-315) and pET 11d (Studier *et al.*, p. 60-89, In *Gene Expression Technology: Methods in Enzymology* vol.185, Academic Press, San Diego, CA, 1991). Target gene expression from the pTrc vector relies on host RNA polymerase transcription from a hybrid trp-lac fusion promoter. Target gene expression from the pET 11d vector relies on transcription from a T7 gn10-lac fusion promoter mediated by a co-expressed viral RNA polymerase (T7 gn1). This viral polymerase is supplied by host strains BL21(DE3) or HMS174(DE3) from a resident prophage harboring a T7 gn1 gene under the transcriptional control of the lacUV 5 promoter.

One strategy to maximize recombinant protein expression in *E. coli* is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, p. 119-128, In *Gene Expression Technology: Methods in Enzymology* vol. 185, Academic Press, San Diego, CA, 1990. Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in *E. coli* (Wada *et al.*, 1992, *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

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In another embodiment, the expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari *et al.*, 1987, *EMBO J.* 6:229-234), pMFa (Kurjan and Herskowitz, 1982, *Cell* 30:933-943), pJRY88 (Schultz *et al.*, 1987, *Gene* 54:113-123), pYES2 (Invitrogen Corporation, San Diego, CA), and pPicZ (Invitrogen Corp, San Diego, CA).

Alternatively, the expression vector is a baculovirus expression vector. Baculovirus vectors available for expression of proteins in cultured insect cells (e.g., Sf 9 cells) include the pAc series (Smith et al., 1983, Mol. Cell Biol. 3:2156-2165) and the pVL series (Lucklow and Summers, 1989, Virology 170:31-39).

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, 1987, *Nature* 329:840) and pMT2PC

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(Kaufman et al., 1987, EMBO J. 6:187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells see chapters 16 and 17 of Sambrook et al., supra.

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (e.g., tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissuespecific promoters include the albumin promoter (liver-specific; Pinkert et al., 1987, Genes Dev. 1:268-277), lymphoid-specific promoters (Calame and Eaton, 1988, Adv. Immunol. 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore, 1989, EMBO J. 8:729-733) and immunoglobulins (Banerji et al., 1983, Cell 33:729-740; Queen and Baltimore, 1983, Cell 33:741-748), neuron-specific promoters (e.g., the neurofilament promoter; Byrne and Ruddle, 1989, Proc. Natl. Acad. Sci. USA 86:5473-5477), pancreas-specific promoters (Edlund et al., 1985, Science 230:912-916), and mammary gland-specific promoters (e.g., milk whey promoter; U.S. Patent No. 4,873,316 and European Application Publication No. 264,166). Developmentallyregulated promoters are also encompassed, for example the murine hox promoters (Kessel and Gruss, 1990, Science 249:374-379) and the α-fetoprotein promoter (Camper and Tilghman, 1989, Genes Dev. 3:537-546).

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The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operably linked to a regulatory sequence in a manner which allows for expression (by transcription of the DNA molecule) of an RNA molecule which is antisense to the mRNA encoding a polypeptide of the invention. Regulatory sequences operably linked to a nucleic acid cloned in the antisense orientation can be chosen which direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen which direct constitutive, tissue-specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid, or attenuated virus in which antisense nucleic

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acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub et al., 1986, Trends in Genetics, Vol. 1(1).

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic (e.g., E. coli) or eukaryotic cell (e.g., insect cells, yeast or mammalian cells).

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, et al. (supra), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (e.g., for resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418, hygromycin and methotrexate. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (e.g., cells that have incorporated the selectable marker gene will survive, while the other cells die).

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce a polypeptide corresponding to a marker of the invention. Accordingly, the invention further provides methods for producing a polypeptide corresponding to a marker of the invention using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding a polypeptide of the invention has been introduced) in a suitable medium such that the marker is produced. In another embodiment, the method further comprises isolating the marker polypeptide from the medium or the host cell.

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The host cells of the invention can also be used to produce nonhuman transgenic animals. For example, in one embodiment, a host cell of the invention is a fertilized oocyte or an embryonic stem cell into which a sequences encoding a polypeptide corresponding to a marker of the invention have been introduced. Such host cells can then be used to create non-human transgenic animals in which exogenous sequences encoding a marker protein of the invention have been introduced into their genome or homologous recombinant animals in which endogenous gene(s) encoding a polypeptide corresponding to a marker of the invention sequences have been altered. Such animals are useful for studying the function and/or activity of the polypeptide corresponding to the marker and for identifying and/or evaluating modulators of polypeptide activity. As used herein, a "transgenic animal" is a non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal includes a transgene. Other examples of transgenic animals include non-human primates, sheep, dogs, cows, goats, chickens, amphibians, etc. A transgene is exogenous DNA which is integrated into the genome of a cell from which a transgenic animal develops and which remains in the genome of the mature animal, thereby directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal. As used herein, an "homologous recombinant animal" is a nonhuman animal, preferably a mammal, more preferably a mouse, in which an endogenous gene has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule introduced into a cell of the animal, e.g., an embryonic cell of the animal, prior to development of the animal.

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A transgenic animal of the invention can be created by introducing a nucleic acid encoding a polypeptide corresponding to a marker of the invention into the male pronuclei of a fertilized oocyte, e.g., by microinjection, retroviral infection, and allowing the oocyte to develop in a pseudopregnant female foster animal. Intronic sequences and polyadenylation signals can also be included in the transgene to increase the efficiency of expression of the transgene. A tissue-specific regulatory sequence(s) can be operably linked to the transgene to direct expression of the polypeptide of the invention to particular cells. Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 and 4,870,009, U.S. Patent No. 4,873,191 and in Hogan, Manipulating the Mouse Embryo, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986. Similar methods are used for production of other transgenic animals. A transgenic founder animal can be identified based upon the presence of the transgene in its genome and/or expression of mRNA encoding the transgene in tissues or cells of the animals. A transgenic founder animal can then be used to breed additional animals carrying the transgene. Moreover, transgenic animals carrying the transgene can further be bred to other transgenic animals carrying other transgenes.

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To create an homologous recombinant animal, a vector is prepared which contains at least a portion of a gene encoding a polypeptide corresponding to a marker of the invention into which a deletion, addition or substitution has been introduced to thereby alter, e.g., functionally disrupt, the gene. In a preferred embodiment, the vector is designed such that, upon homologous recombination, the endogenous gene is functionally disrupted (i.e., no longer encodes a functional protein; also referred to as a "knock out" vector). Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous gene is mutated or otherwise altered but still encodes functional protein (e.g., the upstream regulatory region can be altered to thereby alter the expression of the endogenous protein). In the homologous recombination vector, the altered portion of the gene is flanked at its 5' and 3' ends by additional nucleic acid of the gene to allow for homologous recombination to occur between the exogenous gene carried by the vector and an endogenous gene in an embryonic stem cell. The additional flanking nucleic acid sequences are of sufficient

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length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector (see, e.g., Thomas and Capecchi, 1987, Cell 51:503 for a description of homologous recombination vectors). The vector is introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced gene has homologously recombined with the endogenous gene are selected (see, e.g., Li et al., 1992, Cell 69:915). The selected cells are then injected into a blastocyst of an animal (e.g., a mouse) to form aggregation chimeras (see, e.g., Bradley, Teratocarcinomas and Embryonic Stem Cells: A Practical Approach, Robertson, Ed., IRL, Oxford, 1987, pp. 113-152). A chimeric embryo can then be implanted into a suitable pseudopregnant 10 female foster animal and the embryo brought to term. Progeny harboring the homologously recombined DNA in their germ cells can be used to breed animals in which all cells of the animal contain the homologously recombined DNA by germline transmission of the transgene. Methods for constructing homologous recombination vectors and homologous recombinant animals are described further in Bradley (1991) 15

Current Opinion in Bio/Technology 2:823-829 and in PCT Publication NOS. WO

90/11354, WO 91/01140, WO 92/0968, and WO 93/04169.

In another embodiment, transgenic non-human animals can be produced which contain selected systems which allow for regulated expression of the transgene. One example of such a system is the *cre/loxP* recombinase system of bacteriophage P1. For a description of the *cre/loxP* recombinase system, see, *e.g.*, Lakso *et al.* (1992) *Proc. Natl. Acad. Sci. USA* 89:6232-6236. Another example of a recombinase system is the FLP recombinase system of *Saccharomyces cerevisiae* (O'Gorman *et al.*, 1991, *Science* 251:1351-1355). If a *cre/loxP* recombinase system is used to regulate expression of the transgene, animals containing transgenes encoding both the *Cre* recombinase and a selected protein are required. Such animals can be provided through the construction of "double" transgenic animals, *e.g.*, by mating two transgenic animals, one containing a transgene encoding a selected protein and the other containing a transgene encoding a recombinase.

Clones of the non-human transgenic animals described herein can also be produced according to the methods described in Wilmut *et al.* (1997) *Nature* 385:810-813 and PCT Publication NOS. WO 97/07668 and WO 97/07669.

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IV. Pharmaceutical Compositions

The nucleic acid molecules, polypeptides, and antibodies (also referred to herein as "active compounds") corresponding to a marker of the invention can be incorporated into pharmaceutical compositions suitable for administration. Such compositions typically comprise the nucleic acid molecule, protein, or antibody and a pharmaceutically acceptable carrier. As used herein the language "pharmaceutically acceptable carrier" is intended to include any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration. The use of such media and agents for pharmaceutically active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, use thereof in the compositions is contemplated. Supplementary active compounds can also be incorporated into the compositions.

The invention includes methods for preparing pharmaceutical compositions for modulating the expression or activity of a polypeptide or nucleic acid corresponding to a marker of the invention. Such methods comprise formulating a pharmaceutically acceptable carrier with an agent which modulates expression or activity of a polypeptide or nucleic acid corresponding to a marker of the invention. Such compositions can further include additional active agents. Thus, the invention further includes methods for preparing a pharmaceutical composition by formulating a pharmaceutically acceptable carrier with an agent which modulates expression or activity of a polypeptide or nucleic acid corresponding to a marker of the invention and one or more additional active compounds.

The invention also provides methods (also referred to herein as "screening assays") for identifying modulators, *i.e.*, candidate or test compounds or agents (*e.g.*, peptides, peptidomimetics, peptoids, small molecules or other drugs) which (a) bind to the marker, or (b) have a modulatory (*e.g.*, stimulatory or inhibitory) effect on the activity of the marker or, more specifically, (c) have a modulatory effect on the interactions of the marker with one or more of its natural substrates (*e.g.*, peptide, protein, hormone, co-factor, or nucleic acid), or (d) have a modulatory effect on the expression of the marker. Such assays typically comprise a reaction between the marker

and one or more assay components. The other components may be either the test compound itself, or a combination of test compound and a natural binding partner of the marker.

The test compounds of the present invention may be obtained from any available source, including systematic libraries of natural and/or synthetic compounds. Test compounds may also be obtained by any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; peptoid libraries (libraries of molecules having the functionalities of peptides, but with a novel, non-peptide backbone which are resistant to enzymatic degradation but which nevertheless remain bioactive; see, e.g., Zuckermann et al., 1994, J. Med. Chem. 37:2678-85); spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the 'one-bead one-compound' library method; and synthetic library methods using affinity chromatography selection. The biological library and peptoid library approaches are limited to peptide libraries, while the other four approaches are applicable to peptide, non-peptide oligomer or small molecule libraries of compounds (Lam, 1997, Anticancer Drug Des. 12:145).

Examples of methods for the synthesis of molecular libraries can be found in the art, for example in: DeWitt et al. (1993) Proc. Natl. Acad. Sci. U.S.A. 90:6909; Erb et al. (1994) Proc. Natl. Acad. Sci. USA 91:11422; Zuckermann et al. (1994). J. Med. Chem. 37:2678; Cho et al. (1993) Science 261:1303; Carrell et al. (1994) Angew. Chem. Int. Ed. Engl. 33:2059; Carell et al. (1994) Angew. Chem. Int. Ed. Engl. 33:2061; and in Gallop et al. (1994) J. Med. Chem. 37:1233.

Libraries of compounds may be presented in solution (e.g., Houghten, 1992, Biotechniques 13:412-421), or on beads (Lam, 1991, Nature 354:82-84), chips (Fodor, 1993, Nature 364:555-556), bacteria and/or spores, (Ladner, USP 5,223,409), plasmids (Cull et al, 1992, Proc Natl Acad Sci USA 89:1865-1869) or on phage (Scott and Smith, 1990, Science 249:386-390; Devlin, 1990, Science 249:404-406; Cwirla et al, 1990, Proc. Natl. Acad. Sci. 87:6378-6382; Felici, 1991, J. Mol. Biol. 222:301-310; Ladner, supra.).

In one embodiment, the invention provides assays for screening candidate or test compounds which are substrates of a marker or biologically active portion thereof. In another embodiment, the invention provides assays for screening candidate or test

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compounds which bind to a marker or biologically active portion thereof. Determining the ability of the test compound to directly bind to a marker can be accomplished, for example, by coupling the compound with a radioisotope or enzymatic label such that binding of the compound to the marker can be determined by detecting the labeled marker compound in a complex. For example, compounds (e.g., marker substrates) can be labeled with ¹²⁵I, ³⁵S, ¹⁴C, or ³H, either directly or indirectly, and the radioisotope detected by direct counting of radioemission or by scintillation counting. Alternatively, assay components can be enzymatically labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product.

In another embodiment, the invention provides assays for screening candidate or test compounds which modulate the activity of a marker or a biologically active portion thereof. In all likelihood, the marker can, *in vivo*, interact with one or more molecules, such as but not limited to, peptides, proteins, hormones, cofactors and nucleic acids. For the purposes of this discussion, such cellular and extracellular molecules are referred to herein as "binding partners" or marker "substrate".

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One necessary embodiment of the invention in order to facilitate such screening is the use of the marker to identify its natural *in vivo* binding partners. There are many ways to accomplish this which are known to one skilled in the art. One example is the use of the marker protein as "bait protein" in a two-hybrid assay or three-hybrid assay (see, e.g., U.S. Patent No. 5,283,317; Zervos et al, 1993, Cell 72:223-232; Madura et al, 1993, J. Biol. Chem. 268:12046-12054; Bartel et al, 1993, Biotechniques 14:920-924; Iwabuchi et al, 1993 Oncogene 8:1693-1696; Brent WO94/10300) in order to identify other proteins which bind to or interact with the marker (binding partners) and, therefore, are possibly involved in the natural function of the marker. Such marker binding partners are also likely to be involved in the propagation of signals by the marker or downstream elements of a marker-mediated signaling pathway. Alternatively, such marker binding partners may also be found to be inhibitors of the marker.

The two-hybrid system is based on the modular nature of most transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA constructs. In one construct, the gene that encodes a marker protein fused to a gene encoding the DNA binding domain of a known

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transcription factor (e.g., GAL-4). In the other construct, a DNA sequence, from a library of DNA sequences, that encodes an unidentified protein ("prey" or "sample") is fused to a gene that codes for the activation domain of the known transcription factor. If the "bait" and the "prey" proteins are able to interact, in vivo, forming a marker-dependent complex, the DNA-binding and activation domains of the transcription factor are brought into close proximity. This proximity allows transcription of a reporter gene (e.g., LacZ) which is operably linked to a transcriptional regulatory site responsive to the transcription factor. Expression of the reporter gene can be readily detected and cell colonies containing the functional transcription factor can be isolated and used to obtain the cloned gene which encodes the protein which interacts with the marker protein.

In a further embodiment, assays may be devised through the use of the invention for the purpose of identifying compounds which modulate (e.g., affect either positively or negatively) interactions between a marker and its substrates and/or binding partners. Such compounds can include, but are not limited to, molecules such as antibodies, peptides, hormones, oligonucleotides, nucleic acids, and analogs thereof. Such compounds may also be obtained from any available source, including systematic libraries of natural and/or synthetic compounds. The preferred assay components for use in this embodiment is an breast cancer marker identified herein, the known binding partner and/or substrate of same, and the test compound. Test compounds can be supplied from any source.

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The basic principle of the assay systems used to identify compounds that interfere with the interaction between the marker and its binding partner involves preparing a reaction mixture containing the marker and its binding partner under conditions and for a time sufficient to allow the two products to interact and bind, thus forming a complex. In order to test an agent for inhibitory activity, the reaction mixture is prepared in the presence and absence of the test compound. The test compound can be initially included in the reaction mixture, or can be added at a time subsequent to the addition of the marker and its binding partner. Control reaction mixtures are incubated without the test compound or with a placebo. The formation of any complexes between the marker and its binding partner is then detected. The formation of a complex in the control reaction, but less or no such formation in the reaction mixture containing the test compound, indicates that the compound interferes with the interaction of the marker and its binding

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partner. Conversely, the formation of more complex in the presence of compound than in the control reaction indicates that the compound may enhance interaction of the marker and its binding partner.

The assay for compounds that interfere with the interaction of the marker with its binding partner may be conducted in a heterogeneous or homogeneous format.

Heterogeneous assays involve anchoring either the marker or its binding partner onto a solid phase and detecting complexes anchored to the solid phase at the end of the reaction. In homogeneous assays, the entire reaction is carried out in a liquid phase. In either approach, the order of addition of reactants can be varied to obtain different information about the compounds being tested. For example, test compounds that interfere with the interaction between the markers and the binding partners (e.g., by competition) can be identified by conducting the reaction in the presence of the test substance, i.e., by adding the test substance to the reaction mixture prior to or simultaneously with the marker and its interactive binding partner. Alternatively, test compounds that disrupt preformed complexes, e.g., compounds with higher binding constants that displace one of the components from the complex, can be tested by adding the test compound to the reaction mixture after complexes have been formed. The various formats are briefly described below.

In a heterogeneous assay system, either the marker or its binding partner is anchored onto a solid surface or matrix, while the other corresponding non-anchored component may be labeled, either directly or indirectly. In practice, microtitre plates are often utilized for this approach. The anchored species can be immobilized by a number of methods, either non-covalent or covalent, that are typically well known to one who practices the art. Non-covalent attachment can often be accomplished simply by coating the solid surface with a solution of the marker or its binding partner and drying. Alternatively, an immobilized antibody specific for the assay component to be anchored can be used for this purpose. Such surfaces can often be prepared in advance and stored.

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In related embodiments, a fusion protein can be provided which adds a domain that allows one or both of the assay components to be anchored to a matrix. For example, glutathione-S-transferase/marker fusion proteins or glutathione-S-transferase/binding partner can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtiter plates, which are then

combined with the test compound or the test compound and either the non-adsorbed marker or its binding partner, and the mixture incubated under conditions conducive to complex formation (e.g., physiological conditions). Following incubation, the beads or microtiter plate wells are washed to remove any unbound assay components, the immobilized complex assessed either directly or indirectly, for example, as described above. Alternatively, the complexes can be dissociated from the matrix, and the level of marker binding or activity determined using standard techniques.

Other techniques for immobilizing proteins on matrices can also be used in the screening assays of the invention. For example, either a marker or a marker binding partner can be immobilized utilizing conjugation of biotin and streptavidin. Biotinylated marker protein or target molecules can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques known in the art (e.g., biotinylation kit, Pierce Chemicals, Rockford, IL), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). In certain embodiments, the protein-immobilized surfaces can be prepared in advance and stored.

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In order to conduct the assay, the corresponding partner of the immobilized assay component is exposed to the coated surface with or without the test compound. After the reaction is complete, unreacted assay components are removed (e.g., by washing) and any complexes formed will remain immobilized on the solid surface. The detection of complexes anchored on the solid surface can be accomplished in a number of ways. Where the non-immobilized component is pre-labeled, the detection of label immobilized on the surface indicates that complexes were formed. Where the non-immobilized component is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; e.g., using a labeled antibody specific for the initially non-immobilized species (the antibody, in turn, can be directly labeled or indirectly labeled with, e.g., a labeled anti-Ig antibody). Depending upon the order of addition of reaction components, test compounds which modulate (inhibit or enhance) complex formation or which disrupt preformed complexes can be detected.

In an alternate embodiment of the invention, a homogeneous assay may be used. This is typically a reaction, analogous to those mentioned above, which is conducted in a liquid phase in the presence or absence of the test compound. The formed complexes are then separated from unreacted components, and the amount of complex formed is

determined. As mentioned for heterogeneous assay systems, the order of addition of reactants to the liquid phase can yield information about which test compounds modulate (inhibit or enhance) complex formation and which disrupt preformed complexes.

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In such a homogeneous assay, the reaction products may be separated from unreacted assay components by any of a number of standard techniques, including but not limited to: differential centrifugation, chromatography, electrophoresis and immunoprecipitation. In differential centrifugation, complexes of molecules may be separated from uncomplexed molecules through a series of centrifugal steps, due to the different sedimentation equilibria of complexes based on their different sizes and densities (see, for example, Rivas, G., and Minton, A.P., Trends Biochem Sci 1993 Aug;18(8):284-7). Standard chromatographic techniques may also be utilized to separate complexed molecules from uncomplexed ones. For example, gel filtration chromatography separates molecules based on size, and through the utilization of an 15 appropriate gel filtration resin in a column format, for example, the relatively larger complex may be separated from the relatively smaller uncomplexed components. Similarly, the relatively different charge properties of the complex as compared to the uncomplexed molecules may be exploited to differentially separate the complex from the remaining individual reactants, for example through the use of ion-exchange chromatography resins. Such resins and chromatographic techniques are well known to one skilled in the art (see, e.g., Heegaard, 1998, J Mol. Recognit. 11:141-148; Hage and Tweed, 1997, J. Chromatogr. B. Biomed. Sci. Appl., 699:499-525). Gel electrophoresis may also be employed to separate complexed molecules from unbound species (see, e.g., Ausubel et al (eds.), In: Current Protocols in Molecular Biology, J. Wiley & Sons, New York. 1999). In this technique, protein or nucleic acid complexes are separated based on size or charge, for example. In order to maintain the binding interaction during the electrophoretic process, non-denaturing gels in the absence of reducing agent are typically preferred, but conditions appropriate to the particular interactants will be well known to one skilled in the art. Immunoprecipitation is another common technique utilized for the isolation of a protein-protein complex from solution (see, e.g., Ausubel et al (eds.), In: Current Protocols in Molecular Biology, J. Wiley & Sons, New York. 1999). In this technique, all proteins binding to an antibody specific to one of the

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binding molecules are precipitated from solution by conjugating the antibody to a polymer bead that may be readily collected by centrifugation. The bound assay components are released from the beads (through a specific proteolysis event or other technique well known in the art which will not disturb the protein-protein interaction in the complex), and a second immunoprecipitation step is performed, this time utilizing antibodies specific for the correspondingly different interacting assay component. In this manner, only formed complexes should remain attached to the beads. Variations in complex formation in both the presence and the absence of a test compound can be compared, thus offering information about the ability of the compound to modulate interactions between the marker and its binding partner.

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Also within the scope of the present invention are methods for direct detection of interactions between the marker and its natural binding partner and/or a test compound in a homogeneous or heterogeneous assay system without further sample manipulation. For example, the technique of fluorescence energy transfer may be utilized (see, e.g., Lakowicz et al, U.S. Patent No. 5,631,169; Stavrianopoulos et al, U.S. Patent No. 4,868,103). Generally, this technique involves the addition of a fluorophore label on a first 'donor' molecule (e.g., marker or test compound) such that its emitted fluorescent energy will be absorbed by a fluorescent label on a second, 'acceptor' molecule (e.g., marker or test compound), which in turn is able to fluoresce due to the absorbed energy. Alternately, the 'donor' protein molecule may simply utilize the natural fluorescent energy of tryptophan residues. Labels are chosen that emit different wavelengths of light, such that the 'acceptor' molecule label may be differentiated from that of the 'donor'. Since the efficiency of energy transfer between the labels is related to the distance separating the molecules, spatial relationships between the molecules can be 25 assessed. In a situation in which binding occurs between the molecules, the fluorescent emission of the 'acceptor' molecule label in the assay should be maximal. An FET binding event can be conveniently measured through standard fluorometric detection means well known in the art (e.g., using a fluorimeter). A test substance which either enhances or hinders participation of one of the species in the preformed complex will 30 result in the generation of a signal variant to that of background. In this way, test substances that modulate interactions between a marker and its binding partner can be identified in controlled assays.

In another embodiment, modulators of marker expression are identified in a method wherein a cell is contacted with a candidate compound and the expression of mRNA or protein, corresponding to a marker in the cell, is determined. The level of expression of mRNA or protein in the presence of the candidate compound is compared to the level of expression of mRNA or protein in the absence of the candidate compound. The candidate compound can then be identified as a modulator of marker expression based on this comparison. For example, when expression of marker mRNA or protein is greater (statistically significantly greater) in the presence of the candidate compound than in its absence, the candidate compound is identified as a stimulator of marker mRNA or protein expression. Conversely, when expression of marker mRNA or protein is less (statistically significantly less) in the presence of the candidate compound than in its absence, the candidate compound is identified as an inhibitor of marker mRNA or protein expression. The level of marker mRNA or protein expression in the cells can be determined by methods described herein for detecting marker mRNA or protein.

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In another aspect, the invention pertains to a combination of two or more of the assays described herein. For example, a modulating agent can be identified using a cell-based or a cell free assay, and the ability of the agent to modulate the activity of a marker protein can be further confirmed *in vivo*, *e.g.*, in a whole animal model for cellular transformation and/or tumorigenesis.

This invention further pertains to novel agents identified by the above-described screening assays. Accordingly, it is within the scope of this invention to further use an agent identified as described herein in an appropriate animal model. For example, an agent identified as described herein (e.g., an marker modulating agent, an antisense marker nucleic acid molecule, an marker-specific antibody, or an marker-binding partner) can be used in an animal model to determine the efficacy, toxicity, or side effects of treatment with such an agent. Alternatively, an agent identified as described herein can be used in an animal model to determine the mechanism of action of such an agent. Furthermore, this invention pertains to uses of novel agents identified by the above-described screening assays for treatments as described herein.

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It is understood that appropriate doses of small molecule agents and protein or polypeptide agents depends upon a number of factors within the knowledge of the ordinarily skilled physician, veterinarian, or researcher. The dose(s) of these agents will vary, for example, depending upon the identity, size, and condition of the subject or sample being treated, further depending upon the route by which the composition is to be administered, if applicable, and the effect which the practitioner desires the agent to have upon the nucleic acid or polypeptide of the invention. Exemplary doses of a small molecule include milligram or microgram amounts per kilogram of subject or sample weight (e.g. about 1 microgram per kilogram to about 500 milligrams per kilogram, about 100 micrograms per kilogram to about 5 milligrams per kilogram, or about 1 microgram per kilogram to about 50 micrograms per kilogram). Exemplary doses of a protein or polypeptide include gram, milligram or microgram amounts per kilogram of subject or sample weight (e.g. about 1 microgram per kilogram to about 5 grams per kilogram, about 100 micrograms per kilogram to about 500 milligrams per kilogram, or about 1 milligram per kilogram to about 50 milligrams per kilogram). It is furthermore understood that appropriate doses of one of these agents depend upon the potency of the agent with respect to the expression or activity to be modulated. Such appropriate doses can be determined using the assays described herein. When one or more of these agents is to be administered to an animal (e.g. a human) in order to modulate expression or activity of a polypeptide or nucleic acid of the invention, a physician, veterinarian, or researcher can, for example, prescribe a relatively low dose at first, subsequently increasing the dose until an appropriate response is obtained. In addition, it is understood that the specific dose level for any particular animal subject will depend upon a variety of factors including the activity of the specific agent employed, the age, body weight, general health, gender, and diet of the subject, the time of administration, the route of administration, the rate of excretion, any drug combination, and the degree of expression or activity to be modulated.

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A pharmaceutical composition of the invention is formulated to be compatible with its intended route of administration. Examples of routes of administration include parenteral, e.g., intravenous, intradermal, subcutaneous, oral (e.g., inhalation), transdermal (topical), transmucosal, and rectal administration. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the following

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components: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediamine-tetraacetic acid; buffers such as acetates, citrates or phosphates and agents for the adjustment of tonicity such as sodium chloride or dextrose. pH can be adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampules, disposable syringes or multiple dose vials made of glass or plastic.

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Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersions. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor EL (BASF; Parsippany, NJ) or phosphate buffered saline (PBS). In all cases, the composition must be sterile and should be fluid to the extent that easy syringability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as mannitol, sorbitol, or sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

Sterile injectable solutions can be prepared by incorporating the active compound (e.g., a polypeptide or antibody) in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound

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into a sterile vehicle which contains a basic dispersion medium, and then incorporating the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum drying and freeze-drying which yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

Oral compositions generally include an inert diluent or an edible carrier. They can be enclosed in gelatin capsules or compressed into tablets. For the purpose of oral therapeutic administration, the active compound can be incorporated with excipients and used in the form of tablets, troches, or capsules. Oral compositions can also be prepared using a fluid carrier for use as a mouthwash, wherein the compound in the fluid carrier is applied orally and swished and expectorated or swallowed.

Pharmaceutically compatible binding agents, and/or adjuvant materials can be included as part of the composition. The tablets, pills, capsules, troches, and the like can contain any of the following ingredients, or compounds of a similar nature: a binder such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, Primogel, or corn starch; a lubricant such as magnesium stearate or Sterotes; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring.

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For administration by inhalation, the compounds are delivered in the form of an aerosol spray from a pressurized container or dispenser which contains a suitable propellant, e.g., a gas such as carbon dioxide, or a nebulizer.

Systemic administration can also be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished through the use of nasal sprays or suppositories. For transdermal administration, the active compounds are formulated into ointments, salves, gels, or creams as generally known in the art.

The compounds can also be prepared in the form of suppositories (e.g., with conventional suppository bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

In one embodiment, the active compounds are prepared with carriers that will protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Methods for preparation of such formulations will be apparent to those skilled in the art. The materials can also be obtained commercially from Alza Corporation and Nova Pharmaceuticals, Inc. Liposomal suspensions (including liposomes having monoclonal antibodies incorporated therein or thereon) can also be used as pharmaceutically acceptable carriers. These can be prepared according to methods known to those skilled in the art, for example, as described in U.S. Patent No. 4,522,811.

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It is especially advantageous to formulate oral or parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the subject to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms of the invention are dictated by and directly dependent on the unique characteristics of the active compound and the particular therapeutic effect to be achieved, and the limitations inherent in the art of compounding such an active compound for the treatment of individuals.

For antibodies, the preferred dosage is 0.1 mg/kg to 100 mg/kg of body weight (generally 10 mg/kg to 20 mg/kg). If the antibody is to act in the brain, a dosage of 50 mg/kg to 100 mg/kg is usually appropriate. Generally, partially human antibodies and fully human antibodies have a longer half-life within the human body than other antibodies. Accordingly, lower dosages and less frequent administration is often possible. Modifications such as lipidation can be used to stabilize antibodies and to enhance uptake and tissue penetration (e.g., into the breast epithelium). A method for lipidation of antibodies is described by Cruikshank et al. (1997) J. Acquired Immune Deficiency Syndromes and Human Retrovirology 14:193.

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The nucleic acid molecules corresponding to a marker of the invention can be inserted into vectors and used as gene therapy vectors. Gene therapy vectors can be delivered to a subject by, for example, intravenous injection, local administration (U.S. Patent 5,328,470), or by stereotactic injection (see, e.g., Chen et al., 1994, Proc. Natl. Acad. Sci. USA 91:3054-3057). The pharmaceutical preparation of the gene therapy vector can include the gene therapy vector in an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery vector can be produced intact from recombinant cells, e.g. retroviral vectors, the pharmaceutical preparation can include one or more cells which produce the gene delivery system.

The pharmaceutical compositions can be included in a container, pack, or dispenser together with instructions for administration.

V. Electronic Apparatus Readable Media and Arrays

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Electronic apparatus readable media comprising a breast cancer marker of the present invention is also provided. As used herein, "electronic apparatus readable media" refers to any suitable medium for storing, holding or containing data or information that can be read and accessed directly by an electronic apparatus. Such media can include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as compact disc; electronic storage media such as RAM, ROM, EPROM, EEPROM and the like; general hard disks and hybrids of these categories such as magnetic/optical storage media. The medium is adapted or configured for having recorded thereon a marker of the present invention.

As used herein, the term "electronic apparatus" is intended to include any suitable computing or processing apparatus or other device configured or adapted for storing data or information. Examples of electronic apparatus suitable for use with the present invention include stand-alone computing apparatus; networks, including a local area network (LAN), a wide area network (WAN) Internet, Intranet, and Extranet; electronic appliances such as a personal digital assistants (PDAs), cellular phone, pager and the like; and local and distributed processing systems.

As used herein, "recorded" refers to a process for storing or encoding information on the electronic apparatus readable medium. Those skilled in the art can readily adopt any of the presently known methods for recording information on known media to generate manufactures comprising the markers of the present invention.

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A variety of software programs and formats can be used to store the marker information of the present invention on the electronic apparatus readable medium. For example, the nucleic acid sequence corresponding to the markers can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and MicroSoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like, as well as in other forms. Any number of dataprocessor structuring formats (e.g., text file or database) may be employed in order to obtain or create a medium having recorded thereon the markers of the present invention.

By providing the markers of the invention in readable form, one can routinely access the marker sequence information for a variety of purposes. For example, one skilled in the art can use the nucleotide or amino acid sequences of the present invention in readable form to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of the sequences of the invention which match a particular target sequence or target motif.

The present invention therefore provides a medium for holding instructions for performing a method for determining whether a subject has breast cancer or a predisposition to breast cancer, wherein the method comprises the steps of determining the presence or absence of a breast cancer marker and based on the presence or absence of the breast cancer marker, determining whether the subject has breast cancer or a predisposition to breast cancer and/or recommending a particular treatment for the breast cancer or pre- breast cancer condition.

The present invention further provides in an electronic system and/or in a network, a method for determining whether a subject has breast cancer or a pre-disposition to breast cancer associated with a breast cancer marker wherein the method comprises the steps of determining the presence or absence of the breast cancer marker, and based on the presence or absence of the breast cancer marker, determining whether

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the subject has breast cancer or a pre-disposition to breast cancer, and/or recommending a particular treatment for the breast cancer or pre- breast cancer condition. The method may further comprise the step of receiving phenotypic information associated with the subject and/or acquiring from a network phenotypic information associated with the subject.

The present invention also provides in a network, a method for determining whether a subject has breast cancer or a pre-disposition to breast cancer associated with a breast cancer marker, said method comprising the steps of receiving information associated with the breast cancer marker receiving phenotypic information associated with the subject, acquiring information from the network corresponding to the breast cancer marker and/or breast cancer, and based on one or more of the phenotypic information, the breast cancer marker, and the acquired information, determining whether the subject has breast cancer or a pre-disposition to breast cancer. The method may further comprise the step of recommending a particular treatment for the breast cancer or pre- breast cancer condition.

The present invention also provides a business method for determining whether a subject has breast cancer or a pre-disposition to breast cancer, said method comprising the steps of receiving information associated with the breast cancer marker, receiving phenotypic information associated with the subject, acquiring information from the network corresponding to the breast cancer marker and/or breast cancer, and based on one or more of the phenotypic information, the breast cancer marker, and the acquired information, determining whether the subject has breast cancer or a pre-disposition to breast cancer. The method may further comprise the step of recommending a particular treatment for the breast cancer or pre- breast cancer condition.

The invention also includes an array comprising a breast cancer marker of the present invention. The array can be used to assay expression of one or more genes in the array. In one embodiment, the array can be used to assay gene expression in a tissue to ascertain tissue specificity of genes in the array. In this manner, up to about 7600 genes can be simultaneously assayed for expression. This allows a profile to be developed showing a battery of genes specifically expressed in one or more tissues.

In addition to such qualitative determination, the invention allows the quantitation of gene expression. Thus, not only tissue specificity, but also the level of expression of a battery of genes in the tissue is ascertainable. Thus, genes can be grouped on the basis of their tissue expression per se and level of expression in that tissue. This is useful, for example, in ascertaining the relationship of gene expression between or among tissues. Thus, one tissue can be perturbed and the effect on gene expression in a second tissue can be determined. In this context, the effect of one cell type on another cell type in response to a biological stimulus can be determined. Such a determination is useful, for example, to know the effect of cell-cell interaction at the level of gene expression. If an agent is administered therapeutically to treat one cell type but has an undesirable effect on another cell type, the invention provides an assay to determine the molecular basis of the undesirable effect and thus provides the opportunity to co-administer a counteracting agent or otherwise treat the undesired effect. Similarly, even within a single cell type, undesirable biological effects can be determined at the molecular level. Thus, the effects of an agent on expression of other than the target gene can be ascertained and counteracted.

In another embodiment, the array can be used to monitor the time course of expression of one or more genes in the array. This can occur in various biological contexts, as disclosed herein, for example development of breast cancer, progression of breast cancer, and processes, such a cellular transformation associated with breast cancer.

The array is also useful for ascertaining the effect of the expression of a gene on the expression of other genes in the same cell or in different cells. This provides, for example, for a selection of alternate molecular targets for therapeutic intervention if the ultimate or downstream target cannot be regulated.

The array is also useful for ascertaining differential expression patterns of one or more genes in normal and abnormal cells. This provides a battery of genes that could serve as a molecular target for diagnosis or therapeutic intervention.

30 VI. Predictive Medicine

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The present invention pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trails

are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, one aspect of the present invention relates to diagnostic assays for determining the level of expression of polypeptides or nucleic acids corresponding to one or more markers of the invention, in order to determine whether an individual is at risk of developing breast cancer. Such assays can be used for prognostic or predictive purposes to thereby prophylactically treat an individual prior to the onset of the cancer.

Yet another aspect of the invention pertains to monitoring the influence of agents (e.g., drugs or other compounds administered either to inhibit breast cancer or to treat or prevent any other disorder {i.e. in order to understand any breast carcinogenic effects that such treatment may have}) on the expression or activity of a marker of the invention in clinical trials. These and other agents are described in further detail in the following sections.

15 A. Diagnostic Assays

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An exemplary method for detecting the presence or absence of a polypeptide or nucleic acid corresponding to a marker of the invention in a biological sample involves obtaining a biological sample (e.g. a breast-associated body fluid) from a test subject and contacting the biological sample with a compound or an agent capable of detecting the polypeptide or nucleic acid (e.g., mRNA, genomic DNA, or cDNA). The detection methods of the invention can thus be used to detect mRNA, protein, cDNA, or genomic DNA, for example, in a biological sample in vitro as well as in vivo. For example, in vitro techniques for detection of mRNA include Northern hybridizations and in situ hybridizations. In vitro techniques for detection of a polypeptide corresponding to a marker of the invention include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations and immunofluorescence. In vitro techniques for detection of genomic DNA include Southern hybridizations. Furthermore, in vivo techniques for detection of a polypeptide corresponding to a marker of the invention include introducing into a subject a labeled antibody directed against the polypeptide. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

A general principle of such diagnostic and prognostic assays involves preparing a sample or reaction mixture that may contain a marker, and a probe, under appropriate conditions and for a time sufficient to allow the marker and probe to interact and bind, thus forming a complex that can be removed and/or detected in the reaction mixture.

5 These assays can be conducted in a variety of ways.

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For example, one method to conduct such an assay would involve anchoring the marker or probe onto a solid phase support, also referred to as a substrate, and detecting target marker/probe complexes anchored on the solid phase at the end of the reaction. In one embodiment of such a method, a sample from a subject, which is to be assayed for presence and/or concentration of marker, can be anchored onto a carrier or solid phase support. In another embodiment, the reverse situation is possible, in which the probe can be anchored to a solid phase and a sample from a subject can be allowed to react as an unanchored component of the assay.

There are many established methods for anchoring assay components to a solid phase. These include, without limitation, marker or probe molecules which are immobilized through conjugation of biotin and streptavidin. Such biotinylated assay components can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques known in the art (e.g., biotinylation kit, Pierce Chemicals, Rockford, IL), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). In certain embodiments, the surfaces with immobilized assay components can be prepared in advance and stored.

Other suitable carriers or solid phase supports for such assays include any material capable of binding the class of molecule to which the marker or probe belongs. Well-known supports or carriers include, but are not limited to, glass, polystyrene, nylon, polypropylene, nylon, polyethylene, dextran, amylases, natural and modified celluloses, polyacrylamides, gabbros, and magnetite.

In order to conduct assays with the above mentioned approaches, the non-immobilized component is added to the solid phase upon which the second component is anchored. After the reaction is complete, uncomplexed components may be removed (e.g., by washing) under conditions such that any complexes formed will remain immobilized upon the solid phase. The detection of marker/probe complexes anchored to the solid phase can be accomplished in a number of methods outlined herein.

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In a preferred embodiment, the probe, when it is the unanchored assay component, can be labeled for the purpose of detection and readout of the assay, either directly or indirectly, with detectable labels discussed herein and which are well-known to one skilled in the art.

It is also possible to directly detect marker/probe complex formation without further manipulation or labeling of either component (marker or probe), for example by utilizing the technique of fluorescence energy transfer (see, for example, Lakowicz et al., U.S. Patent No. 5,631,169; Stavrianopoulos, et al., U.S. Patent No. 4,868,103). A fluorophore label on the first, 'donor' molecule is selected such that, upon excitation with incident light of appropriate wavelength, its emitted fluorescent energy will be absorbed by a fluorescent label on a second 'acceptor' molecule, which in turn is able to fluoresce due to the absorbed energy. Alternately, the 'donor' protein molecule may simply utilize the natural fluorescent energy of tryptophan residues. Labels are chosen that emit different wavelengths of light, such that the 'acceptor' molecule label may be differentiated from that of the 'donor'. Since the efficiency of energy transfer between the labels is related to the distance separating the molecules, spatial relationships between the molecules can be assessed. In a situation in which binding occurs between the molecules, the fluorescent emission of the 'acceptor' molecule label in the assay should be maximal. An FET binding event can be conveniently measured through standard fluorometric detection means well known in the art (e.g., using a fluorimeter).

In another embodiment, determination of the ability of a probe to recognize a marker can be accomplished without labeling either assay component (probe or marker) by utilizing a technology such as real-time Biomolecular Interaction Analysis (BIA) (see, e.g., Sjolander, S. and Urbaniczky, C., 1991, Anal. Chem. 63:2338-2345 and Szabo et al., 1995, Curr. Opin. Struct. Biol. 5:699-705). As used herein, "BIA" or "surface plasmon resonance" is a technology for studying biospecific interactions in real time, without labeling any of the interactants (e.g., BIAcore). Changes in the mass at the binding surface (indicative of a binding event) result in alterations of the refractive index of light near the surface (the optical phenomenon of surface plasmon resonance (SPR)), resulting in a detectable signal which can be used as an indication of real-time reactions between biological molecules.

Alternatively, in another embodiment, analogous diagnostic and prognostic assays can be conducted with marker and probe as solutes in a liquid phase. In such an assay, the complexed marker and probe are separated from uncomplexed components by any of a number of standard techniques, including but not limited to: differential centrifugation, chromatography, electrophoresis and immunoprecipitation. In differential centrifugation, marker/probe complexes may be separated from uncomplexed assay components through a series of centrifugal steps, due to the different sedimentation equilibria of complexes based on their different sizes and densities (see, for example, Rivas, G., and Minton, A.P., 1993, Trends Biochem Sci. 18(8):284-7). 10 Standard chromatographic techniques may also be utilized to separate complexed molecules from uncomplexed ones. For example, gel filtration chromatography separates molecules based on size, and through the utilization of an appropriate gel filtration resin in a column format, for example, the relatively larger complex may be separated from the relatively smaller uncomplexed components. Similarly, the 15 relatively different charge properties of the marker/probe complex as compared to the uncomplexed components may be exploited to differentiate the complex from uncomplexed components, for example through the utilization of ion-exchange chromatography resins. Such resins and chromatographic techniques are well known to one skilled in the art (see, e.g., Heegaard, N.H., 1998, J. Mol. Recognit. Winter 11(1-6):141-8; Hage, D.S., and Tweed, S.A. J Chromatogr B Biomed Sci Appl 1997 Oct 10;699(1-2):499-525). Gel electrophoresis may also be employed to separate complexed assay components from unbound components (see, e.g., Ausubel et al., ed., Current Protocols in Molecular Biology, John Wiley & Sons, New York, 1987-1999). In this technique, protein or nucleic acid complexes are separated based on size or charge, for example. In order to maintain the binding interaction during the electrophoretic process, non-denaturing gel matrix materials and conditions in the absence of reducing agent are typically preferred. Appropriate conditions to the particular assay and components thereof will be well known to one skilled in the art.

In a particular embodiment, the level of mRNA corresponding to the marker can be determined both by *in situ* and by *in vitro* formats in a biological sample using methods known in the art. The term "biological sample" is intended to include tissues, cells, biological fluids and isolates thereof, isolated from a subject, as well as tissues,

cells and fluids present within a subject. Many expression detection methods use isolated RNA. For *in vitro* methods, any RNA isolation technique that does not select against the isolation of mRNA can be utilized for the purification of RNA from breast cells (see, *e.g.*, Ausubel *et al.*, ed., *Current Protocols in Molecular Biology*, John Wiley & Sons, New York 1987-1999). Additionally, large numbers of tissue samples can readily be processed using techniques well known to those of skill in the art, such as, for example, the single-step RNA isolation process of Chomczynski (1989, U.S. Patent No. 4,843,155).

The isolated mRNA can be used in hybridization or amplification assays that include, but are not limited to, Southern or Northern analyses, polymerase chain reaction analyses and probe arrays. One preferred diagnostic method for the detection of mRNA levels involves contacting the isolated mRNA with a nucleic acid molecule (probe) that can hybridize to the mRNA encoded by the gene being detected. The nucleic acid probe can be, for example, a full-length cDNA, or a portion thereof, such as an oligonucleotide of at least 7, 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to a mRNA or genomic DNA encoding a marker of the present invention. Other suitable probes for use in the diagnostic assays of the invention are described herein. Hybridization of an mRNA with the probe indicates that the marker in question is being expressed.

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In one format, the mRNA is immobilized on a solid surface and contacted with a probe, for example by running the isolated mRNA on an agarose gel and transferring the mRNA from the gel to a membrane, such as nitrocellulose. In an alternative format, the probe(s) are immobilized on a solid surface and the mRNA is contacted with the probe(s), for example, in an Affymetrix gene chip array. A skilled artisan can readily adapt known mRNA detection methods for use in detecting the level of mRNA encoded by the markers of the present invention.

An alternative method for determining the level of mRNA corresponding to a marker of the present invention in a sample involves the process of nucleic acid amplification, e.g., by rtPCR (the experimental embodiment set forth in Mullis, 1987, U.S. Patent No. 4,683,202), ligase chain reaction (Barany, 1991, Proc. Natl. Acad. Sci. USA, 88:189-193), self sustained sequence replication (Guatelli et al., 1990, Proc. Natl. Acad. Sci. USA 87:1874-1878), transcriptional amplification system (Kwoh et al., 1989,

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Proc. Natl. Acad. Sci. USA 86:1173-1177), Q-Beta Replicase (Lizardi et al., 1988, Bio/Technology 6:1197), rolling circle replication (Lizardi et al., U.S. Patent No. 5,854,033) or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such molecules are present in very low numbers. As used herein, amplification primers are defined as being a pair of nucleic acid molecules that can anneal to 5' or 3' regions of a gene (plus and minus strands, respectively, or vice-versa) and contain a short region in between. In general, amplification primers are from about 10 to 30 nucleotides in length and flank a region from about 50 to 200 nucleotides in length. Under appropriate conditions and with appropriate reagents, such primers permit the amplification of a nucleic acid molecule comprising the nucleotide sequence flanked by the primers.

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For *in situ* methods, mRNA does not need to be isolated from the breast cells prior to detection. In such methods, a cell or tissue sample is prepared/processed using known histological methods. The sample is then immobilized on a support, typically a glass slide, and then contacted with a probe that can hybridize to mRNA that encodes the marker.

As an alternative to making determinations based on the absolute expression level of the marker, determinations may be based on the normalized expression level of the marker. Expression levels are normalized by correcting the absolute expression level of a marker by comparing its expression to the expression of a gene that is not a marker, e.g., a housekeeping gene that is constitutively expressed. Suitable genes for normalization include housekeeping genes such as the actin gene, or epithelial cell-specific genes. This normalization allows the comparison of the expression level in one sample, e.g., a patient sample, to another sample, e.g., a non-breast cancer sample, or between samples from different sources.

Alternatively, the expression level can be provided as a relative expression level. To determine a relative expression level of a marker, the level of expression of the marker is determined for 10 or more samples of normal versus cancer cell isolates, preferably 50 or more samples, prior to the determination of the expression level for the sample in question. The mean expression level of each of the genes assayed in the larger number of samples is determined and this is used as a baseline expression level

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for the marker. The expression level of the marker determined for the test sample (absolute level of expression) is then divided by the mean expression value obtained for that marker. This provides a relative expression level.

Preferably, the samples used in the baseline determination will be from breast cancer or from non-breast cancer cells of breast tissue. The choice of the cell source is dependent on the use of the relative expression level. Using expression found in normal tissues as a mean expression score aids in validating whether the marker assayed is breast specific (versus normal cells). In addition, as more data is accumulated, the mean expression value can be revised, providing improved relative expression values based on accumulated data. Expression data from breast cells provides a means for grading the severity of the breast cancer state.

In another embodiment of the present invention, a polypeptide corresponding to a marker is detected. A preferred agent for detecting a polypeptide of the invention is an antibody capable of binding to a polypeptide corresponding to a marker of the invention, preferably an antibody with a detectable label. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment thereof (e.g., Fab or F(ab')₂) can be used. The term "labeled", with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (i.e., physically linking) a detectable substance to the probe or antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently labeled streptavidin.

Proteins from breast cells can be isolated using techniques that are well known to those of skill in the art. The protein isolation methods employed can, for example, be such as those described in Harlow and Lane (Harlow and Lane, 1988, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York).

A variety of formats can be employed to determine whether a sample contains a protein that binds to a given antibody. Examples of such formats include, but are not limited to, enzyme immunoassay (EIA), radioimmunoassay (RIA), Western blot analysis and enzyme linked immunoabsorbant assay (ELISA). A skilled artisan can

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readily adapt known protein/antibody detection methods for use in determining whether breast cells express a marker of the present invention.

In one format, antibodies, or antibody fragments, can be used in methods such as Western blots or immunofluorescence techniques to detect the expressed proteins. In such uses, it is generally preferable to immobilize either the antibody or proteins on a solid support. Suitable solid phase supports or carriers include any support capable of binding an antigen or an antibody. Well-known supports or carriers include glass, polystyrene, polypropylene, polyethylene, dextran, nylon, amylases, natural and modified celluloses, polyacrylamides, gabbros, and magnetite.

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One skilled in the art will know many other suitable carriers for binding antibody or antigen, and will be able to adapt such support for use with the present invention. For example, protein isolated from breast cells can be run on a polyacrylamide gel electrophoresis and immobilized onto a solid phase support such as nitrocellulose. The support can then be washed with suitable buffers followed by treatment with the detectably labeled antibody. The solid phase support can then be washed with the buffer a second time to remove unbound antibody. The amount of bound label on the solid support can then be detected by conventional means.

The invention also encompasses kits for detecting the presence of a polypeptide or nucleic acid corresponding to a marker of the invention in a biological sample (e.g. an breast-associated body fluid). Such kits can be used to determine if a subject is suffering from or is at increased risk of developing breast cancer. For example, the kit can comprise a labeled compound or agent capable of detecting a polypeptide or an mRNA encoding a polypeptide corresponding to a marker of the invention in a biological sample and means for determining the amount of the polypeptide or mRNA in the sample (e.g., an antibody which binds the polypeptide or an oligonucleotide probe which binds to DNA or mRNA encoding the polypeptide). Kits can also include instructions for interpreting the results obtained using the kit.

For antibody-based kits, the kit can comprise, for example: (1) a first antibody (e.g., attached to a solid support) which binds to a polypeptide corresponding to a marker of the invention; and, optionally, (2) a second, different antibody which binds to either the polypeptide or the first antibody and is conjugated to a detectable label.

For oligonucleotide-based kits, the kit can comprise, for example: (1) an oligonucleotide, e.g., a detectably labeled oligonucleotide, which hybridizes to a nucleic acid sequence encoding a polypeptide corresponding to a marker of the invention or (2) a pair of primers useful for amplifying a nucleic acid molecule corresponding to a marker of the invention. The kit can also comprise, e.g., a buffering agent, a preservative, or a protein stabilizing agent. The kit can further comprise components necessary for detecting the detectable label (e.g., an enzyme or a substrate). The kit can also contain a control sample or a series of control samples which can be assayed and compared to the test sample. Each component of the kit can be enclosed within an individual container and all of the various containers can be within a single package, along with instructions for interpreting the results of the assays performed using the kit.

B. Pharmacogenomics

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Agents or modulators which have a stimulatory or inhibitory effect on expression of a marker of the invention can be administered to individuals to treat (prophylactically or therapeutically) breast cancer in the patient. In conjunction with such treatment, the pharmacogenomics (*i.e.*, the study of the relationship between an individual's genotype and that individual's response to a foreign compound or drug) of the individual may be considered. Differences in metabolism of therapeutics can lead to severe toxicity or therapeutic failure by altering the relation between dose and blood concentration of the pharmacologically active drug. Thus, the pharmacogenomics of the individual permits the selection of effective agents (*e.g.*, drugs) for prophylactic or therapeutic treatments based on a consideration of the individual's genotype. Such pharmacogenomics can further be used to determine appropriate dosages and therapeutic regimens.

Accordingly, the level of expression of a marker of the invention in an individual can be

determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual.

Pharmacogenomics deals with clinically significant variations in the response to

Pharmacogenomics deals with clinically significant variations in the response to drugs due to altered drug disposition and abnormal action in affected persons. See, e.g., Linder (1997) Clin. Chem. 43(2):254-266. In general, two types of pharmacogenetic conditions can be differentiated. Genetic conditions transmitted as a single factor altering the way drugs act on the body are referred to as "altered drug action." Genetic

conditions transmitted as single factors altering the way the body acts on drugs are referred to as "altered drug metabolism". These pharmacogenetic conditions can occur either as rare defects or as polymorphisms. For example, glucose-6-phosphate dehydrogenase (G6PD) deficiency is a common inherited enzymopathy in which the main clinical complication is hemolysis after ingestion of oxidant drugs (anti-malarials, sulfonamides, analgesics, nitrofurans) and consumption of fava beans.

As an illustrative embodiment, the activity of drug metabolizing enzymes is a major determinant of both the intensity and duration of drug action. The discovery of genetic polymorphisms of drug metabolizing enzymes (e.g., N-acetyltransferase 2 (NAT 2) and cytochrome P450 enzymes CYP2D6 and CYP2C19) has provided an explanation as to why some patients do not obtain the expected drug effects or show exaggerated drug response and serious toxicity after taking the standard and safe dose of a drug. These polymorphisms are expressed in two phenotypes in the population, the extensive metabolizer (EM) and poor metabolizer (PM). The prevalence of PM is different among different populations. For example, the gene coding for CYP2D6 is highly polymorphic and several mutations have been identified in PM, which all lead to the absence of functional CYP2D6. Poor metabolizers of CYP2D6 and CYP2C19 quite frequently experience exaggerated drug response and side effects when they receive standard doses. If a metabolite is the active therapeutic moiety, a PM will show no therapeutic response, as demonstrated for the analgesic effect of codeine mediated by its CYP2D6formed metabolite morphine. The other extreme are the so called ultra-rapid metabolizers who do not respond to standard doses. Recently, the molecular basis of ultra-rapid metabolism has been identified to be due to CYP2D6 gene amplification.

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Thus, the level of expression of a marker of the invention in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual. In addition, pharmacogenetic studies can be used to apply genotyping of polymorphic alleles encoding drug-metabolizing enzymes to the identification of an individual's drug responsiveness phenotype. This knowledge, when applied to dosing or drug selection, can avoid adverse reactions or therapeutic failure and thus enhance therapeutic or prophylactic efficiency when treating a subject with a modulator of expression of a marker of the invention.

This invention also provides a process for preparing a database comprising at least one of the markers set forth in Tables 1-6. For example, the polynucleotide sequences are stored in a digital storage medium such that a data processing system for standardized representation of the genes that identify a breast cancer cell is compiled. The data processing system is useful to analyze gene expression between two cells by first selecting a cell suspected of being of a neoplastic phenotype or genotype and then isolating polynucleotides from the cell. The isolated polynucleotides are sequenced. The sequences from the sample are compared with the sequence(s) present in the database using homology search techniques. Greater than 90%, more preferably greater than 95% and more preferably, greater than or equal to 97% sequence identity between the test sequence and the polynucleotides of the present invention is a positive indication that the polynucleotide has been isolated from a breast cancer cell as defined above.

In an alternative embodiment, the polynucleotides of this invention are sequenced and the information regarding sequence and in some embodiments, relative expression, is stored in any functionally relevant program, e.g., in Compare Report using the SAGE software (available though Dr. Ken Kinzler at John Hopkins University). The Compare Report provides a tabulation of the polynucleotide sequences and their abundance for the samples normalized to a defined number of polynucleotides per library (say 25,000). This is then imported into MS-ACCESS either directly or via copying the data into an Excel spreadsheet first and then from there into MS-ACCESS for additional manipulations. Other programs such as SYBASE or Oracle that permit the comparison of polynucleotide numbers could be used as alternatives to MS-ACCESS. Enhancements to the software can be designed to incorporate these additional functions. These functions consist in standard Boolean, algebraic, and text search operations, applied in various combinations to reduce a large input set of polynucleotides to a manageable subset of a polynucleotide of specifically defined interest.

One skilled in the art may create groups containing one or more project(s) by combining the counts of specific polynucleotides within a group (e.g., GroupNormal = Normal1 + Normal2, GroupTumor1 + TumorCellLine). Additional characteristic values are also calculated for each tag in the group (e.g., average count, minimum count, maximum count). One skilled in the art may calculate individual tag count ratios between groups, for example the ratio of the average GroupNormal count to the average

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GroupTumor count for each polynucleotide. A statistical measure of the significance of observed differences in tag counts between groups may be calculated.

C. Monitoring Clinical Trials

Monitoring the influence of agents (e.g., drug compounds) on the level of expression of a marker of the invention can be applied not only in basic drug screening, but also in clinical trials. For example, the effectiveness of an agent to affect marker expression can be monitored in clinical trials of subjects receiving treatment for breast cancer. In a preferred embodiment, the present invention provides a method for monitoring the effectiveness of treatment of a subject with an agent (e.g., an agonist, antagonist, peptidomimetic, protein, peptide, nucleic acid, small molecule, or other drug candidate) comprising the steps of (i) obtaining a pre-administration sample from a subject prior to administration of the agent; (ii) detecting the level of expression of one or more selected markers of the invention in the pre-administration sample; (iii) obtaining one or more post-administration samples from the subject; (iv) detecting the level of expression of the marker(s) in the post-administration samples; (v) comparing the level of expression of the marker(s) in the pre-administration sample with the level of expression of the marker(s) in the post-administration sample or samples; and (vi) altering the administration of the agent to the subject accordingly. For example, increased administration of the agent can be desirable to increase expression of the marker(s) to higher levels than detected, i.e., to increase the effectiveness of the agent. Alternatively, decreased administration of the agent can be desirable to decrease expression of the marker(s) to lower levels than detected, i.e., to decrease the effectiveness of the agent.

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D. Surrogate Markers

The markers of the invention may serve as surrogate markers for one or more disorders or disease states or for conditions leading up to disease states, and in particular, breast cancer. As used herein, a "surrogate marker" is an objective biochemical marker which correlates with the absence or presence of a disease or disorder, or with the progression of a disease or disorder (e.g., with the presence or absence of a tumor). The presence or quantity of such markers is independent of the

disease. Therefore, these markers may serve to indicate whether a particular course of treatment is effective in lessening a disease state or disorder. Surrogate markers are of particular use when the presence or extent of a disease state or disorder is difficult to assess through standard methodologies (e.g., early stage tumors), or when an assessment of disease progression is desired before a potentially dangerous clinical endpoint is reached (e.g., an assessment of cardiovascular disease may be made using cholesterol levels as a surrogate marker, and an analysis of HIV infection may be made using HIV RNA levels as a surrogate marker, well in advance of the undesirable clinical outcomes of myocardial infarction or fully-developed AIDS). Examples of the use of surrogate markers in the art include: Koomen et al. (2000) J. Mass. Spectrom. 35: 258-264; and James (1994) AIDS Treatment News Archive 209.

The markers of the invention are also useful as pharmacodynamic markers. As used herein, a "pharmacodynamic marker" is an objective biochemical marker which correlates specifically with drug effects. The presence or quantity of a pharmacodynamic marker is not related to the disease state or disorder for which the drug is being administered; therefore, the presence or quantity of the marker is indicative of the presence or activity of the drug in a subject. For example, a pharmacodynamic marker may be indicative of the concentration of the drug in a biological tissue, in that the marker is either expressed or transcribed or not expressed or transcribed in that tissue in relationship to the level of the drug. In this fashion, the distribution or uptake of the drug may be monitored by the pharmacodynamic marker. Similarly, the presence or quantity of the pharmacodynamic marker may be related to the presence or quantity of the metabolic product of a drug, such that the presence or quantity of the marker is indicative of the relative breakdown rate of the drug in vivo. Pharmacodynamic markers are of particular use in increasing the sensitivity of detection of drug effects, particularly when the drug is administered in low doses. Since even a small amount of a drug may be sufficient to activate multiple rounds of marker transcription or expression, the amplified marker may be in a quantity which is more readily detectable than the drug itself. Also, the marker may be more easily detected due to the nature of the marker itself; for example, using the methods described herein, antibodies may be employed in an immune-based detection system for a protein marker, or marker-specific radiolabeled probes may be used to detect a mRNA marker.

Furthermore, the use of a pharmacodynamic marker may offer mechanism-based prediction of risk due to drug treatment beyond the range of possible direct observations. Examples of the use of pharmacodynamic markers in the art include: Matsuda *et al.* US 6,033,862; Hattis *et al.* (1991) *Env. Health Perspect.* 90: 229-238; Schentag (1999) *Am. J. Health-Syst. Pharm.* 56 Suppl. 3: S21-S24; and Nicolau (1999) *Am. J. Health-Syst. Pharm.* 56 Suppl. 3: S16-S20.

The markers of the invention are also useful as pharmacogenomic markers. As used herein, a "pharmacogenomic marker" is an objective biochemical marker which correlates with a specific clinical drug response or susceptibility in a subject (see, e.g., McLeod et al. (1999) Eur. J. Cancer 35(12): 1650-1652). The presence or quantity of the pharmacogenomic marker is related to the predicted response of the subject to a specific drug or class of drugs prior to administration of the drug. By assessing the presence or quantity of one or more pharmacogenomic markers in a subject, a drug therapy which is most appropriate for the subject, or which is predicted to have a greater degree of success, may be selected. For example, based on the presence or quantity of RNA or protein for specific tumor markers in a subject, a drug or course of treatment may be selected that is optimized for the treatment of the specific tumor likely to be present in the subject. Similarly, the presence or absence of a specific sequence mutation in marker DNA may correlate with drug response. The use of pharmacogenomic markers therefore permits the application of the most appropriate treatment for each subject without having to administer the therapy.

VII. Experimental Protocol

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25 A. Subtracted Libraries and Transcript Profiling

Subtracted libraries are generated using a PCR based method that allows the isolation of clones expressed at higher levels in one population of mRNA (tester) compared to another population (driver). Both tester and driver mRNA populations are converted into cDNA by reverse transcription, and then PCR amplified using the SMART PCR kit from Clontech. Tester and driver cDNAs are then hybridized using the PCR-Select cDNA subtraction kit from Clontech. This technique results in both subtraction and normalization, which is an equalization of copy number of low-

abundance and high-abundance sequences. After generation of the subtractive libraries, a group of 96 or more clones from each library is tested to confirm differential expression by reverse Southern hybridization.

5 B. Proteomics

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Proteins that are secreted by normal and transformed cells in culture are analyzed to identify those proteins that are likely to be secreted by cancerous cells into body fluids. Supernatants are isolated and MWT-CO filters are used to simplify the mixture of proteins. The proteins are then digested with trypsin. The tryptic peptides are loaded onto a microcapillary HPLC column where they are separated, and eluted directly into an ion trap mass spectrometer, through a custom-made electrospray ionization source. Throughout the gradient, sequence data is acquired through fragmentation of the four most intense ions (peptides) that elute off the column, while dynamically excluding those that have already been fragmented. In this way, approximately 2000 scans worth of sequence data are obtained, corresponding to approximately 50 to 200 different proteins in the sample. These data are searched against databases using correlation analysis tools, such as MS-Tag, to identify the proteins in the supernatants.

In addition, protein profiling experiments are undertaken to assess whether the proteins associated with the expression of individual markers of the invention are secreted. Transcriptional profiling experiments are performed on fractions of RNA that are obtained from either (a) endoplasmic reticulum-associated (ER-associated) ribosomes, or (b) free ribosomes. Eukaryotic RNA which is isolated from ER-associated ribosomes tends to encode secreted and membrane bound proteins rather than intracellular proteins. Accordingly, markers of the invention which exhibit significantly enhanced expression in fractions of RNA from ER-associated ribosomes (in comparison with RNA from free ribosomes) are predicted to be associated with secreted proteins.

VIII. Summary Of The Data Provided In The Tables

Table 1 shows 4068 novel nucleotide sequences identified through subtracted library experiments. The sequences of Table 1 were reinterpreted and those sequences are set forth in Tables 3 and 5. These sequences were determined to be novel through various BLAST searches of the available databases.

The library source for SEQ ID NOS: 1-675 was breast cancer cell cultures (ascites and pleural fluid cultures) versus normal (*i.e.*, non-cancerous) human epithelial mammary cell lines (HMEC). SEQ ID NOS: 1-470 are preferred and SEQ ID NOS: 1-315 are most preferred.

The library source for SEQ ID NOS: 676-1644 was cancer tissue samples (clinical invasive lobular carcinomas (ILC)) versus normal breast tissue samples. SEQ ID NOS: 676-890 and 1056-1363 are preferred and SEQ ID NOS: 676-792 and 1056-1254 are most preferred.

The library source for SEQ ID NOS: 1645-2941 was cancer tissue samples (clinical invasive ductal carcinomas (IDC)) versus normal breast tissue samples. SEQ ID NOS: 1645-2454 are preferred and SEQ ID NOS: 1645-2124 are most preferred.

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The library source for SEQ ID NOS: 2942-4068 was cancer tissue samples (clinical ductal carcinomas in situ (DCIS)) versus normal breast tissue samples. SEQ ID NOS: 2942-3626 are preferred and SEQ ID NOS: 2942-3351 are most preferred.

Table 2 shows 4843 novel nucleotide sequences identified through subtracted library experiments. The sequences of Table 2 were reinterpreted and those sequences are set forth in Tables 4 and 5. These sequences were determined to be novel through various BLAST searches of the available databases.

The tester source for SEQ ID NOS: 1-64, 1960-1976 and 3038-3080 was aggressive breast tumor cell lines and the driver source was indolent breast tumor cell lines (detects markers upregulated in more aggressive tumors).

The tester source for SEQ ID NOS: 65-72, 1879, 1977-2004 and 3081-3127 was indolent breast tumor cell lines and the driver source was aggressive breast tumor cell lines (detects markers upregulated in more indolent tumors).

The tester source for SEQ ID NOS: 73-629, 1880-1894, 2005-2296 and 3128-3471 was poor clinical outcome breast tumors and the driver source was good clinical outcome breast tumors (detects markers upregulated in more aggressive tumors). "Poor clinical outcome" is defined as the patient suffering disease recurrence following surgery within a period of less than five years. "Good clinical outcome" is defined as the patient remaining disease free for at least five years or more following surgery.

The tester source for SEQ ID NOS: 630-862, 1895-1900, 2297-2385 and 3472-3602 was good clinical outcome breast tumors and the driver source was poor clinical outcome breast tumors (detects markers upregulated in more indolent tumors).

The tester source for SEQ ID NOS: 863-1262, 1901-1910, 2386-2567 and 3602-3988 was breast tumor lymph node metastasis and the driver source was indolent (colloid and tubular) breast tumor samples (detects markers upregulated in more aggressive tumors).

The tester source for SEQ ID NOS: 1263-1392, 1911-1916, 2568-2735 and 3989-4319 was indolent (colloid and tubular) breast tumor samples and the driver source was breast tumor lymph node metastasis (detects markers upregulated in more indolent tumors).

The tester source for SEQ ID NOS: 1393-1638, 1917-1943, 2736-2940 and 4320-4604 was T1N1 breast tumors (tumors 2.0 cm or less in greatest dimension with regional lymph node metastasis) and the driver source was T1N0 breast tumors (tumors 2.0 cm or less in greatest dimension with no regional lymph node metastasis), good clinical outcome (detects markers upregulated in more aggressive tumors.

The tester source for SEQ ID NOS: 1639-1878, 1944-1959, 2941-3037 and 4605-4843 was T1N0 breast tumors with good clinical outcome and the driver source was T1N1 breast tumors (detects markers upregulated in more indolent tumors).

Table 6 shows novel nucleotide sequences shown to be associated with breast cancer.

The contents of all references, patents, published patent applications, and database records cited throughout this application are hereby incorporated by reference.

25 Other Embodiments

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Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

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What is claimed is:

Claims

- 1. An isolated nucleic acid molecule selected from the group consisting of:
- a) a nucleic acid molecule comprising a nucleotide sequence which is at least 90% homologous to a nucleotide sequence of Tables 1-6, or a complement thereof;
- b) a nucleic acid molecule comprising a fragment of a nucleic acid comprising a nucleotide sequence of Tables 1-6, or a complement thereof; and
 - c) a nucleic acid molecule comprising a nucleotide sequence of Tables 1-6, or a complement thereof.
- 15 2. A vector which contains a nucleic acid molecule of claim 1.
 - 3. A host cell which contains a nucleic acid molecule of claim 1.
- 4. An isolated polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 90% homologous to a nucleic acid comprising a nucleotide sequence of Tables 1-6.
 - 5. An antibody which selectively binds to a polypeptide of claim 4.
- 25 6. A method for producing a polypeptide comprising culturing the host cell of claim 3 under conditions in which the nucleic acid molecule is expressed.

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- 7. A method for detecting the presence of a polypeptide of claim 4 in a sample comprising:
- a) contacting the sample with a compound which selectively binds to the polypeptide; and
- b) determining whether the compound binds to the polypeptide in the sample to thereby detect the presence of a polypeptide of claim 4 in the sample.
 - 8. A kit comprising a compound which selectively binds to the polypeptide of claim 4.
- 9. A method for detecting the presence of a nucleic acid molecule of claim 1 in a sample comprising:
 - a) contacting the sample with a nucleic acid probe or primer which selectively hybridizes to the nucleic acid molecule; and
- b) determining whether the nucleic acid probe or primer binds to a nucleic acid molecule in the sample to thereby detect the presence of a nucleic acid molecule of claim 1 in the sample.
- 10. The method of claim 9, wherein the sample comprises mRNA molecules 20 and is contacted with a nucleic acid probe.
 - 11. The method of claim 9, wherein the sample is isolated from breast tissue.
 - 12. The method of claim 9, wherein the sample is a tumor sample.
 - 13. A kit comprising a compound which selectively hybridizes to a nucleic acid molecule of claim 1.

- 14. A method of assessing whether a patient is afflicted with breast cancer, the method comprising comparing:
- a) the level of expression of a marker in a patient sample, wherein the marker is selected from the group consisting of the markers listed in Tables 1-6, and
- b) the normal level of expression of the marker in a control non-breast cancer sample,

wherein a significant difference between the level of expression of the marker in the patient sample and the normal level is an indication that the patient is afflicted with breast cancer.

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- 15. The method of claim 14, wherein the marker corresponds to a secreted protein.
- 16. The method of claim 14, wherein the marker corresponds to a transcribed polynucleotide or portion thereof, wherein the polynucleotide comprises the marker.
 - 17. The method of claim 14, wherein the sample comprises cells obtained from the patient.
- 20 18. The method of claim 17, wherein the sample is a breast tissue.
 - 19. The method of claim 17, wherein the cells are in a fluid selected from the group consisting of blood fluid, lymph, ascitic fluid, cystic fluid, urine, a breast exudate and a nipple aspirate.

- 20. The method of claim 14, wherein the level of expression of the marker in the sample is assessed by detecting the presence in the sample of a protein corresponding to the marker.
- The method of claim 15, wherein the presence of the protein is detected using a reagent which specifically binds with the protein.

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- 22. The method of claim 21, wherein the reagent is selected from the group consisting of an antibody, an antibody derivative, and an antibody fragment.
- 23. The method of claim 14, wherein the level of expression of the marker in the sample is assessed by detecting the presence in the sample of a transcribed polynucleotide or portion thereof, wherein the transcribed polynucleotide comprises the marker.
- 24. The method of claim 23, wherein the transcribed polynucleotide is an 10 mRNA.
 - 25. The method of claim 23, wherein the transcribed polynucleotide is a cDNA.
- 15 26. The method of claim 23, wherein the step of detecting further comprises amplifying the transcribed polynucleotide.
- 27. The method of claim 14, wherein the level of expression of the marker in the sample is assessed by detecting the presence in the sample of a transcribed polynucleotide which anneals with the marker or anneals with a portion of a polynucleotide wherein the polynucleotide comprises the marker, under stringent hybridization conditions.
- 28. The method of claim 14, wherein the level of expression of the marker in the sample differs from the normal level of expression of the marker in a patient not afflicted with breast cancer by a factor of at least about 2.
 - 29. The method of claim 14, wherein the level of expression of the marker in the sample differs from the normal level of expression of the marker in a patient not afflicted with breast cancer by a factor of at least about 5.

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- 30. The method of claim 14, comprising comparing:
- a) the level of expression in the sample of each of a plurality of markers independently selected from the markers listed in Tables 1-6, and
- b) the normal level of expression of each of the plurality of markers in
 samples of the same type obtained from control humans not afflicted with breast cancer, wherein the level of expression of more than one of the markers is significantly altered, relative to the corresponding normal levels of expression of the markers, is an indication that the patient is afflicted with breast cancer.
- 10 31. The method of claim 30, wherein the level of expression of each of the markers is significantly altered, relative to the corresponding normal levels of expression of the markers, is an indication that the patient is afflicted with breast cancer.
- 32. The method of claim 30, wherein the plurality comprises at least three of the markers.
 - 33. The method of claim 30, wherein the plurality comprises at least five of the markers.
- 20 34. A method for monitoring the progression of breast cancer in a patient, the method comprising:
 - a) detecting in a patient sample at a first point in time, the expression of a marker, wherein the marker is selected from the group consisting of the markers listed in Tables 1-6;
- b) repeating step a) at a subsequent point in time; and
 - c) comparing the level of expression detected in steps a) and b), and therefrom monitoring the progression of breast cancer in the patient.
- 35. The method of claim 34, wherein the marker corresponds to a secreted 30 protein.

- 36. The method of claim 34, wherein marker corresponds to a transcribed polynucleotide or portion thereof, wherein the polynucleotide comprises the marker.
- 37. The method of claim 34, wherein the sample comprises cells obtained from the patient.
 - 38. The method of claim 34, wherein the patient sample is a breast tissue.
- 39. The method of claim 34, wherein between the first point in time and the subsequent point in time, the patient has undergone surgery to remove a tumor.
 - 40. A method of assessing the efficacy of a test compound for inhibiting breast cancer in a patient, the method comprising comparing:
- a) expression of a marker in a first sample obtained from the patient and
 exposed to the test compound, wherein the marker is selected from the group consisting of the markers listed in Tables 1-6, and
 - b) expression of the marker in a second sample obtained from the patient, wherein the sample is not exposed to the test compound,

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- wherein a significantly lower level of expression of the marker in the first sample, relative to the second sample, is an indication that the test compound is efficacious for inhibiting breast cancer in the patient.
 - 41. The method of claim 40, wherein the first and second samples are portions of a single sample obtained from the patient.
 - 42. The method of claim 40, wherein the first and second samples are portions of pooled samples obtained from the patient.

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- 43. A method of assessing the efficacy of a therapy for inhibiting breast cancer in a patient, the method comprising comparing:
- a) expression of a marker in the first sample obtained from the patient prior to providing at least a portion of the therapy to the patient, wherein the marker is selected from the group consisting of the markers listed in Tables 1-6, and
- b) expression of the marker in a second sample obtained from the patient following provision of the portion of the therapy,

wherein a significantly lower level of expression of the marker in the second sample, relative to the first sample, is an indication that the therapy is efficacious for inhibiting breast cancer in the patient.

- 44. A method of selecting a composition for inhibiting breast cancer in a patient, the method comprising:
 - a) obtaining a sample comprising cancer cells from the patient;
- b) separately exposing aliquots of the sample in the presence of a plurality of test compositions;
- c) comparing expression of a marker in each of the aliquots, wherein the marker is selected from the group consisting of the markers listed in Tables 1-6; and
- d) selecting one of the test compositions which induces a lower level of expression of the marker in the aliquot containing that test composition, relative to other test compositions.
 - 45. A method of inhibiting breast cancer in a patient, the method comprising:
 - a) obtaining a sample comprising cancer cells from the patient;
- b) separately maintaining aliquots of the sample in the presence of a plurality of test compositions;
- c) comparing expression of a marker in each of the aliquots, wherein the marker is selected from the group consisting of the markers listed in Tables 1-6; and
- d) administering to the patient at least one of the test compositions which
 induces a lower level of expression of the marker in the aliquot containing that test composition, relative to other test compositions.

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- 46. A kit for assessing whether a patient is afflicted with breast cancer, the kit comprising reagents for assessing expression of a marker selected from the group consisting of the markers listed in Tables 1-6.
- A kit for assessing the presence of breast cancer cells, the kit comprising a nucleic acid probe wherein the probe specifically binds with a transcribed polynucleotide corresponding to a marker selected from the group consisting of the markers listed in Tables 1-6.
- 10 48. A kit for assessing the suitability of each of a plurality of compounds for inhibiting breast cancer in a patient, the kit comprising:
 - a) the plurality of compounds; and
 - b) a reagent for assessing expression of a marker selected from the group consisting of the markers listed in Tables 1-6.

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- 49. A method of making an isolated hybridoma which produces an antibody useful for assessing whether a patient is afflicted with breast cancer, the method comprising:
- isolating a protein or protein fragment corresponding to a marker selected 20 from the group consisting of the markers listed in Tables 1-6;

immunizing a mammal using the isolated protein or protein fragment; isolating splenocytes from the immunized mammal;

fusing the isolated splenocytes with an immortalized cell line to form hybridomas; and

- specifically binds with the protein or protein fragment to isolate the hybridoma.
 - 50. An antibody produced by a hybridoma made by the method of claim 49.

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51. A kit for assessing the presence of human breast cancer cells, the kit comprising an antibody, wherein the antibody specifically binds with a protein corresponding to a marker selected from the group consisting of the markers listed in Tables 1-6.

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- 52. A method of assessing the breast cell carcinogenic potential of a test compound, the method comprising:
- a) maintaining separate aliquots of breast cells in the presence and absence of the test compound; and
- b) comparing expression of a marker in each of the aliquots, wherein the
 marker is selected from the group consisting of the markers listed in Tables 1-6,

wherein a significantly enhanced level of expression of the marker in the aliquot maintained in the presence of the test compound, relative to the aliquot maintained in the absence of the test compound, is an indication that the test compound possesses human breast cell carcinogenic potential.

- 53. A kit for assessing the breast cell carcinogenic potential of a test compound, the kit comprising breast cells and a reagent for assessing expression of a marker, wherein the marker is selected from the group consisting of the markers listed in Tables 1-6.
- 54. A method of treating a patient afflicted with breast cancer, the method comprising providing to cells of the patient an antisense oligonucleotide complementary to a polynucleotide corresponding to a marker selected from the markers listed in Tables 1-6.
 - 55. A method of inhibiting breast cancer in a patient at risk for developing breast cancer, the method comprising inhibiting expression of a gene corresponding to a marker selected from the markers listed in Tables 1-6.

Table 1

Sequence 1

Sequence 2

AGGTACCTGCCCATCCACTGCCTTTTCCATGTATCCTGGAACTGAGCATAGACCTCTTCC CAGGCAGAGCTGACAGCAAGTAAAGGAGATCATAATCAGGGGACCAAACAACTTTGTCTA AAGTGTGAATGTCACCTAAGGAGAAGCTGTGAGATCAGAAGGGTGGGGCAGAGGAGCAGA CACCATGAGGGAGAGTCCTTGGGGGTACCTGCCCG

Sequence 4

Sequence 5

Sequence 7

GGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTGAAAGGATGAAAAGGTGGTGTC
ATGTTTTGGGGAGAATCTTACTTCTCAAATGGAAATTGCACTTTTNGCTGAATCCTTTGC
ATTTTTTTGGTAGTAAGCAGTTCATTGAGTATCAGGTCCTCAAAGGAATGAGTTGGCCCG
GCTAGGGTGGGCCCTCTTGACCTAACTTCAGAGGGGGCCCTTGGCTCAGTAGGTGTGAATC
AGGGAAGCCACATTGTCCTCAGGGTGCTGTATGAAGCTGGGTGTGGGCGGATTCCTCCA

Table 1

Sequence 8

AGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACATGTATTTGTCACTTAAAGGT
TCTTCTGTAAACTGCTTCAGATTCTTTTACTATTCAATTTTTAATTNTTAATATCTGTA
AAGAACGTTAATATTCCTCTTTATAATCAATCTTTCCCAGTTAGCCTTAAAAATGTATTC
CCTACTTTTGCTTCAGGAGATCATTATTTTGCAAATGCAAAGATTTTTTACTTAGACTTTT
GAAATCACTCTTAGTAACTTTAACATTGTTTTTTAGGTATGAAATTGAAGGCTGTGAAGTG
ATTTGGGCCATTAAAGATAAAGCTATAGGGAATACTTTTCTTCGATGCAGGAGCAGCTTG
AATTCTTTGACTTCAAAGCTCATTGCTGGAAAAATCAAGAGGGCTTAAATTTGCCCCTTA
AAAGGAACCNGGATTTTCCCACCTGGANGGAAGGG

Sequence 9

Sequence 10

Sequence 11

CCGGGCAAGGTACACCAGGGATTGGGGGCCCTGCAGCTTCTACGCCCAGGGACATTTG CTTCGGGGACTGGAGTCCTTGCTGTGGCGTGAGGCTGTGTCTGGCGTCTGGGAGGAGGAC TGTGTGGGGTCTGGGTTCCCCAGCCCTAATGACCCAGCTGGTTGAAGGCAGCAGATGAAA GGAGACAAATGACCACGCAAACCCTGGGTGGCCTCATGAACAGGTGGCGGACAAGGGTGA TCCCTGTTGAGCAAGGTCCTGCACTGCGGTGGGTCCAAGGACTAAGCTGCCAGC Sequence 12

Sequence 13

TNCTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACATCATATGCCTGCTG
AAGTGCTCTGACTTTAGGATGAGAAACTCTAACATAGGCCGGAAGACAAATAAACCATAA
ACTGTAACAATGACTAAACAGACACTTGGCCCACTGTGGTGGATTTGTATAACATCTCTT
CGCCAATTTATGAGCTGTTTTTATTTCCTGTTTAGTTCTCTTAGCCATGAGAGGTGGACT
CTTTGACCTGCCCG

Sequence 15

CGGCCGCCGGGCNNGTACCAAAAGGNTNAANACCCANAGGGNAAACCCACCGCGGGNNG AGCAACAAGNAGGCACACANGGGGAAAGACCCCANANACGGGGGAAANGCGGGAAAGC CCCCGAGGAAGCACACACCNCANACAACACCAAAAAANACACACGGGCGAGAAGNCGAN

Table 1

Sequence 16

AGGTGNGAATCAACGCAGGTCAAAATGAAATTTACACTGAAGGCTTCCAAACCAAAGGGA AGGACAGGATGTGTCATCAAATATGTTTNGTCACCTTGTATTATACAAAANGCTATTTTC TAANGAGTCAGAGAAANTNTGTGAANCTTATTGTGCGGCCCCCTTGTAATNAAATGTTAA CTCCCTTGTATTTAATTTTCAACACTACATTAAGAATTAAGTGGTTTNAGTTTGNGGACA TAAGCANCACTTATTAATATCAAGGTGTTTAAGAACTCAGGAG

Sequence 17

GGGCGAATTGGAGCTCCCCGCGGTGGCGGCGGCGAGGTTNTGCTTCCAGTTTATATTTCACA TCCTGTTCAGCTTNATTAATATGCCATGGGTCACAAAACTCAGTGCAATAAAATGTGTAT GAAAGAAACACCCTTCAGAAAAGATGAGACTCTTTCAAGTGTAAATACTCTAAACTAATA TAAGTCAAAATATTTTTTTGTGCCCAGNGATTTTTAAAAAATTACCCAGTCAACCATTTC CTCAATAATTCAAATACTCAAGTGTCCATTTATATTTTTTGGAATAAGCGAGAGTGATCGT AGTACCTGCCCG

Sequence 18

CNATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGGATTGTGTGCAAAATCACGAG GGGGGTGCAAGATCCTGATTTTTNAGGAGTTCAAGCGACAATGGCAGNCCAATACGGCAG TATGAGCTTNAACCCCAGCACACCAGGGGCCAGTTATGGGCCTGGAAGGCAAGAGCCCAG AAATTCCCAATTGAGAATTGTGTTAGTGGGTAAAACCGGAGCAGGAAAAAGTGCAACAGG AAACAGCATCCTTGGCCGGAAAGTGTTTCATTCTGGCACTGCAGCAAAATCCATTACCAA GAAGTGTGAGAAACGCAGCAGNTNATGGAAGGAAACAGAACTTGT Sequence 19

Sequence 20

Sequence 21

CCGCGGTGCCGAGGTACTCTATGTCCCTCCAGTTGCAACAATGTTGTTTCCAGCC
TGGTTCAGCAGCTTGCTGGTGGTTTACTAGGCAGACATGAGCCAGAAACAAAATCAGCAA
CCCTGGAGTGGTCATTTAGGATCAGTTTTGTCTCCTTTTTACAAAGCAATGAGTGCTTTAT
AAAAGCATTTCTCCTCAGGAAACTGGCTCCTCAAAAGTCGTTCTCCAAGCCAGCAGCTCA
CAGTAGATGGATGAGTTTACCTGTCCTAATAATACTTTTTATTATAATACTTTTATTACT
GATACTTTATTATAATACTTTTATTACTGATACCTAGTAATACTTTTATTAGAT

GAAATGTATCCCCAGGCCTCCACATCAGCCTTCTGGGGCCCTGACAGGTGTTTACCAGTA GCTNCACAACCTTCACAGGCTTGTTCTCTCATCCCTGTGAGGGAAGGTTCAAAAGGCAAC

Sequence 23

CCGCGGTGCCGCCCGGGCAGGTACTCGCTCAAATTAAGTTTTTTTAAAAGGTCTGT
AATTTGAAAGGAAAACAATTTTTCACTAAAAATATCCTTATTACATGAAAGCCATAATTT
AAAAGACAGAGAAAAAAGCTTTTTAATTAACAAATAAACAGCATCTCCAGAGACACTTG
GGAATGTTTGTTTTTAATCAGTGGGTCCTAAAAATCACTGCTTCCACCTGCAAACGAACA
CGAATCCACTGTGGATGGCGTCCTCTGACCCACCCTGAAGGGTTCTGTTTCTCTCCACAC
ACTTCCTTTTCTGCAACTTTCAGCAAAGCAGGTTTGGAAGAAAAGAGGATTACAAAGAACT
ACGACTGGCTCCCTAGTGAATAACTTAACACGGTAAAACCCGGTTTTCCATTTACATT
Sequence 24

Sequence 25

Sequence 26

ACGACTNCTATAGGGCGAATTGGAGCTCCCGGGGTGGCGGCCGCCCGGGCAGGTACAAG
CTAAGAAATGTAACAGTATCAACCCTCCCAGTTGCTTAATTATACCCATAGGTAATACAA
AAAGCTCTGAAGACCCAAAGATGACATTACTAATGATGTGATTTCAGGAGCCACAGAAGA
ACCTTACCAGCTTCCCTCAAATCAGTCCTTATCCTCTTTCTATCTTCACTCCCATCATCA
TCTATTTTCACACTATCCAGCTAAGCAAAGATTCCTGGAGGCTGACTTGTATCTTCAGAC
TCACAGAGTGAATTCAGCTNTTCTGAATCAAGACCCACCCAGTN
Sequence 27

Sequence 29

TACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCGAGGTACAGAGAAGGCACTGAAT
AAATTCACAAAGGCCGATTGGTTCACCCATTCTTTTAGAGACAACAGACACGCAATTCTG
ACGAGGACTCCTGTTACTAAAAGACACAGCCTCTGATACAAGAGAGATATCCCTTTGACT
GAAGCATTACCAGGGTCCCCAGGGCCCCCTCCCACTGGGGCGGTAACACTACGGGTCTCC
CCACCATATATTCCATGTCAAAGTATCTACACAAATACAGAGGAAATTAAGCAAGTAAAT

Table 1

ACGGTATGTAATTGTTATCATTTGTATTTCTTTAAGGCATATTTATAAATATTTTAAAGT AAACAATATGAGGTGAGTGCCTTTCATTAGCTATGATCTTTCATACTGATATATTTTGAC TGGATCTGAATAAGGCAGGTTTACTGGNGGGAGCATATTAACATAAAACAGCTTATATGA TTTCAGGTGGGTACCTGCC

Sequence 30

Sequence 31

Sequence 32

Sequence 33

TCGAGGTACCTAAGTCAAAAGGCACTGNTTTGGAGATGGCACACTCATTTTCATGCGTGT
AAAATNTTAAATCATCCACTTTGCAGGCAGTGGCTTTGATAACTCACTGCAGTGTTCAAG
GGGTTTATAAAACTGGTTATAAGCTTCAAACCCATGTTTAGAAAAATTGACACTCATAGA
AAAAAATGCTTTCTCTGGGCTAATTAAAATTAAAAATTGAAATGAAATGTAAACCCAGAAGTA
TGGCTCACAAAGCTATAGAAAAGATCCTTCATATCATCCCTGGCCCTAGCACCGTGAGTA
GATGTTCACCCTGATAAGGCCAGGCGGAGGTGGCCCATGTGAAATTCTTTGGCTTTGAGC
TAATTG

Sequence 34

CCGGGCAGGTACTAACATGATGATAGGTTTTCAAAATATCTTTGTAGTGGATGCTGCATA ATTACATTCACTTCTCTTAGACTGTAAAAGACTTTCTTGACTTGTTTTAACAGTAGAGAT AGCAGTACCT

Sequence 35

Table 1

AGGTACAGAAACCTTCAGAGAGGATAAATAGCTTGCCCTGTAGAAGCAGGACTGAAACCC
TTGTCCGCCTGACTCCCCCAGCTACTCTGCCCACTGTAGCCCCCTNNCTTACTGTCCTGG
CACACCCCTCACCATCCTNTNTACCTTAAATATCAAAGAGGGCAAGAGNGAAAGGGCTTT
AAAGATAAGTTATTTTTTTAAGGAACCTTAATATTATTTTTTAAGNAAGTAACCCAAATTA
GTGACGTGAAATTACAANAAACCTGNCCGGGCCGGCCNGCTCTTAGAACCTAGTTGGAAT
CCCCCCCGGGCTGCAGGGAAATTTNTGANTTTTCAAAGCTTTATTCNATACCCGTNCGAC
CCTTNAGGGGGGGGGNGCCCCGGGTACCCAAACNTTTTTGGTT
Sequence 39

Sequence 40

CCGCGGTGGCGGCCGAGGTACGCGGAACACCCATGGCAGTGGGATATATCCCGGAAACCC
ACAGGATGAGAAAAGCTTGGCGCAGATGTGATAGAGGTGGCTTTTGGGCAGATGATGA
TTATTCTCGCTGTCAGTATGCAAATGATGTCACTAGAGTTCTTTATATGTTTAATCAGAT
GCCCCTCAATCTTACCAATGCCGTGGCAACAGCTCGACAGTTACTGGCTTACACTGTGGA
AGCAGCCAACTTTTCTGACAAAATGGATGTTATATTTGTGGCAGAAATGATTGAAAAATT
TGGAAGATTTACCAAGGAGGAAAAATCAAAAGAGCTAGGTGACGTGATGGTTGACATTGC
AAGTAACATCATGTTGGCTGATGAACGT

Sequence 41

AGGTGGAAAGCTGGTGCTGCTGCTGCCTGATTCCCGCCGACAGACCTTGGGACCGGGGCC AACACTGGCAGCTGGAGATGGCGGACACCGAGATCCGTGCACGAGACTAGGTTTGA Sequence 42

CCGCGGTGGCGGCCGAGGTACCCTTTGCCTCCTTTTGTGGGGAGATATCTGGAAAATAGC TGAACAAACTCTACATGTGGCAAAACAAAGTGACAGTTGTTATAAAATGTCCACTAAAAT TACCTGCTAGCATTACTACGTATAACTGAAGTTTTTGCATATCCGCATAAGAAGAAATCC ACATTACAAGGAAAAGTACACCTGCCCG

Sequence 43

CAACTTCGGCGCCACCCAATCGCTCACCTGGAACGGCTTGCGGATCAACCGTTGCTGCGA TGCCAGATNCACTTTGTCCTGCAACTTGGCGAGGAACACCGGGTCGAGGGTCGACGGGAA AATCTCGCTGAGTTTCTGGTCTTTCAAATCATTGGTCAGGATCACCGGTGGATAACTCGC CAGCCCCGACACCAACTGGATGTAGGCCTGCTTGTTGTTGTCATCGGTCAGCCATTGCAC CGCTTGCTGCTGCGCCTTGAGCAACGTGGCCACGGCTTCAGGATGCTCATCGACAAACTT GCCGCTGCCCACCAGCACACTCTGGATACT

Sequence 44

Sequence 45

AGTATTTTCTGATGCCACAAGCTTACTAAGAAAATTACTTCTAAAAATTGGTNATATAAA TCATCAATGGATTTACCCTACTTTAAAAAAGAGGGGTATCTGGNTTTCTCTTACATTTAA TAACCTGAAAATGGAGGTCTATAAAAATATTTTTTAAAAAAATACAGNGACNCCTGNTGGA GGTTTTGGTAGGGCCCCTTGGTTTTTTNAAN

Sequence 46

Sequence 48

CCGCGGTGGCGGCCGAGGTACAAGAGAACAAATTAAAATTGAAAAATTCATTTCACTTAG
AAAAACTTCTAGGAACAGGGTGAACCACTGATTTTAATTTTGCCTAATTATCTTATGACAA
GTATCAAATTAAGATGACACTTAAAGATCCTTAGCATTAACTTAATGATGAGAAGAGATG
CTCAACAGACAGTTCCCAGTAAGGTAATGAGATGCCATTTTCAGAGACACTTCTAAGAAGA
TATTTTGATTCATTAAAACATTAAATAAAAAAGCCCTCCTCAGATTGGAACCCCCCAAATCG
ATGGAGCCACATTAATAATACTTTTCATGCCTCACTTTGACATGACAGGCATTTNGATTT
TTTTAAAGATCTTTAATACTTT

Sequence 49

CGCNGGCGCCGCCCGGGCAGGTNCGAGAAAAGAGCTAGGGTAGGCAACTTAAACTTACA
CAGTGCCAGTCTCAGGAGGTCAGTAGCTCACAGAACTCAACAGATAAACTGGATTAAAAC
TTAAAAGTCTTCTTTCTATTTGAGCCCATAATGACTATTTTGAACATGGCTCTTTTGCTG
CTGCCTATATATAAATTTTTTATTAATTTTCTTGTATTGGGAAGATCTTGAATACGCTCC
AGGATGAGAAAAAAATACGCTGACACTGCTAAATCGGGTATATGTTTTTTGCAATAAAG
AACACTGGTCAATATACAACTGAGGAAAAACTGAAACAGATGTGAGTCCTANAACCACAA
GAGTTTGAATTTGCCCAGAAATGCTATTTTAAACACTCTATATGTTGGCTGCTGTTTTTT
GGGGGAATAATGCATTCTTGGCATCCTTAAAAGGTTTCAATATGTTACAAAGGTTATCCCG
GAAAGAGAAAAAGC

Sequence 50

TTAGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCCTCTGTCTTCTGGACCAG
TCAGTCTATGAGCTCTTCTTTGAAACAGTCTTAGACCCAGAATGGTCATCTCACCCCCAG
AAGACATGGTTTCCAAGGGTGGGAGGTGTTAGTTATGGGTGCCGAGCCCCACTTCCTGGG
CGACAAGGCAAAGGTCAATTTCTCCCTGCTTCAAGAATGAAGAGGGAACTGGTGCTCCTT
GAACCAAAGATTCTTGGAAGGGTCATTGTCACCAAAGTGGCTGGTGTGGGCAGGAGCACC
AAGTGCAGACAAACCCACCGGGGCCTGGCGGGGCAGCCCTGTCATGGTTTCTGTCTTTGT
TCCTGTTAGTGAAACAGAAGACCCCCGACCCCCGCCACCTAGCAGCATGGAACACCTGCT
GCCCAGATACAGACAAGGCTCTGCTTTGTCTCCTTGTGCTGGTTTTTGGCAGAAACGTTA
AAGGGGCTGAAGGCCTGTGGGACAGAA

Sequence 51

Table 1

TTTCTTGAGGCTGCCCTCTATCATTTTATCTTTCCCATGGGCAGAGATGTTGTAAGTGGG
ATTCTTAATATCACCATTCTTGGGACTGGTATACATAAGGCAGCCGTGAAACTGGAAAGT
CATTTTGATGACTGATGTGATACATCCAGAGGTAAAATGCATTTAAACATATTAAAGGAT
TTGCCAAAGATCAATTTTCTTGCTGACATAAAAATCACACAAACCAGTCCCCCCAAACC
ACAACTGNCTCTCAAATAGCTTAAAAAAATTGGAAAACATTTTAAGGATTTTTCAAGGTT
TCTAGATTTTNAAAAAGGATGGTCAGCTTTTAGAGGGNATGGTNAAAAATTTT
Sequence 52

Sequence 53

Sequence 54

TTÁGGGCGAATTGGAGCTCCCGCGGTGGCGGCGAGGTACCTCACGCGCATAAATTTGC
TGCTCCTATTTTTTTCTGTTTATGTGTTTTTTATGGATCTAAGTTAAATCTTTTGGCAAT
ATATAAAAATGTAAATAGTAAACTTTATTTATTTATTAAGAATGTCATCTTTTTTAATTTATAT
TTACACAATTGTTCATCTAATTTATTTTTTCTATACAGTTTTAAATACTCAGACATATTT
TGCTGTTCATGATATTTTTATCCTGTTCTCATGGATTTGTTTTCCCATACTGTTTTCTCT
GATCTCAATTACAGGTTGGATCTCACAAATAATAATGTCAGAGACAGAAATATTTTGCCA
CTGTTGATTACTATACTTTAAAGTTCTATATTATGAAAAATATATAATAGCTTGTACCTGC
CCG

Sequence 55

Sequence 56

Sequence 57

ACTTAGGGCGAATTGGAGCTCNCCGCGGTGGCGGCCGAGGTACCCCGTTCTGCCTGAGCA
TTTTTTCCTAAAGGGAAGAATCAATAGTTTCTGACTGTTTTAACAGCTGAAAGCTCCAAC
TGGAGGCAGAAGATGGGTTTTCACACACGTGCGTGCAAGTTTAGCCACCTCCAAA
GGCCTTGTTCTTAAAGCA

Sequence 58

CCGCGGTGGCGGCCGAGGTACTGGGAAAATTTATAGAAATCATCTAGTCTTACCCTTCAT

Table 1

Sequence 59

CTATAGGGCGATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTCGTAAAACAAGGATCAT
CGATGTTGTCTACAATGCATCTAATAACGAGCTGGTTCGTACTTTTAGTAACAGTTCAGA
ATTCATCTTTATCTCCTACCTGCCTCATCGGTGGAAGTTTAAAGTCATGATTTTTTTAG
ACATTGATACTTGTGTCTATAGACAAATAAACTCATATTAGATGACAATTGATTTTTTAA
AAGTCCAGGTAGAGAAAGGAGCAATCATTTTGAACTAAAATCTTTCTATGTTTTTTGATT
ACTATTCAACTTGCTATTTTTTAGCAAAAAGCCGAAGTTTCAATTAGTGTTCATCTCAAA
TCTTATTGCTTTCAACCCGGGGTACCTGCCCGGGCGGCCGCTCTAGAACTAGGTG
Sequence 60

Sequence 61

TAGGGCGATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACATTTTTGAAAAGCACAATAAC
TTGTATTNTTTGCACTNAACACAATGAACCTTTANTNTCCAACCAGTTTTCATTCTCTGC
ANACCCGGGCTTTNTTTTTATAAAAACTGCTTTCAAAAGGCATAGAGACACCACACATGG
TCCACAGTAAATTCAAATAGAGAGGNGCAATAGTTGCAGTGGTAAACACACAAAAAAATA
CATTTTTTTGGACTAAAAATCTGGTCACGGATAAAAGCATGTGCCTTTTCATTCTTCTCT
GGGATGTTACAACAGCAACACGCTCTAAAACAATTAAGTTACATGCCTAATGCTAAAAGA
AATGTGAGCAATCCTATAACCAGCT

Sequence 63

Sequence 64

CCGCGGTGGCGCCCCTCTGAAGACCTCCTTTTTGGGCACCGGACGCCAGGTGTTCTA CAAGTATGGGAAACTCTCCAAGTTATCAGAGATTGTCTACGACAGTACCGCCGTCACCTT CGGGTATGACGAGACCACTGGTGTCTTGAAGATGGTCAACCTCCAAAGTGGGGGCTTCTC CTGCACCATCAGGTACCGGAAGATTGGCCCCCTGGTGGACAAGCAGATCTACAGGTTCTC CGAGGAAGGCATGGTCAAT

Sequence 65

Table I

ACCTGNTTTTNAAAAAATTTTTTTTNACCCANCAAACCCTAAAAAACCTGCAAAANGGG GGTTGGGTTTTANNTTTTNAAAAATTNTGGGGAAAAATTAAAAANTTTCCCAAAGAAACC CCCTTTTNGAACNTNNTNCTNNNNANNCNNNAAATTTTAANANNANTNTTAAAAANTTTT

Sequence 66

CCGCGGTGCCGCCCGGGCAGGTACGTGGAGTCGCAGCTGCAGCGCACAGAGACTGG AGCGACGGACCGTCACGCCCTCAGAGGCCCCGGTGCTGGCAGCTGAGCCCGAGGCTGA CAAGGCACTGTGTTGGCACTCACTGAAAATAACTTCGATGACACCATTGCAGAAGGAAT AACCTTCATCAAGTTTTATGCTCCATGGTGTGGTCATTGTAAGACTCTGGCTCCTACTTG GGAGGAACTCTCTAAAAAGGAATTCCCTGGTCTGGCGGGGGTCAAGATCGCCCGAAGTAG ACTGCACTGCAACGGAATATCTGCAGCAAGTATTTCGGTACCTCGGCCGCTCTAGAAC TAGGTG

Sequence 67

CTCCCCGCGGTGGCGGCCGAGGTTTTTTGTTCAATACATTTTAGATTAAGGATTGACAAG TAAAGATACTGCTATGGAATGATACATTGTATTTTCTGCATTGTGTGAAATAAGTTTTTA TTGAAAGTCAAGTGACATTTCAAAAGAAGTTCTATAACAATTATGTTTCATGCTTAAAGT AAAAATTCCCAGAGTTTAGTTTAGAAAATGTAATCTTTTAAATTTCAGACTGATATATTC CCAAGTATTTCAT

Sequence 68

CGCACATTCACTCAAGCATACATACTAGACATAAAAATTGTGCAAGATCAAGCATCAGCT TTCTATTTTAAAAGCCTTAATTTAAAAAAACTTAGATAGGCTCACTGCAGTTCCTTTAAA GACCTTCGAGGGGGGGGCCCCGGGTACCCAGCTTTTTG

CCGGGCAGGTCCAGGGGTAAAAAAACCCTTGTGAATCCTGCACACATCCCTTCCTGTGT TGGTGTTTCCTTTAGACTGGCCTAGCCTGGGCATCACTGTAAAGTATGTGCAGTTGGTCT CTGTCCTGTACCT

Sequence 70

CCGCGGTGGCGGCCGCGGGCAGGTACAAAAATACCAGTGCTTGTTATACTAGTTACTA AAAGAAGAAGAACTCAAAATTCCTATCTGCGTGCTAATTTGAAAAGAACAACGTAGATA GATTTGTTGGCACATATATATGGCATATTCACATATGGCATATATACATATGGGGAGAAA ACATGAACCAAAGGCCAATTCAGTTATGGGAGCTCATCTCCTTCCATCTCCTAATCAA GAGCAAAGGGAACAGCAAGGCCTAACAGCAGGGTTGGGGAAGGCAAAAGGACTGGGCACT GAACTAAGTGAAAGGGGCGTCTGGTCTTATTTCAGAGGAAGAGGCTGGAATTGGGCTTT

CTCCCGCGGTGGCGGCCGAGGTGTGCTATAGACGCACAAACGACCGCGAGCCACAAATC AAGCACACATATCAAAAAACAAATGAGCTCTTATTTTGTAAACTCATTTTGCGGTCGCTA ATTCAGGGACTCGGCGAGCATGCACTCCGGCAGGTACCTGCCCG Sequence 72

TACTATAGGGCGAATTGGAGCTCNCCGCGGTGGCGGCCGCCCGGGCAGGGTACCCCTGCT GCTGGCTGGGTTCTCAGCCCCTGACCATGAAATGGTTCCACATCGATCTACAGAAAAAAC AGCCACTTTGGCCCGTGGGCCCTGACGCGTAATATCATTATGGAGTCAGCAGCGCATCCC GTCCCATTATCGCCTGGCCAAGCTTTTCCAAGGCCAGCCTGGCTGCAAATGGCTTTCTCC TGTCTAGGGGGGCCACAGCCACTGTTTGCCCTCCACTACCGGAGGAGAAATTTTATCTTT AATTGACACTGCCTGCCACCCCCTTGCCTTCGGCTGGCCCAGGCTCCAAGCCCGGA TCTTTTCCTTACACTTCAGGAACAGGCTTCCCCTGGCTTCTTCCCCTTCTTCTCGGCAATT CCCGTCCTCACCTTGGTTGTTCTACACTGGCCAAGACAGTCCNGGGGGGGNGGGTCTTTGG CCTTT

Sequence 73

CTGAGCCGGGAGGAGCTGGAAGCACTCTTCCTCCCCTATGACCTGAAGCGGCTGGAGATG

TATTCACGGAATATGGTGGACTATCACCTCATCATGGACATGATCCCGGCCATCTCTCGC
ATCTATTTCCTGAACCAGCTGGGGGACCTGGCCCTGTCTGCGGCTCAGTCGGCTCTTCTC
TTGGGGATTGGCCTGCAGCATAAGTCTGTGGACCAGCTGGAAAAGGAGATTGAGCTGCCC
TCGGGCCAGTTGATGGGGACTTTTCAACCCGGATCATCCGCAAAGTTGTGAAGCTATTTA
ATGAAGTTCAGGAAAAGGCCATTGAGGAGCAGAATGGTGGCAGCGAAGGATTGTTGGTCA
TGGGAGCCCACGATGAAAGACCCTCAGTGACGACCTAANATGAAGCAGCAAAG
Sequence 74

Sequence 75

Sequence 76

Sequence 77

GGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACTTTTTTTCTCTTTGA
AATCTCATAGGATAGTCACACTTATAAACATTCCCAATATTCGGATTCTAGAAGAAATGC
AATTCATTAAAATTTTCCTGGCACTGAGAGTTAATCTTTAGCAGATTGCATGAAAATACT
GAATTCCTGGTAAGGAGATATTTTGTTTTAAAAATAATGTGTTTTGATACGAATCAGTGT
ATTAACTGATAACTAAAAAGTACCT

Sequence 78

CCGGGCAGGTACGTTGAACGTTTATTACAACTAATTGGCGATGTGATAAGACAGTGCTCA CGTGGCCTGAATGTTGGTCACAATCACAACAAAGCTTAATCCAGCCCAGCATATATAAGT GAAAATATAAACCATGAAGACATGTTTAGATATGTATAAGTACCT

Sequence 80

Sequence 81

GGTACTTTAACTTTTGAAGGTGGTTTCTGGTTCCCCCAATCGGTGAGCCCAAAGACCTCA

Table 1

Sequence 82

Sequence 83

ACTTAGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACCCTGTGCGTA
GGTGGAGCGGTTGAAGCAAGGTGGGTGTGAAGCCCCGAGAGTGGTGCTTTGGTCGGACTG
GCACACTCCGGGCAGCTGGGAGAGTGACAGGGAGGCTGAGAAGGGGCCCGCTGGATCCCG
CAGCTGGCGCGCACATAGTGTCTCGCTGCCCTGCTTAGGACAGTTCTCTTTGCATCCGTGA
GGAGCCAAGACAAGTCACAACTGCAAGTGAGGGGGTTGCCAAAGAGGTTGATCGATAGGA
CCTGGGAGGAATCCAGGGTCCAAGGAGGGAAGCAAGTTCCAAGTTCTGGAACAGAA
GGACCTATAGATGTGGAGTATCTTGAAAGATGTGTGTGGCGACAGAAGCAAGTGCTGGGG
GAGTCTTGACAGTCCAGCTGTTGCAGGTGGGGGGTCATCTTGAAAAATGTCCCCCTCAGG
GGTCGTCAAGCCGAGGCATNTTCACCTNGGNCCGCTTTAAAACTAAGTNGGATCCCCCCG

Sequence 84

Sequence 86

Sequence 88

Sequence 89

Sequence 90

TACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACCGAACAATG
ACAGGGGAAGGGTATTGGACACGGCAGCGTCCTCCTTATTGAAAACACATTATGTCAGTT
GGGAATTTTAAATAAGCTTTTAGCAAACCTAACACTAAAAGCAAAATANAAGAAAGCTAT
ACCATTACCATAATACATTTTTCATCTCATGGCTACAATGGAATTNTTGAAAAGGAAAAA
AAAATCCTATCTACATATAAAAAACCTGCATGAATGAATCACTACATATGCTTATAATGAG
GAAGAGTTATGGGTCCTGAGTGTAATTTTTTATCCTTTCTTAAAAAGTTTCTGTATTATG
CATTTTTGATAACACTCTGATGATCCTTCCCTTACATTTGAAATGTTATGTACCCTNGGC
CGCTCTAGAACTAG

Sequence 91

Sequence 92

Sequence 93

Sequence 94

CTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTTGCTGAAATTGAGA CTCTTCTCCCTTTTGAGCAGAGGTCATTTTCTCTTGACATTGAATTCCAGTATTTGTGCA GAAAAGAGGTGTCAATGAGGACTCCATGGATACTTTCAGTTGATCAGTATTGGCTCTGCT

GCAGGGTGATTTTGGCTTCACACATAAATGTTGCAGTGGCATTTGTCCAGGGGAAAGCCC GCTTGGAGGCTGTAGGATGACCCTGATGGAGGCTGTCACTCAAACAGCTCCAGGTAGTCA GGCAGCTGGTCCTGACCACAGGGATAGAGAAGGAGCTCCTTCCCCGGGGAAGTGATG GGTT

Sequence 95

Sequence 96

CCGGCCAGGTACCTAACCTACCTTTAAGACTGGGATAACTATTGGAAACAATAGCTAATA CCGGNTATAGTNATTTATCGCATGATGAGTAATAGAAAGGAGCTTCACAGCTTNACTTAA AAATGGGGGTGCGGAACATTANTTAGTTGGTAGGGTAATGGCCTACCAAGACGATGATGG TTAGCCGGGCCGAG

Sequence 97

Sequence 98

TATNCTGGAACTGAGCATAGACCTNTTNCCAGGCAGAGCTGACAGCAAGTNAAGGAGATC ATAATCATGGGGACCAAACAACTTTGNCTAAAGTGTGAATGTNACCTAAGGAGAAGCTGT GAGATCAGAAGGGNGGGGCAGAGGAGCACCATGAGGGAGAGTCCTTGGGGGTACCT GCCCGGN

Sequence 99

Sequence 100

GGNAACCCCCCCNGNGGCGGCCGCCCGGGCAGGNTCNCTTAGGGGGGGGGNAAACCACC CCCCCCCNGNGCGAAAGNCNACCNNNGATGTTTTCAGNTNCANGGGGGGAANCNCCCNG NAAAACGGGNGNGCAGGCNGNAANNNNCNNNCNNNANAAANNCNGCAAANCNAAAGAACG ATTTTTCC

Sequence 101

Sequence 102

Sequence 103

CCGGGCAGGTACAGTTGGATTGACTACAAAAAAAATTTAGGCCTTGTCCATTTATCCAGA GGTTTCCTTCAAAACTTTTAAAAAATTTTATCACCTAAAATGGATTTTAAATTATCAGAA TTTAGATGTAGCAATTAAGTAAATCTTAAAGGAGGTGTAGAATTCCTTTAAGAAGTTATT

Table 1

Sequence 104

Sequence 105

AACCCCACCGCGTGGCGCCCCCGGGCAGGTACTTTTTGCCATGTCAGTNATGACTCC
AATTTTCTGTGTGCAAGAGCAATCACACGGAAGCCCTGTTTAGTGAAGTCTTCCAAAACG
TTTTGAAAATCGACAGGAACTGTTTCAGGTTTACAGAGACCGGCAATGGCCTCGGGCGCT
CCTTTNATGTAGGCNTCCATTTTCCTATCCCCCAGCACCCTGGCAACCACACTCATACGT
TGCAAAGCAGAAGAAAATGGGAACTGGCGAACAATTCCTATCTCATAAGTAGCTGGAAGT
TCAAACAGCTCCATTTCTTGGTTTCCTGCAGGGGTAGATTCAGGAAGCAGTTGTTTGGGA
GGACGAACCACTGTGGGCA

Sequence 106

Sequence 107

NNNAANCTCNCCCNCCAAACCNNNCCCGGGNNNNNNNNNGGGGGGGNTTTTNTTGGGGGGA NGGGGNNNNNNCCCNGNNNNNNNNGGCCGCCCGGGCAGGTACATTCNCAAGGGTTGGAAC CCAAGCCCCACCCTGGGTTTTCTTAAGTTCATTATTCCCCCACCCCAGNAATTCCCTTGG GAGTTCCTTGGCCAGAAGCCATCAGAGACAGCAGGCGAAAAGCAGGGCTTAACTGAATNC CATATTGGGG

Sequence 108

AGGTACATCCCGAAAGACAGCAAAAAGAAGAAGCACCGAGCTGAAGATTACTCAGCAGGG CACGGACCCGCTTGTTCTCGCCGTCCAGAGCAAGGAACAGGCCGAGCAGTGGCTGAAGGT GATCAAAGAAGCCTACAGTGGTTGTAGTGGCCCCGTGGATTCAGAGTGTCCTCCTCCACC AAGCTCCCCGGTGCACAAGGCAGAACTGGAGAAACTGTCTTCAGAGAGACCCAGCTC AGATGGGAAGGGTGTTGTGGAAAATGGAATTACCACATGTAATGGAAAGGAGCAAGTGAA GAGGAAGAAAAGTTCCAAATCAGAGGCCAAGGG

Sequence 109

Sequence 110

Sequence 111

CCGGGCAGGTACTACCATTTAGGAAACTGCTATAACACATAATTTCATGAAGTAACACCT AATACGGTGTAGTTCCCTGGTCATATTTTATACAATTCAACCATATAAAAGGGTGTCACT GTAATTTCAGTAGTGTGGGTTTACAAATAATCTGCTGGTTAGCTTATTACCTTGAGGTTT TGAAAAACTAGAATTATATTGAGGCATTTCATAAACATATCTCTTGCACCCTCTTCATGG TGGAGTTAAGGATAACTTGCAGGTGGTTGGCCAAGGCCCAATATAGATGATTATAACATT

Table 1

TAGAATTGGCAATTAGAAGTTGATAATCCATATAGGACCATAGG

Sequence 112

AGGTACCACCTCACATTCTTTAACACTTAAGGTTTTTCTGGGTAGTAAGTGCAATACAT
TCTTATTATAAAACAATATGGACAGTTCAGTATGTATAAATGAGGATAAAATCAAAATCA
CCCACAATCTCACCACTTTGTGATAATAACCATTAACTTCAATATTGATGAATTTCCTTG
AATGTTTTATCTACAATATTTCTTTCATATAGTTGATATCACTCTGTATGCACAAACTTG
TATCCTTTTTCTAAATCTTAATATCATAATATTAGCATTTTCTAATGTTAGTAGATGTAC
CTGCCCG

Sequence 113

Sequence 114

AGGTACTGCACTGGTCATTGATAAAGATGTATTCAAAGGCTCACTTAAAGACTTCGAATA
CAAGCTGATGGGAATCTGATTACTATTTTCACTGCTTGGAGCTGATCCAAATTCAGAGAG
AGAAGGTTCTGACCCAAATTCCAGAGCCCCAAACTGCACATTTAATCCTGTGACATCTGC
TGAACCAGGCATTTCCACTGCAGAAGCTGGGATCTTAGAAGCTGGGGGTATCCGCCGCTT
AGCAAGTTTGATGTGTTTGGGCTGTGGCTGGTGACACAGAGATATTTTCAATGGT
CGTGCTGGGAAGCTGCAAAAGCTTGTTCACAGTGGAGGACTGTC

Sequence 115

CCGGGCAGGTACCTGGTTCTACAGATGGTTCTCATGCACAAAATTTCAGAACCACATTGT AGAAAAGTAAAGCAGTATGACATGCTTTGGAAACTGCAGATAATTTAGTGCAACTGTATT ACAGGTTACAGATAATAAGAGATGAATCTGGAAAAGAAAAGAATGTTATGGTACCT

AGGTTTTTTTCACTNNCGTATTGTTTATGGAAGAAGAGATTAGAGGACAATACAAGTAG
CCACAGCTATGATGCATGGAATACTACAGAATATGGTGAAATGCTATGTAAGGGCTAGAA
ACAATTCATTAGGTGTACCTGCCCGGGCGGCCGCCCGGNCAGGTACATGCAAATCGCCTG
TGGTAGCCATAGTCACAGGATGTGTCTTCAAGACAGAAACTTGCTTTGTGGCCCTCAGCC
ACTCTCCTNTGGGTGTTGNCATCAAGCANGTCATAGAGNCTAAACTCATCCATACTGTGG
NAATG

Sequence 117

CNGGGCAGGTACCTAACCTTTAAGACTGGGATAACTATTGGAAACAATAGCTAATA CCGGATATAGTTATTTATCGCATGATGAGTAATAGAAAGGAGCTTCACAGCTTCACTTAA AAATGGGGGTGCGGAACATTAGTTAGTTGGTNGGGTAANGGCCTACCAAGACNATGATGT TTAGCCGGGCCGAGAGGCTGTACCT

Sequence 118

Sequence 119

TTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTGGAAGAAATTGCCAAGGA CAAAGTTTTAAAAGACTTTTATGTTCATACAGTAATGACTTGTTATTTTAGTTTATTTTGG

Table 1

AATAGACAATATGGCTCCTAGTCCTGGTCATATATTGAGAGTTTACGGTGGTGTTTTGCC TTGGTCTGTTGCTTTGGACTGGCTCACAGAAAAGCCAGAACTGTTTCAACTAGCACTGAA AGCATTCAGGTATACTCTGAAACTAATGATTGATAAAGCAAGTTTAGGTCCAATAGAAGA CTTTAGAGAACTGATTAAGTACCTGCCCG

Sequence 121

GAAATAAAAATTAGCAAACAATTATTCTAGGGATATTTTCAGATTTTACTTCATTTCTTG
AAATGCGNGTGCCATATGCAATTGCATTTCTTGTGCCAAGAAACTAATAGAACTTATTTC
ACTTTACCTTTTTTTAAAATGTGAATTTAGTTATTATAGTTTCAATTTTATGGCCTTACA
GATGGCTTTTATTTTGTTTGCAGCNTGACACTGCAGTTCCTTTCATGCAAAATACCCATA
AACTGTTTTGATGGAAAAATTCATTGCCCCTTAATGGGAAAACCTCTCTAGTTTTTTCCC
ATTATAAACTANTTCCCTACTGNTACCCTGCCCCCGGGGCCGGGCNCGCTTTTCGACCCA
AACCATTNGTNGGGTNGAAGCNATTTTCCCAACGGGNGCCGCCAATTGGAAANGTCCTNG
GGGTNGCCTTGGTGCCTTNCCGAAGTCNTNCTTGGNAAATAATTTTTTTTGGATANGGGAA
AGCCGGACCANAGGGAAAAAAAATTT

Sequence 123

TACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACAATAAAGTT
CACCCACCTGCACTTTGGCCCTTAGATCAATCCTAAGTAGCCATTGCCAGTAGGCCAAG
TITAATCAGAGGACAGTGCCTACCAGTAAATACTGAATAGTTACAATAGTTATGTCCATC
CAACCAGTAGCAGATGAACAGCTAATACATCATGATGCTATGCTCTCCTAACAGGGTCCC
CTCAGATCCTCAGTGAGCACATAAAGAAAGGGAGGTCATATCCCTTACATCTCTACCAGG
TATTAACACCTAACTACTCTCTAGCCAGAGGCAATTCCCTTTATTTCCTTACTCTCGTCG
TCTTCTCTTTAGCCCAATCTCCTGACAATAGTTAAAACAAAAAGACCCCCAAAATATCTC
TTGCTAAAACAGAAGTAGTCCCTAAACTCTCTCATCTTAGACTACTGTCAGGTACCTCGG
CCGCTCTAGAACTAGGTGGATCCCCCGG

Sequence 124

CCGGGCAGGTACAAAGCACTGGAATTGGGGAAATAGCAGGGTGTTTCCCCCACAATTAGA AGCAGTGTTGCTTTTCATTTTCCTTTTACTGATTAGCACTAAGTAGACATTAACCTATAT GAATTTTTCAAAAACAGCATTTAGGGTCCACATTTATTTTAATTCTGATCTTCTCTAATC TAATTGGGTGAAACTTATGGTGAAAAAATATGCATAGTTACTTTTGACATAGATTTGTTT AAGCATGAAAGCTAGGAATTGATTAAAACCAATACATAATATTTAGTTTTGTGTTACTTA GTTTCTTTGTAATAGTGTGAGAATCATGTGAATTACTG Sequence 125

Sequence 126

AGGGCGAATTGGAGCTCACCGCGGTGGCGGCCGAGGTCGNCCGCCTGACCTGGGGCAAGT GCTTTCAACTCTCTGAACTTCGGTTCCTCATCTGCCAGTTGGCAGACGCTCAGCAAATCT TCCTAGACTCACGGGGCGAATTGTACCTGCCCGGGCGGCGTTAGAACTAGTGGATCCCCG N

Sequence 127

CTTAGGGCAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACATTCCCAACAGCATGTCCT TCCTGGTTCTCTACCCCCACAGCACTTCTTAGAGCAGAGGCAGAGCCCAGAAGCTGTGTG GGTCACAGGCAAGAGCTGAAGTAAGACCTGCAAGAGGCGGCAGGGAGCTAACTGTAGCAC

Sequence 128

Sequence 129

Sequence 130

CCGCGGTGGCGGCCGAGGTACATCATATGCCTGCTGAAGTGCTCTGACTTTAGGATGAGA AACTCTAACATAGGCCGGAAGACAAATAAACCATAAACTGTAACAATGACTAAACAGACA CTTGGCCCACTGTGGTGGATTTGTATAACATCTCTTCGCCAATTTATGAGCTGTTTTTAT TTCCTGTTTAGTTCTCTTAGCCATGAGAGGTGGACTCTTTGACCTGCCCG

Sequence 131

Sequence 132

Sequence 133

Sequence 134

CCGCGGTGGCGGCCGCCCGGGCAGGTACAAAGCTTATTCACATTTTTACTAAATCCAACA CAACTTTCACAAATGGCAAAATGATTGCCTCTTCAAAGCAATGCAGCCTAGTTTTTGGTG

Sequence 135

CTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTGGCCTCTTTGAGTATGA
ATGAACTTGGAAGAATAAAGCCTTCCAGTTGGATGAAAGCACATCCAGCCTTTTGTGAGT
GACAGCTTTGTATATAATCTTATGCAGAGCTGATATGGATTCCCTCCAGGCAGCTCAAAT
CTGGAAGTTGTAAATGAATGGCTATGCCACCTTGGAGTATCACCATAATACATCTCTGCT
TTAGAGCTGATATACAGATGTGAAACGATCGAACAACATGATTTCTCATTCTAGTGCTCC
TTAGAAAGGAGTTCTGATAAGCCCCAAAGCAGACCTGGGTTGGAATCGTGGTTATTATTC
AAGTACCTGCCCGGGCGGCCGCTCTAGAAACTGGTG

Sequence 136

Sequence 137

Sequence 138

CTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCAGNGCCCNTTTTCAGA
CAGTTNTNGATTCGCTCTAGACTTTTTTTTTTTTTTAATAGGGAGGAAAAAATTTGATA
ATTTCTTTTTCTACATGCACTTAAGACTAAAACACAGGTTTGGATTAATTTTATTTGC
TTCCTTTTTCCGCTTTTCTTCCCGCAGAGCCTGATGGGAGAATGTCCAGGGCAGGGAAAC
CACATTTTTTGTAGGTGATAACTCAATGAAAATTGGTGCTTATTTTTTACACTTCTCTC
TGTGGCTCTCTTGNGGTGCTATCTGTTTTAAGGTCTCCTTGAAGGCGCACTGGGGTCCCT
GGCCATGCCTCGTTCTCCCTGCTTTCTTTA

Sequence 139

ACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTGTGCTATAGACGCACAAAC GACCGCGAGCCACAAATCAAGCACACATATCAAAAAACAAATGAGCTCTTATTTTGTAAA CTCATTTTGCGGTCGCTATCCAAATGGCCCGGACTACCAGTTGCATAATTATGGAGATCA TAGTTCCGTGAGCGAGCAATTCAGGGACTCGGCGAGCATGCACTCCGGCAGGTACCTGCC CG

Sequence 140

Sequence 141

GACTACTATAGGGCGNATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACAGATTGTTCTCA AGAGGGCCATCAGAAGGAAGCCAAAGAGTTCACAGCCTCAGCACCAACAACTCAACATGG TCATCATGTTTTCTATATGGTTTTTCCAGCTAGCAGTACCTGCCCG

Sequence 142

CCGCGGTGGCGCCCCCGGGCAGGTACCCTGAGAAGCATGGGGCAGTAGAAAGAGCATG TGGGCTTTAGAGTTCAAACCAAGTCAGGCTCAAACATAGTTCTGTGATAAGCCCTGAGCA

Table I

AGTTACCCGGGTCTTCCATTTCCCCCTTCTGGAGAAGTCCTTTGGAGGATGAGTCCTTCT GGAGGATGAGTCCTTCTGGAGGATGAAGTCCTTCTGGAGGATGAGTTCGTTGTAAGAATA AAATGAGAATGTAAGACACCTAGAGGATGCCCGAGTAAAAAATGACAGTTGCTAGTAGTA GTAATTTGTAGGGCTCATTATCTAGAATAATTTTGTTTGACGTTACTAATTAAAATGAAC TCTTAAAGAAAAGCAGTGTATTTAGACTCTTGTAGTTAAGAAAAATTACACCACAGAGCC CTTTTTACTTTTTAAATTCATTTTTACATTTTAAATTCATTGCATGTATTCATTATG

Sequence 143

TAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACTATATTAAGTGGT
TCTATAAAAGCTATTCACAAGTTCTACTGTGATGGACATCCTCATCATAGACAAACCTCC
CCTGTTTTATCCTCAATTTCTAGTTACAGAAATTTGGTGATGCTTATTTTTTGCCAATTTT
ATGTCAAAATAAGNTAAAACTTCCCTCCTGTTCACCTCTTTGGGTCTCTATCCTGTGTAAC
CTNTGGTGTAGTATTTGCCCATAGGCAACCAGAGCCACTTCCTCTGAACCCAACATCTNC
TGGGGACCTTCGCAGCANGAGGAAAGCACTGAGACAATAGCTTGCTAAGCAGGGCCCAG
NGGTGTCTCAAAGAAACCATGGNTGTNCTCGCCACTTCCCAGGGNGGGTGANGNGAGCTC
GGGAACATAACGATGGTTTTG

Sequence 144

Sequence 145

CCGCGGTGGCGGCCGAGGTACCTGCCGGAGTGCATGCTCGCCGAGTCCCTGAATTGCTCG CTCACGGAACTATGATCTCCATAATTATGCAACTGGTAGTCCGGGCCATTTGGATAGCGA CCGCAAAATGAGTTTACAAAATAAGAGCTCATTTGTTTTTTTGATATGTGTGCTTGATTTG TGGCTCGCGGTCGTTTGTGCGTCTATAGCACCCTTGCACAATTTATGATGAATTATGGAA ATGACTGGGACATGTACCTGCCCG

Sequence 146

ACTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACAACCTCATCAATGT
CTCTAAAACTAGGTCTTGAATCTAAAATGGAATTATACATAGAACTATTACATGAAGCAG
TTCTTTCACTACAATCATTTTTAGCCCCCCAGTGACCAATCTCCTCAGGTAAACAATGTC
TAATGACTGATGATTGTTTACTGTATGCCAATTACTGCTAAATCCCTCATATAGATTATC
TCATCTATGAAGACACAAGGATTATTAATAACCCCACTTCAGAGATAAACAGACACAGGT
TAACACATCTCGCTAACACCTNTTGTAAGTGAAAAACCAAGTTCAGAGCCCAAAAAGTT
Sequence 147

Sequence 148

Sequence 149

CCGCGGTGGCGGCCGAGGTACAGAAGTTAGAATTTTTGACTCCAGGCAGCAGTTTGCTCA GTGATCTTGAACAAGTTATCCAATTGCCTCTACATTTGCATCAGTTTCTCTAGCTGCAAA

Sequence 150

CCGCGGTGGCGCCGAGGTACTCAGGTGACTTTCTGGTTAAAAATATTGAAGACGGATGA
CAACTGGGCTTTTTTTACTTTGACAACTGAGACAAAATGACAAATTGTCAGTGTTCAGAG
ATCCAGACCAACTTCTCAAAAAAAATATGTTTACCCCTGATATCATCATTATTTTAGCCCA
ACTGTGCCTTTTTGGGGGGGATCACAACTCATTACTGGCTTTTTTGTTTTAAAGNTAAAAA
TTTTTTGGGCCCTTAAAGCNAGGGGGTTTAGGGNANNATAACNCCCCCTTNTNNNNGANN
GGGGTTNGAAAAACCCAACCCCCCTTTTTTNGGTCCNCGGGGNGGCCCAANNCCCTTTTT
TNTTTCNTTAANGGGGGTTTCCCCCGGGGGGGGGGCCTNTTTTTNTNGGNNGNNGNTA
AAAAAAAAAA

Sequence 152

CCGCGGTGCCGCCCGGGCAGGTACATTATTTTGATGGACGAAAACGGATGATCTTG AGCACTATTTCATGGATGGAGGAAAAAATCCATTTTTGGGGATTGCTTACATCGCTGTT GGATCCATCTCCTTCCTTCTGGGAGTTGTACCT

Sequence 153

Sequence 154

Sequence 155

Sequence 156

CACTACTTAGGGCGAATTGGAGCTCNCCGCGGTGGCGGCCGAGGTACTCGCGATGCCCCCGAGTGGCCTCTCGCGCTGCCAGGGCTGTCCCGGGCCTCCCGGGGACCCAGTGGTGTAGGCACCGTGGACCATGTTGTAGGCACCATCCCGGAGACGCCGCTGGACACAGTATGCCTCATACA

Table 1

GCTCATCGATCTTGCTGGCATGGAACTCCAGTCGTCGCAGGAAGCGTTCAATGGACTTGA CTTGCTTGTCCAGATCATACAGGAAGCCCAAGCGGGAATTCCTCTTGGACTCCCTTATCT GCCCTGGAGTTTCTCTTGCTCCTGCTGGTGCACTTCCAAGTAGGCCGTCAGGCCCCGCT TCAGCGCCCGTGTACCTGCCCG

Sequence 157

CCGCGGTGGCGCCCCCGGGCAGGTGGCGGAGAAGTTTGACCACCTAGAGGAGCACCTG GAGAAGTTCGTGGAGAACATTCGGCAGCTCGGCATCATCGTCAGTGACTTCCAGCCCAGC AGCCAGGCCGGGCTCAACCAAAAGCTGAATTTTATTGTTACTGGCTTACAGGATATTGAC AAGTGCAGACAGCAGCTTCATGATATTACTGTACCT

Sequence 158

CTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACATNNAAATNATACGT TTTAATAAAATACATCTTTAGATCAAAGCTGAAAGAAGACATCAGTAGTAGATCAGAGNA TTCCATTT

Sequence 159

ACACTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTCTTGGGTCTGAAAG TCGATGAAGGACGCGATTACCTGCGATAAGCTTCGTGGAGTTGGAAATAAACTATGATAC GGAGATTTCCGAATGGGGTAACCTAACTGAGCAAACCTCAGTTGCATTTTGATGAATCCA TAGTCAAATTAGCGAGACACNGTTGCGAATTGAAACATNTTAGTAGCACCGGGAAAAAAA AAAAA

Sequence 160

Sequence 161

Sequence 162

CCGCGGTGGCGGCCGAGGTACCACAGTCTTGCACATAAGTGCAGATTTGGCTCAAGTAAA GAGAATTTCCTCAACACTAACTTCACTGGGATAATCAGCAGCGTAACTACCCTAAAAGCA TATCACTAGCCAAAGAGGGAAATATCTGTTCTTACTGTGCCTATATTAAGACTAGTA CCTGCCCG

Sequence 164

Sequence 165

TATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCCCCGGGCAGGTACATAAATATGGA AGAGCAGTTTGTAATATGAATACATTTTCTCTAGACGAGATCACAGTTTTATTTTGTAAA TATTACATTTAAGTATATATATACACACATATATGTACCT

Sequence 166

TTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACAAAACCTCAGGGTTATTTACGAAGCCAAAGGACTTTGCTATATCAAGTAGTTCATTTCTTATCTAAGACCAACTATAGGTATGATGCTACTGTATTCAGGCAATGCCGACTGGATTGGAACATGCTAATTTAAGGTGAGTTGGTACCT

Sequence 167

Sequence 168

Sequence 169

Sequence 170

TATAGGGCGAATTGGAGCTCNCCGCGGTGGCGGCCGAGGTACGAACCATGCTCGTTATTA
GATGCATTGTAGACAACATCGATGATCCTTGTTTTACGAGTACCTGCCCG
Sequence 171

Sequence 172

CCGCGGTGGCGGCCGAGGTACCAACTCACCTTAAATTAGCATGTTCCAATCCAGTCGGCA TTGCCTGAATACAGTAGCATCATACCTATAGTTGGTCTTAGATAAGAAATGAACTACTTG ATATAGCAAAGTCCTTTGGCTTCGTAAATAACCCTGAGGTTTTGTACCTGCCCG Sequence 173

CCGCGGTGGCGCCGAGGTACCAACTCACCTTAAATTAGCATGTTCCAATCCAGTCGGCA TTGCCTGAATACAGTAGCATCATACCTATAGTTGGTCTTAGATAAGAAATGAACTACTTG ATATAGCAAAGTCCTTTGGCTTCGTAAATAACCCTGAGGTTTTGTACCTGCCCG Sequence 174

Table 1

Sequence 175

Sequence 176

CTATAGGGCGAATTTAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACACGCGTCGCAA
TTCAGGATGGCTCTCTTGGATCTTAGCTTGCAACTCGGCCTCCAAGCTTGTCACAGACAT
GGAACTTTTCTGAGGAAACAGGGCACAACACAGGGGTGTAGCAAACACCAAACAGAAGCC
AACTAACCCAACTTGAATGGGTGCACTCATCCATGGGAACCTCTTCAAAAAGGCTTTCTT
TTCCAAAGTGTTCATAATGAATGGAGGGATGGCCATGCCAGGGGCTGCCATGAGAATCCT
GGACACGACAACTTGCGTGATGGCTTGTTTCGCAAGCGTTCGCCGACTCCCCAAGCGGT
TCCCATTCTCATTCCCGTGACGGGGAAT

Sequence 177

CCGCGGTGGCGCCGNGGTACACGAAGGTTAGAATTTTTGACTCCAGGCAGCAGTTTGCT CAGTGATCTTGAACAAGTTATCCAATTGCCTCTACATTTGCATCAGTTTCTCTAGCTGCA AAATGGGGATAATACTATATACCTACCTCACAGNGGGAGGGCAGGAGATTTTGAGGCCCT GAGGTTTTAGGTGGGCTGTGAGGGCCAACGCTTGACACAAAGTCCAT

Sequence 180

CACTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCCCCGGGCAGGTACTCATGG

Sequence 182

CACTNCTATAGGGCNAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACAATAA AGTTCACCCACCCTGCACTTTGGCCCTTAGATCAATCCTAAGTAGCCATTGCCAGTAGGC CAAGTTTAATCAGAGGACAGTGCCTACCAGTAAATACTGAATAGTTACAATAGTTATGTC CATCCAACCAGTAGCAGATGAACAGCTAATACATCATGATGCTATGCTCTCCTAACAGGG TCCCCTCAGATCCTCAGTGAGCACATAAAGAAAGGGAGGTCATATCCCTTACATTCTCTA CCAGGGATTAACACCTAACTACTTCTCTAAGCCAGAGGCAATTCCCTTTATTTCCTTACT CTCGGTCGNNCTTNTTTTTAACCCAAATCTTCTGACCAATAGGGTAAAAACAAAA Sequence 183

Sequence 184

Sequence 185

Sequence 186

Sequence 187

Sequence 188

CCGCGGTGGCGGCCGAGGTACATTTCTAAATAAATATCTTTGATCTATAACCCTTGAAAA

Table 1

Sequence 189

Sequence 190

Sequence 191

TTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTGTTCTTATAAAAGATTCT
TTCTCCCAGAATTATATCTCCTCAGAGCAACAGCAAGGTTCTCAGGATCGAAGCCTACTC
TAGCCTGAAGGGCTAGGAAGATTAGGATAAGGATAAGGATAATAATCCAAAAGTCTCGAC
AATTCCAGTAGTCTCTGGATGGCTCCAACATCATAGAAATTTAACACTGTTCCACTTGTT
TACAAAATCTAACACTGGCTTAGACATTCTGGACTTTCAGTGAGGGTTCCAGCATCTGAT
GTCCCTCAACTCCTTTCCAGGGTGAGAGGCCCACTTACAGGAAACTTAACTTCTCACCAT
GTGGACCCATGGAGGGGTTTTTCTCTTTGCAGAAAGGGCTAAAAAAGTGAGGAGGCTATGGA
AAAAATGGTGGGTCACTTTTAAGGCAGACTGTTNGGGTTGGGTGGGAATTTTT
Sequence 192

Sequence 193

Sequence 194

CTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGGTGGACCGTGAAANGCTGTAG
TTTGCAACCCTGCGAGTATGTCTGGATCACAGGAGAATGGTCAGAGTGCTCAGTGACCTG
TGGAAAAGGCTACAAACAAAGGCTTGTCTCGTGCAGCGAGATTTACACCGGGAAGGAGAA
TTATGAATACAGCTACCAAACCACCATCAACTGCCCAGGCACGCAGCCCCCCAGTGTTCA
CCCCTGTTACCTGAGGGACTGCCCTGTCTCGGCCACCTGGAGAGTTGGCAACTGGGGGAG
CTGCTCAGTGTCTTGTGGTGTTGGAGTGATGCAAGAGATCTGTGCAATGTTTAACCAATG
AGGACCAACCCAGCCACTTATGCCACACTGATCTGAAGCCAGAAG

Sequence 195

CTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACAAGTTGGGGTCATAATT

Table 1

Sequence 196

TACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTGTGCTGCACAGATTGATA
CATTAGCCTTTGCTTTTTCTCTTTCCGGATAACCTTGTAACATATTGAAACCTTTTAAGG
ATGCCAAGAATGCATTATTCCACAAAAAAACAGCAGACCAACATATAGAGTGTTTAAAAT
AGCATTTCTGGGCAAATTCAAACTCTTGTGGTTCTAGGACTCACATCTGTTTCAGTTTTT
CCTCAGTTGTATATTGACCAGTGTTCTTTATTGCAAAAACATATACCCGATTTAAGCAGT
GTCAGCGTATTTTTTCTTCTCATCCTGGGAGCGTATTCAAGATCTTCCCAATACAAGGAA
AATTAATAAAAAAATTTATATATAGGCAGCAGCAAAAGAGCCATGTTCAAAATAGTCATTA
TGGGCTCAAATAGAAAGAAGCTTTTTAAGTTTTAAATCCAGTTAATCTGGT
Sequence 197

Sequence 198

Sequence 199

CTACTTAGGGCGATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACTGATGAACA
CCAACATGTTCCAGAAGACCCAAGAGAAAAATCACAAGATGAAGTCTTGAGAGATGACCC
TCCAAAAAAAGAACATCTACGGGATACAAAGTCTACATTTGCTGGCAGTCCAGAGCGTGA
GTCCATTCACATCCTGAGTGTTGATGAGAAGAACAAGTTGGGAGCCAAGATTATCAAAGC
AGAGATGATGGGAATATGGAATTAGCTGAACAACTTAAAGTTCAACTTGAAAAGGCAAA
TAAATTCAAAGAAACTATAACACAGATACCAAAAAAAATCTGGGGTAGAGAATGAAGACCA
GC

Sequence 200

Sequence 201

Sequence 202

TATATTTACTATTTTGCAGTCTTCTGCTCTTAGGAATAAAGTGAAATTCAATCACCTGTA TAGAAAGTATTTCACACATGTTTGAATATATGTAGAATAAATTCCCAA Sequence 203

CCTTAGGGCGATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACAAAGCTATAAA GGAACGTTTTTAGAGAAAGCACTGAAGACACACATTTTGCTGACCTAAAAGATTTTAAAA TGAATTAGAATAATTTACATCATATAAAGAGGTATTTAGTCTTTAAGTGGAGAAAGTTGC TAGTCACATGTAAGAAAAACAAGTATTATGGGCCTTCCTAAGACAAATGGAATAAATTCC ATCACTTTTGGCTTTTTTATAAACCAGACTTCTAACAAATAACCATATTAATTTTCCAGT AATCAAACATATCCTAAAAGAGGAAAAAGAGAATGTCTACTTTTAAATCACATCCAATGT GAATTTGCGTGAATGCAAGGCATAAAATACCT

Sequence 204

Sequence 205

Sequence 206

ATAGGCCGAATTGGAGCTCNCCGCGGTGGCGGCCGCCCGGGCAGGGTACAGTGCCCCCTG CTTGTGGTGCAGGGGGGTGCCATTGCCGTGGTGCTTGGCATTGAGGGGCTGCAGGTGATG CATTGCACGGGACACCAGGTCACTCAATTCGGCGATGCTGCCTACGCGCGTGGCCAGCAA AGACTGCTCGATGGTCCTCAGCTCCGACTGGCTGAACATGGGCAGTTCCCCTGGACCT Sequence 207

CCGCGGTGGCGCCCCGGGCAGGTACCAAGCTAAAGAAGGCAGAGAAAGTTTTTG
AGGATGGTGTGTAATCGGTCACTATTTACTGTGTGAGTTCCACTGGAGACAAGCACAC
TTTCTCCAATCCCAGAGTCTACACCTGACTGGGAATTTTTCATTCTGGATTCTGATTGAG
GGAAAATACTGATATCCAATGGGCTATAAGGAGGACCTTTCAGTTTCTGTAACAGCATCT
GAGTTCTATGCATGTCCTGGAAAGGCACCTGCCCACTGGCTAATTCACATGCTGTAATCC
CAACACTGTAAATATCTGACTTCACATTATACCC

Sequence 209

ACTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGCCGAGGTTTTTACTAAATTATCT ATGTCAAAAAAATTCTGTGCCTGGCGTGGAATTTCACTCCATCAAGTGTTACAATGATTT TTTCATTTTCATTACAAGCAGGAGAATGAATGTAGGACAAGTGTTAGGAAACATGGCAAT AAATTAGAATATAATTTACAAAAGCAAAAAAATTAACAGTGTACCTGCCCG Sequence 210

TATGAGAGGAAATAAGATTTCCTCCTCCTCCTCCATTTTATATTGACTGTTTGCCAGA
AACTGTTTTCTTCTGTTTTCTTATATTTTGTTTTTGAGATGGAGTCTCACTCTCACCC
AGGCTTGGAGTGCAAGTGGTGCAATCTCAAGCTCACTGCAACCTCTGCCTCCTGGGTTCA
AGTGATTCTCCTGCCTNGGCCTCCTGAGTAGCTGGGAATTACAGGCCCGGGCCACTACCN
CCCGGCTACTTTTTGGATTTTGGTTTTTAAGAAAAACCG

Sequence 211

ATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCTNTTTNNCTTAAATTGCT
TTNTAGNTCTAAGATTGTANAATGANCCTNNCAAATTGGACTCTTTTCTAACAGAGNTAT
TTTAATATACTTGNTTTNTTAAAAAACAAAAAAACTACTGTCAGTATTAATACTGAGCCA
GACTGNCNTCTACAGATTTNAGATCTATNATTTTATTGATTCTTAAGCTTGTATTAAAAA
CTAGGCAATATCATNATGGATACATAGGAGAAGACNCATTTACAATCATTCATTGGG
Sequence 212

AGGTACTGGATGTTAGAACGGGCTCCAGGAGCCAGGAATCCTGGCTCTGCACTGTTGGAA ACATCTAAGCTAGTCTTGCGCCCATTTACTGGCTTGACAGGGATGCCTGAGGACTTCTGG ATCTTGCTGAGAGTGGCTGAACCACCAGTTTGCATGACAGTGGCTGTGCCTGTGGCAGGA GGAGGCTTCTTGTAGCCAAAGGATCCCGAAGTGGAGGGGGGCGACCAATGCCCGAGGGGGGG

Sequence 213

Sequence 214

Sequence 215

TTAGGGCGATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTGTAAAGTGAAAAGGGATGT GCANAAAAATAAAAAAAACAACAAANAAAGCTAACCTTCTATTAGAAAAGGGGACAGGG GAATGAGTAAACTTCTTTTATTGCGGACAAATGTGCACATAGCCGCTAGTAAAACTAGCC TCAAACAGGATGCTCATAGCTTAATAATAAAAGCTGTGCAAAG

Sequence 216

Sequence 217

CTAAGGGTTCTCAGGAAAAAATGAGAAGGACCCTTTGATCAGGAAAGGAAAAAAGGATAGAGGATAAAACAGTAACCTTTTA

Sequence 218

Sequence 219

CTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGCCGAGGTANTCTTGTTTCTATGAA GGAAAAGTTTGGCTACTAACAGTAGCATTGTGATGGCCAGTATATCCAGTCCATGGATAA AGAAAATGCATCTGCATCTCCTGCCCCTCTTCCTTCTAAGCAAAAGGAAATAAACATCCT GTGCCAAAGGTATTGGTCATTTAGAATGTCGGNAGCCATCCATCAGTGCTTTTAGCTATT ATGAGTGTAGGAAACTGAGCCATCCGTGGGTCAGGATGCAATTATTTA Sequence 220

CTTAGGGCGATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACTGCCAGATCTGT
ATCACTCCGGAGCAACGACCTGTCTCTCTGAATGATCTCTGGCATGGTAAAAGAGTTAAC
TGTATTTCAAAAGGTGAAACAAAACTTTTTTTTGCTTTGTTATGCATGTTTCAAATTGATC
AATGGTTCAGGCCTGGAGTATGCATCAGAATTATCTGTGAAGCTTAGTGAAAGTGCTGAT
GCCAGAGCCCACCCAAAGCTTACTGCTTCANAACCACTGGGGACCTGGGCAGTTCTGATG
TGCACGACTAGTCAAGAATCCTTTAAAGGCTGATAAAGCAATCTTGAAATCACTGTCAAT
GCAAAAGTGGGATGTTCCTTATTAATAAGAACTCAAAAAATAAAGTACCTCGNCCCGCTC
TAGAAACTAGGTGGATCCCCCCGGGCTGCANGAATTCCGATATCAAGCTTATCGATACCC
GGCCGACCTTTGAGGGGGGGCCCCG

Sequence 221

CCGCGGTGGCGGCCGAGGTACGCGTTTCTTGTAAACACGAGGCACCCCAAGATAAGAAGA CAGATAGAGCAAGGGATGGACATGGTCATCTCCTCAGTGATTGGAGAAAGTTACCGGCTT CAGTTTGATTTTCAAGAGGCAGTGAAGAATTTCTTCCCCCCAGGAAATGAAGTGGTTAAT GGAGAAAATTTAAGCTTTGCATATGAATTCAAAGCTGATGCATTATTTGATTTCTTCTAT TGGTTTGGGCTCAGTAATTCCGTTGTAAAAGTAAATGGAAAAGTTCTGAATTTGTCAAGT ACCTGCCCG

Sequence 222

AGGTACTTACATGGGTGTTTTGATCTCTGTTCTTTCATACTACATTTGAACAGGGCAAAA
TGAACTAACTGCCATGTAGGCTAAGAAAGAAATGCTAACCTGTGGAAAGTTGGTTTTGTA
AAATTCCATGGATCTTGCTGGAGAAGCATCCAAGGAACTTCATGCTTGATTTGACCACTG
ACAGCCTCCACCTTGAGCACTATTCTAAGGAGCAAATACCTTAGCTCCCTTGAGCTGGTT
TTCTCTGATGGCACTTTTGAGCTCCTAAGCTGCCAGCCTTCCCTTCTTTTCCTGGGTGCT
CAGGGCATGCTTATTAGCAGCTGGGTTGGTATGGAGTTTTGGCAGACAGGATGTTCAACTT
AATGAAGAAATACAAGCTAAGGCCTTGCCAGCAACACCTGCCGTAAAGTTAC
Sequence 223

CCGCGGTGCCGCCGAGGTACAGTCACCATCATACTTGTCTCCATTTGGAAAGATAAAGC TGATCTTATACACTTCTGAAGTTGGTCGAGAGGTGTTAGAGAGATCTTCCAAACTCTGCG ACTCCCCTGGGCGGCCAGCTCTGCGGCCACCTTGCCCG Sequence 224

Sequence 225

CCCGCGCTGGCCGCCCGGGCAGGTAAAAAAAAAAAGGAGACACAAGACTTACTGCA AAAATATTTTTCCAAGGATTTAGGAAAGAAAAATTGCCTTGTATTCTCAAGTCAGGTAAC TCAAAGCAAAAAAGTGATCCAAATGTAGAGTATGAGTTTGCACTCCAAAAATTTGACATT

Table 1

ACTGTAAATTATCTCATGGAATTTTTGCTAAAATTCAGAGATACGGGAAGTTCACAATCT **ACCTTATTG**

Sequence 226

CTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACTTTCCATT CATTCCAGTGAGAAGCACTAGAACTTTAAAATTTCAGAATTGGATGAAAATAACAAAGAT CACCCAGTTGAATCATATTTTTTTGTTCAGAAGCAAAAACTGAGGCTCAGAGACAAACTG TCCTGTCCAAGATTATACAGAAAATGGTGGGAAGAGTTGAGAAGTTTCTCAATAATGCCA TGACTGTTGAATCATAGGAACAAAAGCCAAGAGATGGATCCTTACAATAGTTTAACAATA TAAACCACATGGAACATTTCAAGAAAGAGTTAAACAATGATCTATGTTTAAAAGCTATCT CTACCTGGCATAGTATCTCACATTCTATAATCCTAGCACTTTTGG

Sequence 227

GCTGGCCCGCCCAGGGGGAGTCGCAGAGTTTGGAAGATCTCTCTAACACCTCTCGGCCAA CTTCAGAAGTGTATAAGATCAGCTTTATCTTTCCAAATGGAGACAAGTATGTTTTTCTCC **TCTGTTTAGATGGTGACTGTACCT**

Sequence 228

GAGAAGTTTTCAAGTATTTCAATGTGCCTTGAAAAGTTTCAAACAGTAATTCTCACAATT GGTTAGACAATCATTTTTTTTTTTTTTTTTTTTTCTTTTCCTCTCATTTAGTCTCAGAGCCTAAAAA GAAATGCCTCCAGTCTNTGTTAGCCCCGATNTTNGGATGGAATTTACCAGGTTTNTCCTT TAAAANAAAAANTTTTGGGGGGTTTTNAAAAANGGGAAAAAATTCCCCCCNCTTTANAA AAAAAANAATTCCCCCCCCGGGGGTTGTTTTTAAANAAGGGGGGGNNNNCCCCCCCCC TTTTTTTTANAAAAAAAANCCCCCCCCCCCCAANNNNNNNGNNNNCCCCCCNTTGG GGGGGGGGGGGNNAANAAAAAAAAAAAAAAAAAACCCCCCNTTTCTCGNGGGGGGGG CCNCNANNNNNNGGGGGGGGGGGGGGGGG

Sequence 229

CTNCTTAGGGCGAATTGGAGCTCCCGGGGTGGCGGCCGCCCGGGCAGGTACAAAATAAC ATCATAAATAACATAAATGAGAAGTTTTCAAGTATTTCAATGTGCCTTGAAAAGTTTCAA AGTCTCAGAGCCTAAAAAGAAATGCCTCCAGTCTCTGTTAGCCCCGATGTTTGGAATGAA ATTAACAAGATTCTACCTTAAAAGAGAAAACTTATGTGGGCTTTTCAAATTGTGAAAATT TGTTCCCTCTTATAAAATATAATCTTTCCCCTGCTGCTGGTTTATAAATATGGGCATATA GCCCANAGCCATTATAAAGAAAAAACAACCCACCACAATAAACTAAGGAGCCTCATCTGA TGGCTAAGGGTTCTCAGGAAAAATGAGAAGAGCCCCTTGATCAGGAAANGGAAAAAANG **GTTGGA**

Sequence 230

TGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTTACATGGGTGTTTTGATCTCTG AAATGCTAACCTGTGGAAAGTTGGTTTTGTAAAATTCCATGGATCTTGCTGGAGAAGCAT CCAAGGAACTTCATGCTTGATTTGACCACTGACAGCCTCCACCTTGAGCACTATTCTAAG GAGCAAATACCTTAGCTCCCTTTGAGCTGGTTTTCTCTGATGGCACTTTTTGAGCTCCTA AGCTGNCAGCCTTCCCTTT

Sequence 231

CCGCGGTGGCGCCCCGGGCATGGTACTAGAAATTGCACTGTCCTAGAAATTCCTCCA TCCCATGAAGCCATTTCCATCATGAAACCTTTGACACACTTGAACACAAGTTCCGCTCTC CTTAAGCACCAGGGTATAGTCATTTNCTCTGACATATAATGTACTTAAGCNCTGCAGAAT NGCTCNAGTAATATNCCNATANGTNCNTTTCCAATTTCAATTA

CTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACTTGGAGCT GACCAAACGGGAGGTCGAATACATTGCCCTGTCAAGGGACACCACTGAAACTGATCTCAA ACAGCGACGAGAGATCCGTGCAGGCACAGCCTTTTACATTGATCAGTGTGCAGTTCGTGC AGCCACAGAAGGCAGAACTCTCATTTTGGAAGGTTTGGAAAAGGCAGAGAGGAATGTTTT GCCTGTTTTGAACAACTTGCTGGAAAACAGAGAGATGCAGCTTGAAGATGGACGCTTCCT TCTTGGAAAATTGTCCCGAGGTTAGTGAAAATTTCCGAGTGATTGCCTTGGGGCTTGCCA

Table 1

GTGCCCAAGGGT

Sequence 233

CTACTATAGGGCNAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTTTTGTTTTGTTTT
AAATTAAGAGATTCCCAAATGCCTTTTTCCCCCTCATCTTGAAATGAGATGAGTTTTTAT
GTGTAAGCAATATTTATTTAACTATTCTATAAAATTATTGAGTGCCTACTGAGGCCTTTA
AGCACCGCTAACATTCCTTTCCATCATTCTTTTAAATGACATAAAATAATTGTGCAATGT
TCCTGATGATGTACCTGCCCG

Sequence 235

CTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACACTAATGTTTGCAAC
ATTTATTGAGATCTAAGTCTGTCTTGCCTTCATTTCTCTTTTTATCTCCCCCTTGCCCTC
ATTCTTGAACAGCTGGAGGAATACATTTTATTCTGTCCATGAAGCATACACTATGAAATT
CAAGTGCTTAAAAATACTTCTATGACTCTNTGCTATCCCACTGTATAGATCCACAGGGAG
CAAACACTTAGAAATGATAGAGAACTGAAGGAGATCAATGGTTTAACAGTTATCCATGCC
AAGTCCCATTGNCAGAAATATTCTTATTACTCAGGCAAACACTCTTTGAGCTTCCCTTNC
TAAAGGTAACCATTCCAGTGAATAGATGTGCCCT

Sequence 236

Sequence 238

Sequence 239

CTACTTAGGGCAATTGGAGCTCCCCGCGGTGGCGGCCCCCGGGCAGGTACTGCTAGCTG GAAAAACCATATAGAAAACATGATGACCATGTTGAGTTGTTGGTGCTGAGGCTGTGAACT CTTTGGCTTCCTTCTGATGGCCCTCTTGAGAACAATCTGTACCT Sequence 240

Table 1

TAATGCAGCTCTTTTAATATAAAGATTCTTGATACAGTGAAATCTCTTATTTCAAGTGTA
AGTTATTCTTCACCCACCCCTTCCCCTGCCATTGTATTTCCCATCTGTTNNANGGNGTTN
NANCANTTNNCATTGNNTCGNATNCAGNAGGTNCCTGCCCG

Sequence 241

AGCTCCCGCGGTGGCGGCCGAGGTACTTATTGAGTGCTTGTATGCACCAGGCTCTGAAC
TAAACGCGCTCCATATTACCCCCATTTAAATTCTTACCATTATTCCTGTCTTACAGAAAG
AAAAAAGGCATGGTGAGTCACACAGGTTCACAAATGAGGGCTAGAACCAAACCCAGGCACT
GTGACCTGCTACACAGGAGAGGCAGATATGAAGATTTCTTCAAGGGTGCTTATTACAGCA
TCATTTATAATAGCAAATAAAGTACCTGCCCGGGCGGCCGCTCTAGAACTA
Sequence 242

CCGCGGTGGCGGCCGAGGTACTCCTCCAGATCCTGGTGCTGCTTTTGTGGTGGTAGAATG TCCAGATGAAAGCTTCATTCAACCCATCTGTGAGAATGCCACCTTTCAGAGGTACCTGCC CG

Sequence 243

CCGCGGTGGCGCCGAGGTACTTTTTAAAAAATCTATAAATTTAATGCACTGTCCAAGTG
AAATGTCCTAGTTGTCATTGTGATTAAGGGGGCCAACTTTCCAGGCAGCTAGCAGAGATAC
TATTCTCTTCCTCCCAGCAAATTTGTATTCCTTCGCCCACGCATTCCTGCTATACTAG
ATGGCAGCCAGTGATGGAACTATAAAGATGTCTGTGGTCATATGTTGAATGTGGCAGCTT
GAAGATGTACCTGCCG

Sequence 244

Sequence 245

GCTNCTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTTTTTGCTTTTCT
TTTGAAAGTATGAAAATGATTTTTACAATGTAAAGAGAGTCTGAGAAATGCAATTGCTAT
TCTTTTATATACTTTTTCAGATTTTTTATATGCTTCTTTACTACTTACATCATAATGCA
CAATTTTATATACTGATTTTTCAATCAATGTATATCATGAGTTTTTAAAATAATGCTAC
AATCTTCATAACTAATATTTTAATGGGGAGTGACTGCTTAATTGGCATGAGGTTTCCTTT
TGAGATGAGGAAAATGTTCTGAAAATATGGTGATGGTTGCACACCATTGTGGAATGGTAC
CTGCCCGGGCGCCCCGAGGTACTTGCCTGGGAGAAG

Sequence 246

GCTCNCCGCGGTGGCGGCCGCCCGGGCAGGTACAGGGTCCCCAGCTTACTCCAGGGATGA
TGTCAGAAAATGAGGTCCTAAACATGCAGCTTTCGGATGAGGACAAGGAGATGTCCCTG
TTGATGAAAACAACTCCATGGTAAACCTGATAAAACCTTGCGCTTTTCCCTCTGCAGTG
ATAATCTGGAAGGAATATCTGAAGGTCCTTCAAATCGCTCCAATTCAGTGTCCTCCCTAG
ACCTAGAAGGAGAGTCTGTCAGAACTTGGAGCAGGACCTTCTGGCAGTAATGAGTTG
AAGCTCTACAGCTGTTAGAACATGAGCAAGCTACAACACAGGATAACCTTGATGATAAAGC
TAAGGGAAGTTTGAAATTCGTGACATGATGGGGATTAACAGATGATAAGGGGACATATCAA
AAACAGTGAGGAGACTTGGAGCTCTTCGGCCCCTTTAGAACTAGGTGGATCCCCCCGGC
TGCAAGGAATTCCATTCAAGCTTATCGATCCGTCCACCTCGAGGGGGGGCCC
Sequence 247

Sequence 248

WO 01/51628

PCT/US01/00798

Table 1

TAGCTGTTCAAATATACTCCATACAGCTTTCAGCAAATCAAAGTGTTTACCTCTCCCACA CCAAGGGAAGAAAAGATGCAGACTGCCTTTAAAGCACCTGTCAGCAAGGCGAGGGGTTTT AAAAGGATCAAGCCTTGAGAATCAAAGCAGCAGCAGAAGTGTCATTCTTNCAGTGCTCTC CTTTCCGGTTC

Sequence 249

TACTTAGGGCGAATTGGAGCTCNCCGCGGTGGCGGCCGAGGTACCCATTGGTCTTACAGA CAAGCATCAGGAACCAGAGGGCCTGGTGGGGGCTGGGAGGAAGCTCGGCAGTGACAGCTGA GGTGCTCATGTCCTTCCATCCCACTGCCCAGTGGATAATGAGCTCATTAGTCAGACGAGG ACCAGCCCAGAATAGCCAGGAGTAAGCATGTCACATTACAGAGCTGTAGCCAGCTTCTGG GTGGAAATAGCACTATCTGGTACCTGCCCG

Sequence 250

CTTAGGGCGATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCCCTTTTTGCACACTGTCA
GCAAAACACGTCCCTTTGAGTATCTCCGGCTCACCAGCCTTGGAGTTATTGGGGCCCTGG
TGAAAACAGATGAACAAGAAGTAATCAACTTTTTATTAACAACAGAAATTATCCCTTTAT
GTTTGCGAATTATGGAATCTGGAAGTGAACTTTCTAAAACAGTTGCCACATTCATCCTCC
AGAAGATCTTGTTAGATGACACTGGTTTGGCTTATATATGTCAAGACGTATGGAGCGTTT
CTCCCATGTTGCCATGATCTTGGGTAAGATGGTCCTGCAGCTATCCAAAGAGCCT
Sequence 251

Sequence 252

Sequence 253

Sequence 255

Sequence 256

Sequence 257

CCGCGGTGGCGCCCCGGGCAGGTACATTTTTTAAAGTTCCTCAAAAAATTCTGCTTC
TAGGCAAATGTAATAGATATTGTGCGTTGCTCATGTTTTTCCTATCAGAACCATGATTTT
AAAAAAACTATCCTTTCTGTCCCCATATATCCCTCATGTGGCCTCACTTCTACTCTCAG
CTCCAGTGGACCTGACTGCCCTAAAGGTTATTCTAGACCCTTTGCCAGTGACTGGCTCAG
GGATGGACAGGTCTAAGTTACTTTAGAGCAATGAGACCTAAGGATATGGAAAGTGAATTC
TGGGAAAGCTTTCTCATACTAGGACAGGGCCCCTAGAATCCAGCCTGACTCTTCCGCTGC
ATGTAAATGAAGATGCACAAGGCTNCAACTGCTACTGGCAATCATCCCATGACCACGAGG
GTAGCCAGCCTTAGGATGATGCCCCATGTTTGTGGGTTGAAAANGGGGGGGGG
Sequence 258

Sequence 259

NNGAATTGGAGCTCCCGCGGTGGCGGCCGAGGTACAACAAAAGCCTGTGAACTGGCTTA AACCAGTTTACATGCTGGATTCCGACCCAGATAATAATGGATTCATAAATGAGGATTTTA TTGTTTGGATGCGTACC

Sequence 260

Sequence 261

ATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTGTATAGGCCATATTCCTT
TACGTGGGACATTAATGAAAAGCTGTCTTTTCCAAACTGAATGCGCCTATTAATAAAAAA
ATACACCTGACCATCTAATGCTGAAGTCATCCGCCAAGGTGGTACCTGCCCG
Sequence 262

CCGCGTGGCGCCGAGGTACAGATTATGGAAAATATGAAGGACTAACAAAGAATTACAT GGATTATTTATCCCGACTATATGAAAGAGAAATCAAAGATTTCTTTGAAGTTGCAAAGAT CAAGATGACTGGCACAACTAAAGAAAGCAAGAAGTTTGGTCTTCATGGAAGTTCGGGGAA ATTAACTGGATCTACTTCTAGTCTAAATAAGCTCAGTGTTCAGAGTTCAGGGAATCGCAG ATCTCAGTCATCTTCCCTGTTGGATATGGGAAACATGTCTGCCTCTGATCTCGATGTTGC TGACAGGACCAAATTTGATAAGATCTTTGAACAGGTACCTGCCCGG

Sequence 263

Table I

Sequence 264

CTTAGGGCGAATTGGAGCTCNCCGCGGTGGCGGCCGCCCGGGCAAGGTACACGGTGGACC TGGAGTCAGGGCTACACTACCTCCTGCGGGTGGAGCTGGCAGCCCACAAGTCCCTGGCCG GAGCAGAGCTGAAGACGCTCAAGGACTTTGTGACTGTCTTTGGCCAAGCTGTTCCCTGGA Sequence 266

Sequence 267

Sequence 268

CTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTTTCATGGTCAAGCTCTAAGA CACAACGAGCTCTGTTATTCAAGAAATCAATTCCAGTGGATTTCCAGTTCCAATTCCTGA GAACTAGGGTAAGGGGGAGAGCTAATGGTTGCTTCCTAAGGCCTTCTGGGTTTATTAGTT CCATTTCAGGACATGACAAGAAAATGTACCTGCCCG Sequence 269

CACTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACCTTCTA
AGGTAGTTAACACCACACAGGCTGATAACTCAGGGCAAGAGAGGGCCTGGAGAGTTGAC
AAGAGTGTGAAGATACTGGAGAGGGGTTCAAAATAGGATCAATTCTTCTAATACTATTCT
TATTTCTTGCTAATAATTTGTCCTTGTAATTATAGTGAAGTAATGGTCTGGATATAAATG
AGATATGGTTTTGTGAGGGAAGAAACATAGAGGATTATTCTTAACAACTGTGGCAGCCTT
GCCAATATGGAACC

Sequence 270

CCGGGGTGGCGCCCCGGGCAGGTGCGNTCTCAGCTCATTGCAACNTNTGCCTTTNTA
AACATGCTATTAAATGTGGCANTGAAGGANTGTTTTTANTGTNATCTTGCTATTAAGTGG
TAATGAATGTTCCCAGGATGAGGATGTTACCCAAAGCAAAAATCAAGAGTAGCCAAAGAA
TCAACATGAAATATATTAACTACTTCCTCTGACCATACTAAAGAATTCAGAATACACAGT
GACCAATGTGCCTNAATATCTTATTGTTCAACTTGACATTTTCTAGGACTGTACCT
Sequence 271

TTĠGAGCTCCCGCGGTGGCGGCCGNGGTACATCCACAGGAGGAATCGGACGAGAGGATG
TGACATTCGGTCCAGGAGAGAAAGAGCAGTTTCTGTTAAAGATGTAACAAATGGATTTCC
AAAGTCTACATGACATTCACTTTTCAAACTTCCCACCAGTTGAATTTCTTTTTTTCCTTA
AGAAACAGGTGATGTCTTGGAAAACAGCTCCTTATGTCTCTCTGTGCATCTCCATTTTCC
TAGTCTCTGGAGTCTCAAAAAGAGTGGCAAAGCACTTTACAGTAGTAACTGAGGAATCAG
AGTCTCTGCTTCAGCGATATCTAGTTTGTACCTGCCCG
Sequence 272

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Table 1

CCGCGGTGGCGCCGAGGTACTTGTCAAATGAAAGAACAGGGATTGCCAGACCTTCAAGG CAATGGGAAAGGAGCAAATCTGCAAAGGTAGGATCTCTTTGGAAGGCAGGTATTGGCCAC CAAGTCAAACTCCTTGAGTCTTATATTCTGATTGGGATGATCTCACATGGATGTTCATCT CTTATATGTGAATGCTCATTTGTGAAAAATAGTAAGAGCCAGCTAGGATATTTGGATTCA GTCAGGCACCATCAGAATAGTGCAGTGAAAGGCCAAACTGGCCACAAGACAGAGGAATGT TTTCAGTTTTCTGGTTTTCCTCTGGTCCATGATAAAGCTCGGAGTAACTCTTCTATCAAG ATGGGGCTATACCTTCNCATGACAGAGGCTGGCAATTGAGCTACCCAGCAGAACGTGTGC TCTCAAAAGGGGAAGTCAAGGGAAC

Sequence 273

CCGCGGTGGCGCCCCGGGCAGGTCAGGCAAGGAGAACTGTGCTATATTGTTGGTGCT
TGCTGTTTTGCTGACATCTTCAATTATTGTTTTTACCTGAAATCAGTAAGACTTTGACA
GGATATCACCTGAATTATTAATGAATGCCCAGGAAGTAATTTTCTTCTCATTCTTCTAAA
ACTACTGCCTTTCAAAGTGCACACACGCGTCCACATACACTGCATTCGTTGCTCCAGT
ATAAATTACATGCATGAGCACCTTTCTGGCTTTTAAGCCAATATAATGGGCTGCAAAATG
AAGACACCAGAGTGTATGCATACAAATCTCACTGTATTAAAGATGCAGGTTTTCTAATTG
TACCTCGGCCGCTCTAGAACTAGGTG

Sequence 274

Sequence 275

Sequence 276

Sequence 277

Sequence 278

ATATTTATAAATTTAAAAAATTTTACACGTGCTGAGTGGTAGCAGTGCTAACATTTTTGT Sequence 279

AGGTACCTACCTTTAAGACTGGGATAACTATTGGAAACAATAGCTAATACCGGAT ATAGTTATTTATCGCATGATGAGTAATAGAAAGGAGCTTCACAGCTTCACTTAAAAATGG GGGTGCGGAACATTAGTTAGTTGGTAGGGTAATGGCCTACCAAGACGATGATGTTTAGCC GGGCCGAGAGGCTGTACCTGCCCG

Sequence 280

AGGTACAGTGCCAGACCATGACTGTCAATCGTCAGATGAAGCGCTACAACGTTCCGTTTC TGAGGTCTAAACTAAATCATAATGCAGCGTTTATGCAGATACCCATGGGTTTGGAGGGTA ATTITAAAGGTATTATAGATCTTATTGAGGAACGAGCCATCTATTTTGATGGAGACTTTG GTCAGATTGTTĆGATATGGTGAGATTCCAGCTGAATTAAGGGCGGCGGCCACTGACCACC GGCAGGAGCTAATTGAATGTGTTGCCAATTCAGATGAACAGCTTGGTGAG Sequence 281

CCGGGCAGGTACTTGTTTATAGACTCAAAACATGATGAAAATTCATTTCATTGTCTTCAC TGAATAGACTTAACCTTGACAGTAAGCTTAAAGCATTAGTGTCATTTAATTACATGTCTG AGGAATTTATGCTAACTAGATTTTGGGCTTTTGCAGCGAATTTTAGTCGGGGCCTCATTC CTGAGCCCAAGTGACCCTTTCACCTCAGCTTCCCAAGTAGCTGGGATTACAGGTGCACAC TTACAAGCCCACAACATCATAGCTTTGCAGTT

Sequence 282

AGGTACAGCACTGGGCTTTATAAAGACTGCACTCAGAACCACACTGCACAGTCCAGTTTT AAACGAAGTAAACAAGAAACATAAAAACCAAATAGCAAATGAATAAAAGCCTGTTCTTGT AACTTATTCAACTTTTGCCAAATTCCTACCAATCACTTGCTTTTTAAAAGAAATGTATAA CAGCCAAAAGAGAAATTATGTCCCTGTTGTACCTGCCCG

Sequence 283

ATTGGAGCTCCCCGTGGTGGCGGCCGCCCGGNCAGGTACGGATACAATTCCGCTGAGTTA AGATTCCAAATTCTAACCTCTCCATCACACGCCCCAGAAAGGACAGTAGCCAGCTTCTCT GGATGCTTTGCCAAGCAATTGACTCCATCACGGNGACCATCCAGCGAAGCAAGGAANGGT TTTGCAAATACTCGNTCCAGTTTGGTAGCATTTAAAGCTCTTATATATTCTCGNGGGACC **TCAAAAGGATGTAAAACCT**

Sequence 284

AGCTCNCCGCGGTGGCGGCCGAGGTACTTACATGGGTGTTTTGATCTCTGTTCTTTCATA CTGTGGAAAGTTGGTTTTGTAAAATTCCATGGATCTTGCTGGAGAAGCATCCAAGGAACT TCATGCTTGATTTGACCACTGACAGCCTCCACCTTGAGCACTATTCTAAGGAGCAAATAC CTTAGCTCCCTTGAGCTGGTTTTCTCTGATGGCACTTTTGAGCTCCTAAGCTGCCAGCCT TCCCTTCTTTTCCTGGGTGCTCAGGGCATGCTTATTAGCAGCTGGG

TTAGGGCGATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACTTACATGGGTGTT GCTAAGAAAGAAATGCTAACCTGTGGAAAGTTGGTTTTGTAAAATTCCATGGATCTTGCT GGAGAAGCATCCAAGGAACTTCATGCTTGATTTGACCACTGACAGCCTCCACCTTGAGCA CTATTCTAAGGAGCAAATACCTTAGCTCCCTTGAGCTGGTTTTCTCTGATGGCACTTTTG AGCTCCTAAGCTGCCAGCCTTCCTTCTTTTCCTGGGTGCTCAGGGCATGCTTATTAGCA **GCTGGGTTGGTATG**

Sequence 286

CCGCGGTGGCGGCCGAGGTACTTACATGGGTGTTTTGATCTCTGTTCTTTCATACTACAT AAAGTTGGTTTTGTAAAATTCCATGGATCTTGCTGGANAAGCATCCAAGGAACTTCATGC TTGATTTGACCACTGACAGCCTNCACCTTGAGCACTATTCTAAGGAGCAAATACCTTAAC TCCCTTGAGCTGGTTTTNTNTGATGGCACTTTTGAGCTCCTAAGCTGCCAGCCTTCCCTT CTTTTCCTGGGTGCTCAGGGCATGCTTATTAGCAGCTGGG Sequence 287

Table 1

AGGTACTTACATGGGTGTTTTGATCTCTGTTCTTTCATACTACATTTGAACAGGGCAAAA
TGAACTAACTGCCATGTAGGCTAAGAAAGAAATGCTAACCTGTGGAAAGTTGGTTTTGTA
AAATTCCATGGATCTTGCTGGAGAAGCATCCAAGGAACTTCATGCTTGATTTGACCACTG
ACAGCCTCCACCTTGAGCACTATTCTAAGGAGCAAATACCTTAGCTCCCTTGAGCTGGTT
TTCTCTGATGGCACTTTTGAGCTCCTAAGCTGCCAGCCTTCCCTTCTTTTCCTGGGTGCT
CAGGGCATGCTTATTAGCAGCTG

Sequence 288

AGGTACAGTAAACATTATTCAGTGAGAGAGATCAGAAGGAAACAAATGGCATCTTTTCAGAA CGCTGTCAACTGTTCCCACAACCCAAGTCTGTTTTTCCAAGTTGCACAAGTGCTTGGAAT AACTCTGAAACAATTCTCTTCAGAGTTTAAAGGCTTCAGAGTATAGGTGATGCTTCCTAA AACAAGAAGCCTGTATTAACATCACAAATTGGAACTCATTCCAAAGCCTCTTCTTAGAGA AAAAAAAATAAAGAAATAAAAAAATGTAAAGAAGGTCATGAAAAAATTCACATGC AGCTAATTATCGTAAAAAATATCAAACAC

Sequence 289

AGGTACAGCATTGATGAACACTTTCAGCCGAAGCAGATTGTCAAGTCTCTTATCCCTTCG
TGGAACAAACTGGTTTTCTTTGAAGTATCTCCTGTGTCCTTTCACCAGGTGTCTGAAGTG
CTGTCTGAAGAAAAGTCACGTTTGTCTATAAGTGGCTGGTTTCATGGTCCATCATTGACT
CGGCCTCCCAACTACTTTGAACCCCCCATACCTNGGAGCCCTCACATCCCACAAGATCAT
GAGATTTTGTATGATTGGATCAACCCTACTTATCTGGACATGGATTACCAAGTTCAAATT
CAAGAAGAGTTTGAAGAAAGTTCTGA

Sequence 290

CCCGCGGTGGCGGCCGAGGNACNGANTNATTTTCNGNATTACTGAACNCCTTTGAACTAT
TTTGAACTNTGAATCTCTCTCTGAATAACTGCCGAAACTCAAAGATAATAATNAGTTGA
TGAAGGTTATCAATTAATAAAATAACNCAGACCANTCTTACCAAACTCTAAATACATTNT
AAAAAATTTTAACTGGCAATGATAAAAAGAATGTTGAGTACCTGCCCG
Sequence 293

Sequence 294

CCGGGCAGGTACATAACATTTCAAATATAAGTGGAAGGATCATCAGTAGTGTTATCAAAA TGCATAATACAGAAACTTTTTAAGAAAGGATAAAAAATTACACTCAGGACCCATAACTCT TCCTCATTATAAGCATATGTAGTGATTCATTCATGCAGGTTTTTATATGTAGATAGGATT TTTTTTTCCTTTTCAAGAATTCCATTGTAGCCATGAGATGAAAAATGTATTATGGTAATG GTATAGCTTTCTTCTATTTTGCTTTTAGTGTTAGGTTTGCTAAAAGCTTATTTAAAATTC CCAACTGACATAATGTGTTTTCAATAAGGAGGACGCT

Sequence 295

Sequence 296

Sequence 298

CCACCGCGGTGGCGGCCGAGGTACTATGTCAGNTTTGTATGTAACTAGCTGTCAGGTCTT
TCCCCGTTGCCTCAGCCTTTCTACACAGACTGGCCTTCAACTTCCCCTGAGTCCAGAAGT
AGACTCTTTCAGCAACTCTATTCAGGAATCTGCAGCAGGAAAACTGCTTCCTCTATTAAC
ATCTATGACTGAAGCACAGATGTGTCTAATAGAAATCACCCTTCACCCAAAAGCTGGGTG
CAGAAAGGGAAGCCCTTAGCTGACTATAGGAGGTGCCTCTTTGTGGCTCCACGTGCTTCTT
ACACACCACCCCCCAGCTTGAGCGATGCCTCAGCCAGCTCACCCTCATCCACACACTCGC
TAGAAA

Sequence 299

CCGGGCAGGTACCTAAGGGGTTACTTGTTTAATGGGATGGCATTGACTTTTTGAAAATCA AGTGGACTGAGTCATTGATAAAACATTTCTAAGAGTGGGGCTAGAGAACATACTTTACAT CTGACATCCTTTGGCCTAACAACATCTATTATTATAGTGCTCAGCAGTGTGGGCATTGAA GAGGCGCAGAATGCTTTGAAAGAAACTAATCAGAATCTTGGAACATCATGATCATGCCAT TCTTAAGTAAATCAACTATTTTCAACACTGAAGAAAATGAAACATTATTTAGAAAACAA TGAGATTACAAGTTCCAAACTCAGCCA

Sequence 301

CCGGGCAGGTACCCTCTACCTCCTTCCCTGTCGGAAAAGTCACCACTTTAGTCCCTGGCC ACCAGCACACCCCAGGAGGGTGAGTGGCCTGAGGTAGTTACCGGCACTTAAAACTCCCTT GCTACCGATCTGGAACTCAAGCCCCAAGACATCCCCTTAGATGATCTGAATACGCATTCA GGGACAGATCTAGGCAGTTTCTAAACAACACTTAGACTGGGGTCTAACGTTGACAAATCC TTCTAGAATTTGCCTCTTTGGGACTGAAGTCTAAGGGGGCTGAGACCAAGAAGGGAGAGCA CAAGACTAACTTTGGTCTCTTGACCTTTT

Sequence 302

AGGTACTCAAATGCATTGATTTTTCCAGCTGGCTTTTCAGAGCAGTGCTAGTGAGAGGCA CCAGTGTAACTTGAAGCAGGAATAGTGATGGCTCAGGTCCCCACAGGTAGCTCCTCCATA

CCTGTGGGACTCAAAGGCTAAGGGCACTAACTCATAGGGCTCAAAGGCTGGATGAAGAGA ACAATCAATGTGTTAAATGTCCTTCAGACCTAGGTCAGAGGACAAATTTTGACTAATTCT TTTGACTAATTCTTTTTGCAACTTCTCTCAACAGGTACCTGCCCG Sequence 304

CCGGGCAGGTACCTATTCACCATTCCAACGTGAAGAAGCTCTGCAGTAGGAAAAATAATT AACACACTTATAGTCTACTGCCTATGTAAGGATCAGCTCCGGCTAAGAGGCCAAAGATGG GTGACATCGTTATGCTCTGCCTTTATTTTTTCTTTCTTACCCACTTAGCTTCCTAATTGG AGGAAGGAGGCGTGGTAAAGGTATATGAAGACTATGGTTTAATTAGACCAGAAAACACTG TCATAATCTCTGGGGTCATCAGAATGTCCAGTTTTGTCTTTGGGCCAAGATAAGGGCAGT GGGATTTATGATGATGTTTTATAGATCTGAAACTACTC Sequence 305

Sequence 306

Sequence 307

Sequence 308

ANCCCCCGCGGNGGCGGCCGAGGTACGCATGTCNTTTGGNNNAGTATGAANCACNGGTT
AAAGTCTGTTTGAACAAAAACAAATGCCCGGGGTAATTTCATAGCTATAAAGTTAACAAC
TAAATTTTGTTCACTAAGAGGACCTTTTCTATGGATTTCCTTCATCTCTCAGTCACACTG
CAAACTTATCTGAAGTGCACTTCCCAAGTGTAGNTAGAGAATAGGAAGGAATGTAAAATT
TTTTTTTTAATTATTTGGTTTGGTNGGTNGGTTGGTTTTTTAAAAACAGCCCTTATTAAC
TCTTCCTTCCACTGATTCTACTGGAAACTCATAAAAGCCTTTT
Sequence 310

Sequence 311

AATGTCTATCCATGATT

Sequence 312

AGGTACAGCCTCTCGGCCCGGCTAAACATCATCGTCTTGGTAGGCCATTACCCTACCAAC
TAACTAATGTTCCGCACCCCCATTTTTAAGTGAAGCTGTGAAGCTCCTTTCTATTAGTCA
TCATGCGATAAATAACTATATCCGGTATTAGCTATTGTTTCCAATAGTTATCCCAGTCTT
AAAGGTAGGTTAGGGTACCTGCCCGGGCGGNCGNCCGGNCNGGNCATAATACATGATTGA
ATA

Sequence 313

AGGTACAACAGTAGAACAATACTGACAAATGCAAACTTAGTCACATGTGCTTTAATAAC
TGACAATACATTCAAGCAGGTTTTTCTAATTCAAGTGTATAGCACATATTCAAATAATAG
GAAACAAATCTCATGCAAAGTAAATAAATCTTGATGTNTAAAAACTGATTAGAACTAGAA
AAGAAGTGGACATGTTTTATTATCTTTGCATTACGTTCTAACAAAAGCAGATTATCAGGG
GCTCTTACTCACTTGCCATTCCTGACATGAGCACTATAAGTGAATACTATGAGTTCTACA
AACAGAACATTTTTCCACATGAATTTGACTTGCAA

Sequence 314

CCGGGCAGGTACGCCGTTTCTTGTAAACACGAGGCACCCCAAGATAAGAAGACAGATAGA GCAAGGGATGGACATGGTCATCTCCTCAGTGATTGGAGAAAGTTACCGGCTTCAGTTTGA TTTTCAAGAGGCAGTGAAGAATTTCTTCCCCCCAGGAAATGAAGTGGTTAATGGAGAAAA TTTAAGCTTTGCATATGAATTCAAAGCTGATGCATTATTTGATTTCTTCTATTGGTTTGG GCTCAGTAATTCCGTTGTAAAAGTAAATGGAAAAGTTCTGAATTTGTCAAGTACCT Sequence 315

AGGTACATTTTGTATTAACTGAACTCAGCTAAACAGTAAAACCTGTTTTACTTAATCCCT GTCTTGACTACCAGACTATCATGATGTTTGTTGGAACTGTAATTCCTGCTCTCCATTTCT CTCTGTCCCCCAAGTTGAAAATATAACCCAAATCTTTAGAATTTTTGCCTCTCATTCCTT GCAACTCCAGTGGGCTAGAATCTTGATCCAGTTTTCTCCAGACTAGATTTCAAGCTACTC TGCATGATGTAGAACATGTAACCATGTAACCTCATCAGCTACCTTTTCCCTTTTGACTTT TCCTGTTGCACACAGTTCAGTCTGACTATC

Sequence 316

TAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGCAGGTACGAATGCGATCACT
GTGGGAAGGCCTTCAGCATAGGCTCCAACCTGAATGTGCACAGGCGGATCCACACCGGGG
AGAAGCCCTACGAATGCCTTGTCTGCGGGAAAGCCTTCAGCGACCACTCATCCCTCAGGA
GCCACGTGAAAACTCACCGGGGAGAGAAGCTCTTTGTGTCATCCGTGTGGAAAAGGCTCC
AGTGAGCGCGCCTGCTTTAGAGACACAGGATGATTCAGACCGGAAACAGACCTCGTGGGT
GTAAGAGGAAGCCTCTGTGAGCTCGCACCTTACTGGGTGCAAAAGAATCCACGGAACTTG
GGAGAAGTCCAGTTCCTGTAAAAACTGGGAAGACGAGGCGTTCTCATCCCATAGGAGGTT
TGTGAGAACTCACGCCGGGGGTGAAAATGTACCT
Sequence 317

Sequence 318

TCTGGCGAACATACATGGCATATAGAATATCNCCTTCTTCCACATGCAGCCTGAACTTCT
TCACCTTCTCAAATAAGGCCTTAGCCTGCTCACCTTCTTTTTATCCAGAGCCCCTGCAG
TGGATTTATCAACTACAAACTTCTCAGGAATGGACTTTAAAGACTGAGAGTTGACCAGGC
TGCCTTCTGGACCAGATTGGATGGTGTTGGACCTGTTCATGTTGTTCTTCCTGTTGTCCT
TTTCTTCTGAGTCCTCCCCAGACACTTCAGATAAAGCCCCGTGTGGTCCAAGGGAGAGTC
AAAACACTTCCCCAGAATGGGAGATGAAAATGTTCTATTTTGGGAGCTGGGACCAGGGGA
ATTTGAACCAAAAAGTTACTGGCAGAGCATAAANACCCAGGGTNTNGATGAAGGCCAAGG
TAAGGGNAATCTTGGCTTACCAGTGGAGGGCTCGCTTATACACATTTTGNTNANAACGGN
NNCCTTCCCCGGGCCGGCCCCCCGGCAG

Sequence 319

TNCTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACTTAAACAT CTCTTAGTAATTGAGAAAATTGAAAGAAAAAGAAAAAGAGAAAAGGGAGAAAGAGAAAACAG

Table 1

Sequence 321

Sequence 323

Sequence 325

Table 1

Sequence 326

CCGGGCAGGTACCGCCATGATGAGAACATCTTGGAGTCCGAGCCCATTGTCTATCGACGG
ATCATAGTGCCCCACAACGTGAGCAAGGAGTTCTGCACGGACTCTGGCCTGGTTGTCCCA
AGTATTTCCTATGAGCTGCATAAAAAGCTGTTGTCCGTGGCTGANAAGCATGGGCTGACC
CTTGAGCGGAGACTGGAGATGACAGGTGTGTGTGCCAGTCAGATGGCACTGACCCTCCTN
GGAGGACCTAACAGGTTGAATCCCAAAAATGTTCACCAGAGGCCTACAGTGGCTCTACTG
TGTGGACCTNATGTGAAGGGGGCTCAGGGTATCAGCTGTGGAAGGCACCTAGCCAACCAT
GATGTCCAGGTCATCCTTTTCCTGCCCAATTTTGTCAAGATGTTGGAATNTATCACCAAT
GAGCTGTCGNTCTTCAGCAAGACCCAAGGCCAACAAGTGTCTAGCCTCAAAGATCTGCCC
ACTAGCCCTGTGGACCTGGTCATCAACTGCCTGGATTGCCCTGAGAACGTCTTCCTGCGC
GAT

Sequence 327

Sequence 328

AATNGGAGCTCCCCGCGGTGGCGGCCGAGGTACAGATGATGCCAGTGTTCCGGGCTGTGA
TGGGTGGTGAATCAATGTCCAGGCGGCACATGTGCTCCAGGAATGTGTCAGCCATGGCTG
CGTGCAGCTGCTGGGTCTGAATGAAGGCAGTCCCGGCTTCACTATGGGGCTTCGACATGG
CTGCTGAGGTCCTCCGGCGCTGACCGACTCGACAATTAGAAAACCTGCATNTTTAATACA
GTGAGATTTGTATGCATACACTCTGGTGTCTTCATTTTGCAGCCCATTATATTGGCTTAA
AAGCCAGAAAGGTGCTCATGCATGTAATTTATACTGGAGCAACGAATGCAGTGTATGTGG
ACGCGTGTGTGTGCACTTTGAAAGGCAGTAGTTTTAGAAGAATGAGAAGAAAATTACTTC
CTGGGCATTCATTAATAATTCAGGTGATATCCTGTACCTGCCGGGCGCCGCTCTA
Sequence 331

ANGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCAGACTCTTATTTNCTGCAGC
TNTTGAGAATACTAAAGATACCTGAGTNATTTTAAATAAATTTCAGGTTNCTTTACCAAA
CTACCCTTAACCGGATTCTCCTTGAAATGACATCACCTGACACCCATGGCATGCTGNATG
CCCACAGNTAGATTACTTTTTAGTGCGCCCACCCNCTTCTGCTTTTATTAGGNGAGGCAN

Table 1

AATCAAGATTCCCTTTTGNTGNATCTTGNACCTGTTCATGCCACTTTGATATTCTAAATTCATACATAAACCAAT

Sequence 332

Sequence 333

Sequence 334

ATAGGCGAATTGGAGCTCCCCGCGGTGGCGCCGCCCGGGCAAGGTACGGGGGCGCAGG
TCCAGGTGGCGGGGATATGCTGCCCAACTCCACCGAGCGGGCCATCACNATCGCTGGCG
TGCCGCAGTCTGCACCGAGTGTGTCAAGCAGATTTGCCTGGTCATGCTGGAGACGCTCT
CCCAGTCTCCGCAAGGGAGAGTCATGACCATTCCGTACGGCATGATGAGTTCTGAGCTGC
GGAGGAACCCTCATTTCCTCAAAAGTAATTTATTTTTACAGCTTCTGGTTTCACATGAAA
TTGTTTGCGCTACTGAGACTGTTACTACAAACTTTTTAAGACATGAAAAAGCGCGTAATGAA
AACCATCCCGTCCCCATTCCTCCTCTCTCTGAGGGACTGGAGGGAAGCCGTGCTTCTGA
GGAACAACTCTAATTAAGTACCTCGGCCGAGGTACCGGATTCTCTTTTAACCCTCCCC
TTTCGTGGTTTCCCCCAATGGTTAAAATGTTTGGATGGT

Sequence 336

Table 1

GTATCTTGTCACTTGGGGGGAATTGAGGGGGGGACAGAATTTGCTCTTAAAAACCCANGGG TTTGCTTCCATGTNTTATTACCATNTTNTTTTGTAGGCCTCCATTTGGGATTGANNGGTT AAAAAA

Sequence 337

AATTGGAGCTCCCCGCGGTGGCGGGCGNGGTACTTTGGTCCAGATAACACTGGTGATATC
ATGACCCTGAAATTCTTGACTGGACTTCAGAATTTCATAAGNGGCATGGNTACTGTTCAC
TTGGTCACTGCAGATGGGAGTTTTGATTGCCAAGGAAACCCANGCTGAACAAGAAGCTTT
AGTTTCTTTTGCATTACTGTGAAGTTGNCACTGCTCTGACCACTCTTGGAAACGGAGG
CTCTTTTGTTCTAAAGATGTTTACTATGTTTGAACATTGTTCCATAAACTTGATGTACCT
GCCCG

Sequence 339

CTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGCCCCGGGCAGGTACCCCTTCATCCA
CCAACCTCCAGAGAATAACCTGGCTGCCCTCACTTCTCCAGCTTTTCTCACAAGGCACTT
GTTACAGGGCTGCTGATGGGAGAGGGAGGGAAGGCCTGGGAGGGGGATCTGGTGGTGGCGC
CCAATCTACAGGGTCCGGAATCAGGGTGGAAGTTGTCAGGGACTAGCGGCTGCCATAGTA
CCTCGGCCGCCCGGGCAGGACGTGTAGTGGGCCGGAATGGAGAATCCAGTGAACTGGACC
TACAAGGCATCCGAATCGACTCAGATATTAGCGGCACCCTCAAGTTTGCGTGTGAGAGCA
TTGTGGAGGAATACGAGGATGAACTCATTGAATTCTTTTCCCGAGAGGCTGACAATGTTA
AAGACAAACTTTGCAGTAAGCGAACAGATCTTTGTGACCATGCCCTGCACATATCGCATG
ATGAGCTATGAACCACTGGAGCACCCCACACTGGCTTGATGGATCACCCCCAGGANGGGA
AAATGGTGGCAATGCCCTTTATATATTATTTTTTTTTACTGGAATTAACTGGAAAA
Sequence 340

GGAGCTCCCCGCGGTGCCGCCCCGGGCAGGTACCGACCGCTCCGAGATCTGTATGAG
TTGGAGGCAGGCCAGTGTGAAGGTGTGGGAGGAATCCGCCCACACNCAGCTTCATACAGC
ACCCTGAGGACAATGTGGCTTCCCTGATTCACACCTACTGAGCCAAGGCCCCCTCTGAAG
TTAGGTCAAGAGGGCCCACCCTAGCCGGGCCAACTCATTCCTTTGAGGACCTGNTACTCA
ATGAACTGCTTACTACCAAAAAAATGCTNAGGATTCAGCAAAAAGTGCAATTTCCATTTG
AGAAGTAAGATTCTNCCCAAAACATGACACCACCTTTTCATCCTTTCAGTACCTNGGCCG
AGGTGGACTAACTGCAACGGAGAGACTCAAGATGATTCCCTTTTTACCCATGTTTTCTCT
ACTATTGCTGCTTATTGGTAACCCCTATAAACGCCAACA

Sequence 341

TATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACTTCACTCAGAT
ACTAAATAGTAGTTTATTCTTTAATATAAGTTACATTCTGCTCCTCAACCAAATGCAATT
TTTTGTGTGTGTTTGAAAGCTAATTTGAGAAAAATTTCATAGGTTACATTTCCTGCAGCCT
ATCTTTATCCACAGAAAGTGTTTTCTTTTTTTAAATCAAGACTTTTAAAACTGGATTTCC
TCCCATCACTGTTTTTTGAAGGTCCTCCAAGTCCGTGTTAAGGTAAATATCTGTTTTCTT
CCTGATGTCACAGCCTGAGCATACTCTGTGCATTAGGAAGACCTGAGTGCATTTCCCACC
ATTGTCCTTTCCACATTATGTTGTAGCTGGCTGGCTGTCAGGCGACTACAAGACTGAGGG
TCTTGTGCCTTATAGATCTTTGTATCCCCCATGGCTGACACATAGTAGGTACCT
Sequence 342

NATTGGAGCTCCCGCGGTGGCGGCCGCCCGGGCAGGTACTGCATGTTACATATTCTTCT
TTAAAATTTTGTAATAAACATTGACAGTGTTTGGTAGGCACAGGGAAACAGGATAACGTA
GAGTCATTACAGAAGAAAAAACTTATTGCTAACATTGCAGTATTCCTTTTATCAGAATT
AGGTGAGTATTGATTGTAAAAAGCTCTATCAACTCTTGCTCTTATTTGATGACTTTGAGAC
TTTTTTACTCTTGCTATAAAAAGAAGGCTACTTTCTTTCCCTAATATATTTCTACCAATG

Table 1

Sequence 343

AGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGNNGGGAACNANAGNANAACTAAACGAT GATGAATGCNNAANNTNCANNAAACGGNGGANNGGNTGNANNGATGNGGNNCCCACTGTN NNCANCNNNATTACATGACATNAAATCAGANACNANGGAGGCCCTGCTACAAAGAAGCAC AAGATGTGGTGTTGCTTAAAAAGTCCTGTATGTGAGGAACTCTTTCATTTTCTTGGGGAT TGGCAGTGCTAGGACTTGGTAAGTTGTTAGGAAACTTCGAAGGGCTTTCCGGCATAAGTG CTTCAAGTGAGCACAGGACCCTAGGAGCTGTCCAAGAACTGGA

Sequence 344

AGGTACCAGACTCTTATTTCCTGCAGCTTTTGAGAATTCTAAAGATACCTGAGTCATTTT
AAATAAATTTCAGCTTTCTTTACCAAACTACCCTTAACCGGATTCTCCTTGAAATGACAT
CACCTGACACCCATGGCATGCTGCATGCCCACAGCTAGATTACTTTTTAGTGCGCCCACG
CACTTCTGCTTTTATTTAGGTGGAGGGCAGNAATCANAGATTCCCTCTTTGTTGGGATCN
TTGAACCCTNGATTCATGCCACTTTTTGGATAATTTCTAAAAATNCCATTACCATAAAAC
CCAAATTGAAAATTATATTGNTGTTTANGAAAAAAATTTGGCTTATNTT
Sequence 345

CTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACNCCGGCCTGCANAAG CCCTCGTGGCACCCGCCCCACTGNGTGCTGGGCCCTGTCTGGGGCACGCTCTACTCAGCC ATGGGGTACTATATNTTTAGCTTGCAATGACATGACTCCAGAGCAAATGGCTACAAATGT GAACTGTTCCAGCCCTGAGCGACACACAAGAAGTTATGATTACATGGAAGGAGGGGGATAT AAGAGTGAGAAGACTCTTCTGTCGAACACAGTGGTACCTGCCCGGGCGGTCGNCCGGGCA GGTCTCCAGAGCCTTCTCTCTCTGNGCAAAAATGGNAACTTTTAAGGAA Sequence 346

Sequence 348

Sequence 349

GGGCNAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTGATTTAACACTCTGTATTACT GAACTTCTTTGAACTATTTTGAACTTTGAATCTCTCTCTGAATAACTGCCGAAACTCAA

Table 1

Sequence 350

CCGGGCAGGTACAACTTAAATAGCATNCTAGGGTAAAGAGTAACATATTCCCCAAGAAAC
AGAACTAAAATATTTCCTATTTTATGAGAAGAGTGAGTNAGAACAAACAGGGATACCTNN
CTCACCAGCNNCACTTAATAAAACATTTNATTTCCATACNAAATCCACAAGCCTTTTCGG
TCAGACTTTAAANGAATGTATNATTCGAAAAAACAATNAGTTTATCTTCAATTTNAAAAA
ATNTCANTTGGAAAGACNTAANTAAACCNAGTGGAATTCTTTTGGCTTNAACAAATTATT
GGTTACAAATTTNCCCAAAAAGGGGTTTNAAATTAAACCTTTANTNAAGNGTTATAAAAN
TANACNCNGTTAAAAATTAANTTGGGNAAAATAACNTATTNTTTTAGNTTCCCTTGCGGG
GCCCGGTTTCTNAANGAAACTTAAGNTTGGGAATCNCCCCNCCGGGGNCTNGCTAAGGGG
AAATTTNCAATTATTTAAAGCCTTTAATTCGANTTCCCCGNCNCGAACCCTTNGAGGGGG
GGGGGGCC

Sequence 351

TTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACATGCAGGGAATATTACAAT
TGCAATCATTATTTTAACACCATCTCCTCCCCCTCTTCCCTTCCCAAAAGATATAAAGAC
ATAAACATCATCTGCTGCCAAATAAATCCTGAAATTCGAGGGGCGATGCTGGGAAGGTAT
GAAATTAGAGGGAGGCATGTTGCTTTTGCACTTTCAGATCCAATGCCTGAATTCCAGACCC
GGGGAAGCCTTTCAGATCCGCATGTAATTTGTTTAAACAATTGCTGTTCATCTGCCACAG
CAGCACTTGTAATGCCGCAGGGAGGAACTTGCAGCATTTCTTGCTCACTTCAAGAAATCA
ACTATAACAAACCTNTTNCAGAAGACTACCGACATNCATATTTCTGCAATAGTTAGATAA
AAGTTAAAGAACTGGTCCTTTTTGTGAATATTCACAGTCCACTGCATATAAATCGGTTTA
TGA

Sequence 352

GCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCCAGAGACTATGATTTATATTGAT TGCACTTGCCTGCCATGATTTAGATAAGATTTTTTTTGCATGGTTTTTATTCTTTCCTAAC GGATCCTGTTTTATAATACTTCCAAGCCTGTCCATGGATATATCAAATGTCTTCACTTGT ATATTTTCATGGCTAGGTATTTCTAATGTTTATTCTTCCCTGTGTACTGCAGGGGATGCT CTGCCGGTCCAGGGACAACAGCCTTTCTCTTGCTACTGCTCTGATTCTTGTCTCCGTTCCG

Table 1

TTTTTCCTTCTCACCATCTTTCTGTGTGCTGTTTTCTTCATTCTGATCATGGTCCCGAC
TGTCATCATCTTTCAAAGCGTCGAACTTGTTGTTCATCCTCTCGCCGCCGCTGTCGCCCC
CGCGTACCTGCCCGGGCGGCGCCG

Sequence 356

Sequence 357

Sequence 358

CCGCGGTGGCGGCCGAGGTACTTCTTTTCCAGAGCAGGTGGCACAAAACGACCCCCCAGG
TAATGGTAGCGACCGGTAAACTGGGTTGCAGATTTTTTTGGGGGCTGTGAGGGAGATGAGC
AAGTCTGGCTGGATCCCTCCAGCATTTCCCTTCTCCACGTCCCATCCTGAGGGAATGTCG
ATGCTGGCAATGGGCACAGTGAGCCCTTCAGGACACTCAGCATGCTGGAACCGTTCC
CGAACATCGCCCTTGAAGCTGAAGCCAAAGATGGCATCCACCACCAGCTCATACAGTTCA
TCAATCGTCATGGGCTCTGCGGGCATTTCCCCAAGGAAAGGGATGTCCATTTTCTGACAC
TGGGTCACCAATGCAGTGAAGAGGGGCTTGTTAGGCCTTTTTGGGGTAATAGATGGTTGGC
TCGTAGCCAAAGAGTTTGAGGTGTCGAGCACAGACCAGACCATCTTCTTCATTATTCCCC

Sequence 359

Sequence 360

CCGGGCAGGTACCAGCGCGTCCCATACGTGGAGCCGCCGAATACGAGTTCTTTTGGGGC
TCCCGGGCCAGCCGCAAATCACCAAGATGCAAATCATGAGTTCCTGGCCAGGGTCTTT
AAGAAAGACCCCCAGGCCTGGCCCTCCCGATACAGAAAGCTCTGGAGGAGGCCAGAAGC
TCTGCGGGAGGCTAATCCCACTGCCCACTACCCTCGCAGCAAGTTGTCTTCTGAGGACTA
GCCAAAGTTCTGGGAGGNCAAGATTGAATGGGTTTTCNTGACCCCTCAACNCANGGGCTT
GTTGGGAAAGGGGNAGGGGTGGCTGGCGTTCATTAATAGGTATTTCANGGGATTTTAACA
GGCTGGCAANTAATTTNCACNGTTNTAAACCTTTTTTAAAGTATTTCCAAGGTNACCCTT
CTTTNCCGCNTCTTANGAAACCTAAGGTGGGGAATACCCCCNCGNGGGCTTTGCTAAGGG
GAAATTTTCCGANNAATTCAAAGNCTTTNATTTTGANTACCCGGCTNCGTANCCCTTCCC
AGGGGGGGGGGGGGCCCCCGGGTTAACCCCCAAGCTTTTTTNGTTT

Sequence 361

Table 1

Sequence 362

CCGCGGTGGCGCCCCGGNCAGGTACAATGTTGTTATGGTAGAGAAACACACATGCCT
TAAAATTTAAAAAGCAGGGCCCAAAGCTTATTAGTTTAAATTAGGGTATGTTTCAAGTTT
GTATTAATTTGTAATAGCTCTGTTTAGAAAAAAATCAAAGACCATGATTTATGAAACTAAT
GTGACATAATTTCCAGTGACTTGTTGATGTGAAATCAGACACGGCACCTTCAGTTTTGTA
CCTNGGCCGCCCGGGCAGGTACAAAAAAGGGATCAGAAGGGCAAGGGCATGCTAACGTCA
TCGGGGGGCCAGTCTCCAAGTCGCAGNCNCGTGCCCCCCGGAGGCCGGTGGCTATCTGAA
CTCTATGCATTCGC

Sequence 365

CCGCGGTGGCGCCCCCGGGCAGGTACACTGTCACCTGGAAGTGGTTCTTCTTCTGGCA
CACAAAGGCGTCGTCGCCCACCGAAAAGTTGAAGCCCTTGTCCGCATCCACGCGGTAGGT
GAGCATGGGCAGCTCCTTGTAGTTAGCATCGTACCTATAAAGTAAAGCTAAAATGATTTT
ATCTGTGAATTCAGATTTTAAAAAGTCTTCACTCTCTGAAGATGATCATTTGCCCTTAAG
GACAAAAATGAACTGAAGTTTCACATGAGCTATTTCCATTCCAGAATATCTGGGATTCTA
CTTTAAGCACTACATAAACTGACTTTATCCTCAGACTAGATGATTTTTGTGCTGTTT
CAGGATGTTTGCACTGAAGAAAAACAGAAAGCTTATCTGAAATTTATAAAACTTTTTGTT
TTGCTACATAGAAAACAGAAAGGTA

Sequence 367

Sequence 368

TNCTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACAGGAGTTTCCCTATTTTGGTGTTCAGCTTGAAAAAGGACTTGTCAGAATCAACTGTGTCATCAAAATTTAAGTAAT

Table 1

Sequence 370

Sequence 371

Sequence 372

CCGCGGTGGCGGCCGAGGTACCTGAGGAACATAGATTCTCTGCATCTTTCTCAAGGGGAA CCCTCTCCAGCTTCCCTGGTGTGACCCTTCACATGCCAGATTGGGTAGGATCACTTTGAA CTGCCTGAAGTTCAGGAAGGTCATCAAGCTC

Sequence 373

ACTACTCAGGGCGAATTNGAGCTCACCGCGGTGGCGGCCGCCCGGGCCGCGTGAAGAGGA
AGAATGCCNNGAATTCCAGGGTGGGGCTGGGGCTGGAGACGACGAGGAGGAGGATTAAGT
CCACCTGTCCCTCCTGGGCTGCTGGATTGTCTCGTTTTCCTGCCAAATAAACAGGATCAG
CGCTTTACACCATGTTGTTACATGTAAACAAACTTCAATTTGAAGTGCAGCTATTATGTG
GTATCCATGTGTATCGACCATGTGCCATATATCAATTATGGTCACTAGAAAGTCTCTTTA

TGATACTTTTATTGTACCTCGGCCGCTCTAGAACTAGT

Sequence 375

CCGCGGTGGCGGCCGAGGACAAATGTGGTGTGTCTTCCAACTTTCATTGAAAATGCCATA TCTATACCATATTTTATTCGAGTCACTGATGATGTAATGATATATTTTTTCATTATTATA GTAGAATATTTTTATGGCAAGATATTTGTGGTCTTGATCATACCTATTAAAATAATGCCA AACACCAAATATGAATTTTATGATGTACCTGCCCG

Sequence 376

ATACACTACTATAGGGCGAATTGGAGCTCACCGCGGTGGCGGCCGCCCGGGCAGGTACGA GTTCAGCCTGACCCGTGAGACAAAGAAGCACGTGCTCTTTGGCACTGTGGGGGTGCCTGA GCACACATACCGCTCCCGAACCAACTTCACCAGCAAATACAACATGAAGGTCCTCTACTT ATCCGCCTTCACTAGCAAGGACGAGGGCACCTACACGTGTGCACTCCACCACTCTGGCCA TTCCCCACCCATCTCCCCAGAACGTCACAGTGCTCAGAGACAAACTGGTCAAGTGTGA GGGCATCAGCCTGCTGGCTCAGAACACCTCGTGGCTGCTGCTGCTCCTGCTCTCCTCTC GGAAGCCTTCAAGTTTCCAAGTGCAAGAAGATCCTACTTNTTTTGAGTCAAGCTGACCCC CTCCCCCAATCCCTCAAACCTTGAGGGAGAAGTGGG

Sequence 377

CNGGTTCGCTGTGCCTAATACATGCATGTTGAACGGGATGTAGCAATACATTCAGTAG CGAATGGGTGAGTAACACGTACCTAACCTTTAAGACTGGGATAACTATTGGAAACA ATAGCTAATACCGGATATAGTTATTTATCGCATGATGAGTAATAGAAAGGAGCTTCACAG CTTCACTTAAAAATGGGGGTGCGGAACATTAGTTAGTTGGTAGGGTAATGGCCTACCAAG ACGATGATGTTTAGCCGGGCCGAGAGGCTGTACCCTCGGCCGCCCGGGCAGGTACAAGAG TGATGGCAATGTGACTGGAACAGAAATAGTTTCTACCAGGCACACAAAAGCTTCTGTAAG CCCCGTANTTCCGTCCTGCAAAGGGCCTTNAGTGGGAACCAGGTCTGCAGACCCCAGTGG GCANAAAGACCGGGTGGAAGCAGG

Sequence 378

CTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACAAAAGGAGAAA AACTATGTCTAAGGAGGGAAGCACATAATAGAATTCTATTATTACAATAGAATTCTATAA ATACAAAATTGGATAAACTTTATCAGAAGCAGGTGTTTGTCACCATTTTATATGTGAAAC TCAGGAAGTTCTTGATTTTTTAAGAGCTGTATTCCTTAATCTGGTTACAGGCTATAAAGG AGATAATCATTTACATGATCATATTCTCAAACAGATGGTCACCAAATGGAATCAAAGGAC TGATTTGATGTAGCCGGTAGTATGATAATTTTTGTAGGTTAAATGGAAAAATACNGGATA GGATCCNAGAAAAATAANGTAATTTTNCCAGGTAGGCCNGGTTTAATAAAATTACCAGGA CCTAGGAATAAGCCAATTTTA

Sequence 379

CATCTGTTTATTGACAATTCCAGGTCATTCCTAACACGCCGNANCAGGGCTNTGTACCTG CCCGGCCGCCCGGGCAGGTACTTCATGAAGCANACCATTGGGAATTCCTGNGGCAC AATCGGACTTATTCACGCAGNGGCCAATAATCAANACAAACTGGGATTTGAGGATGGATC AGTTCTGAAACAGTTTNTTTNTGAAACAAAAAAAAATGTCCCCTGAAAACAGAACCAAAA TGCTTTTGAAAAAAANNGGGGCCTTACCAGGCAAGCCCAATNAATGCCCCGGGGCACAA AGNAAGGCCCAATTGTTNGGGGTAAAAANAAAAAGGGGGGAAAATTCCCCATTTTTTNT TTNTTNTTTNAAANANCCCGGGGGGGGGGGCCCCCNTTTTANAAAAANTTGGGGGGGAA CCTTTTGANGGANCCNCCCNNNNTAANANAAAAAAAAA

Sequence 380

ATTGGAGCTCACCCGCGGGGNCGGCCGCCCGGGCAGGACCTCTTTGCCTTAAATTGCTTT TTAAGTTCTAAGATTGTAGAATGATCCTTTCAAATTGTAATCTTTTCTAACAGAGATATT TTAATATACTTGCTTTCTTAAAAAACAAAAAACTACTGTCAGTATTAATACTGAGCCAG ACTGGGCATCTACAGATTTCAGATCTATCATTTTATTGATTCTTAAGCTTGTATTAAAAA TTTATCTGTCTATCCATCCATCATCTTGAAGGCCTAATATATGCCCAAGGACCTCGGC CGCTCTAGAACTAGGNGGGATCCCCCGGGCTGCAN

Sequence 381

TAGGGCGAATTGGAGCTCCCCGCGGNGGCGGCCGAGGNNCTAAGCCCCAGGACCNATTGG TAGACGACNTANNANCNNAGGCGCATNNCACTGAAACANGTCAGNGTATATGNTGGCACG

Table 1

TATTAAANTTAAGATGAANGNNGAAGCAAAAAGATTTACAAGAATTAGCNGTAACAANAT TGATGCTNAAGAGACATNATTGTACCTGCNCN

Sequence 382

TNCTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGCCCCGGGCAGGTACTGCCGGCAT
TGTCTTAGGGGTTAATAAGGTTAACCTATGGTTACAAAACAAAGGGTAACTTGAAGTATT
GAGTAACTGCTTCTGTAATATGGGGGAGAATAAATTTTTAAATTTGGTTTATTTAGAGGA
AAAATTTTGACTTAAATTTAACACTGATTTGGCACATAAGCATTGAGAGTGTATTTGGTT
AATGGTTTAGAAGCAAACCAGCAAAGGAAAAAAGCAAACCCTAGCAAACCTTTCACAAAT
GTTAAAGAGACACTGCTCCATTTTAAGCAGTGCGGGTCATTTTGAGTTTAATGAATCCCC
ATCAAATGGGTGGTATAGTAGATAGCTATGGTGTGGTTTGTAAGGGTTTGTAGCTTGCAA
GGACGTGCACTAATAATATTTTATATGATCTTTCCTGGTTGGCAGGACCCATGGATGAA
Sequence 383

Sequence 384

AGGTACCAGACTCTTATTTCCTGCAGCTTTTGAGAATTCTAAAGATACCTGAGTCATTTT
AAATAAATTTCAGCTTTCTTTACCAAACTACCCTTAACCGGATTCTCCTTGAAATGACAT
CACCTGACACCCATGGCATGCTGCATGCCCACAGCTAGATTACTTTTTAGTGCGCCCACG
CACTTCTGCTTTTATTAGGTGAGGCAGAATCAAGATTCCCTTTTGTTGGATCTTGAACCT
GTTCATGCCACTTTGATATTCTAAATTCATACATAAACCAATGAAATATATGTGTTAGAA
AAATTGCTATTTCTAGCTGGACGCAGTGGCTCATGACTATAATCCTACCA
Sequence 386

AGGTACCCAGTATTTCTAATTAAATTTCACATGCTAAATTAATGAAAGTAACAAGATTGT
AATTTTTTAAAGTCAGTTGATTAAATGCAATAAATATTGGGTTGCTCAAATATGCCACAA
ATAACTCGAAATTTTTCATTTACTTTCAACAGCATAAGATTCTTTAATATTTAGGATTGA
CTGNTTCTTTCCAGTTAAGCACTGAAGGATTATGTCTTGTAGCTTCCCCAAGAGAAGGGG
AAGGAAAAAAAAGCACTATGTTAAGGATAATACAGAACTCTTTTGAACTATTTTGGGTAG
TACCCTGCCCGGGCGGCCGNCCGGNCAGGTACCAGTGGAGG

Sequence 389

Sequence 390

Sequence 391

CCGGGCAGGTACCGCATCAGCAAAAGTGCCTGGCTGAAGGACACTGTTGACCCAAAACTG GTGACCCTCAACCACCGCATTGCTGCCCTCACAGGCCTTGATGTCCGGCCTCCCTATGCA GAGTATCTGCAGGTGGTGAACTATGGCATCGGAGGACACTATGAGCCTCACTTTGACCAT GCTACGTCACCAAGCAGCCCCCTCTACAGAATGAAGTCAGGAAACCGAGTTGCAACATTT ATGATCTATCTGAGCTCGGTGGAAGCTGGAGGAGCCACAGCCTTCATCTATGCCAACCTC AGCGTGCCTGTGGTTAGGAATGCAGCACTGTTTTGGTGGAACCTGCACAG Sequence 393

AGGACAAATTCAGTCCCAATACTCAATACGTATTATAGATGACTATGAGTGCAAACCTTA GGATGTGATTTTCTGAATAATTGTTCTTTGTAGGATTTGGTTACATTATTTAAAATGAAA AAGATCTAGTTTTAGTGTGAGCTCAGTAATGTTAATTGGTTAAGTTCATTGTGAATCTTG AGTTTTAGATAAGNAGTTATTTTTTTCAATATCACTTCTGTTTTTAGTGATATTATATCA AGAAACAACGTATTCAAGAGCCATGGCTGACAGTGCCAGATATACTTAGGGATAAACATC AAAATGCAATTATAGTTGCTATAACGTTAGATACTCGGAATCAAAATTT

Sequence 394

Sequence 395

AGGTACATAATAAACAAGTTTCAACCAGCAAGAAATTACTAATATTGACTGTGGAGTTTT GGCTGTTTTAATAGTTCTAACTCATTATTCCGTAATTCAACACAGCACTACCAACACAGC TGGCAATGACAAGACTGGGAGTATCAAACTAGGATTATTAGGCACAATCCAGGTGGCCTC TGCAGCTGTGTCTCTCTTTCCTCTTCTGTTCCTATAAGGGCAGGGCCTCCTTCAGGAACA GCCACCAGTGAGCTTCCTCCTCCCTTCTGGTCAGTTGGATTTGTCACTGTTCAGCATCTT TTCGATGATTTACCTGCCCG

Sequence 396

Table 1

GCTTTTCTTTAAGAGTTCATTTTAA

Sequence 397

TTGTCTGAGCTACTGGAATGAAGTTCACAGGTCTTGAAGACCAATATTATTTGTCAATAT GTGGGGATAACCTGTAGCTGCATTCATGAGGTAGCAAATAGCAGTTTTGGCCTGTGGGGT GAACAGCTAAACAGTGTTCTGGCATCAGATAACACGGCACAAAGGGATTGTGTCTAGCTC TTTTGGAGAAAATTTATGTCCAGTCTCAGGATCTGTGGACAATAACGGAAAACTTTGAAT ATTCCTGACAAGTTGCCATATTAGGAGTCAGTTCTTTACTTCTCTGAGATTCCCAGGTCA TCCATGATTTTTTTTTTAATTTGAGACAAAGCCTCACT

Sequence 398

NACACCCACCGCGGNGGCGGCCGCCCGGGCAGGTATGGNTCCGNGGATGCAAAACCCCTG GGCCGCAAGAGGGAGCCAAGCTGACTCCTGANGAAGAAGAGANNNGAAACAAAANCCGA GNACCNGACAGNAGTTTAAGANGAGAGAGGNNAGGGNCCACNCGGNNNAAGCAAGAGANA GAGNAAGGAAANAAAG

Sequence 399

CTCACCGNGGTGGCGGCCGCCGGGCAGGTACACGGACCGCACGGAGAAGCTGAGGCCTG AGATGGAGGGCCCGGCAGCTTCACCATCTTCGCCCCTAGCAACGAGGCCTGGGCCTCCT TGCCAGCTGTGAGATGACCTCCGTCTGCCCGGGGGACTCTTATGGGGAACTGCCTTACTT CCCCGAGGGGTGGGCATGATGAATGGGAGCCTGCAGTCATTTCCTACTGTTTCAGGAAGC TTTCTCCTTAACCCCTTAGAAAAGGCTGTGGAACTTGAGCTAAAATATGTCTTACCAGGT TGCGTCTAATGCCCCCGTTCCCTACTGGGCAGAAAGACTTGGGTGCTTCCTGAGGAGGG **ATCCTTGGCA**

Sequence 400

AGGTACTGCTTAATTCTTTTTCTCCCTCCCTCTAATCCTTTTTTTGACTGTCACATTTG TCCTAATAGCAAGTTAGGACATGTCTGTTGGCTCTCGAGATTCATGGGACAGCAATGCAG CAAATCTAGCCATAGTATTTGCTCTCTCTAGCCCTGCCCTTTTTCCTGTCCAGTGAATAT CAAAACAGGTAGAAAACATGGCCTGAAGGATTGTCTCTGCCACCACCTCCATATGCATTT TACCAGTAGTCCTGTCATACAGGTTGAATTAGTTTTATGTAGAACAAGTCATGAACACTT TAGTGTGGAAAAATAGTATTATATAAAGCTTAATATTAA

AGGTACATTATCAGANACAGTGGTTGACCTCTTTTTTCCTTTACTCCCTTTTCATCTGAG AGAGCCTTTTAGAGATCCGGAATCATTTGCTGTCTGCAATTACTATAGGCTTTGGCTCAC AATTCTGGGGAAAATGCCAATTGAAGGAACCCTGCCTATACATTTTATTTTCTTTTCTT CGAGACAGACAACCTCAAAATAAGGTCCAAATATTNGGTTCCTTNAAATGGTGTCAAAAA GAATAGTATTATGAGGAGGATAGTTATCACAGAATAAGAACTAAAATCCCATTTTTTT TTTTTTAGGAAAAAAGACCTTCNATGATGCAGGTGTNTGTGTATAAGGAACTA

Sequence 402

AGGTCTCAGCGTGGCTACAAGTAACTGTGGTGGGAAGCAGAGTAGAGAAAACTTGTT CCTCATTAGAGAGAGAGCCACACTTCTCACTGCTCACAATGAGAGGCCAAAGATTACCCT TGGACATCCAGATTITCTATTGTGCCAGACCTGACGAAGAGCCTTTTGTGAAGATCATCA CTGTTGAAGAGGCAAAGCGCAGGAAGAGCACATGCAGCTACTATGAAGACGAGGACGAAG AGGTGCTGCCTGCCTACGGCCCCACAGCGCGCTCCTGGGGAATATGCACATCGAGCAGC TGGCCCGACGCCTTCCTGCAAGGGTGCAAGGG

Sequence 403

AGGTACATTTCCATGGGCCCTGTTCCCATTGATGTATACTGCTTCCTTACTAACAGTGAG GGATGACTTTCATCAGTCTTTTATCACCTGAACAGTCTTCCGGCCATAATGATAGTAACT ATAAGCTGATGCAGCTGTGGAAAGCTGTAAAACACCTTTTATGGAAGAAAAAGAAATAA AATGTAGTTGTCAAGTCTAAAAAATAGTAGCAACGGGAATCATAATGAATACATGCAATG AATTTAAAATGTAAAAATGAATTTAAAAAGTAAAAAGGGCTCTGTGGTGTAATTTTTCTT AACTACAAGAGTCTAAATACACTGCTTTTCTTTAAGAGTTCATTTT

Sequence 404

GTGAATGTGTTTGTTGCTGGCTGAATGGCAATAGATGTCTAAGGTGGATTCAGTGTCT GGCACACTGAGACACCTCCAAGAAGGAGATTGATGCATCAGGTTCAGTTTAACCTGGAAT ATCTGACTACCCCTGAATCCACCCAGAAAGGGGGCCCAACACCCTTGTCCATTTATGGGT

Table 1

ATTITITTCGAAGTTATTAAGCATATTCCTTTTCCACGAACCTCTTCTGTACCTGCCCG

Sequence 405

Sequence 406

AGGTACGTTCAGATGTAGCCATGACTGGAGAAATTACACTGAGAGGTCTTGTTCTTCCAG
TGGGTGGAATTAAAGACAAAGTGCTGGCGGCACACAGAGCGGGACTGAAGCAAGTCATTA
TTCCTCGGAGAAATGAAAAAGACCTTGAGGGAATCCCAGGCAACGTACCTGCCCGGGCGG
CCGAGGTACTACTAATTCTACAATGCCTTTCTCTTTAGTCAGTATTAAAAATCTTTTTTA
AAGTATTGGTATGAAAACAAATTTTTGTTGCCCTGATAATGGGAATTTTAAAACTACCCA
CAGTTTAAGAGAAAACATAACTTGGTAAAAAAAGGTAGCCAATAAAACCACA
Sequence 407

CTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACAGAAATAAAAATTAG CAAACAATTATTCTAGGGATATTTTCAGATTTTACTTCATTTCTTGAAATGCGTGTGCCA TATGCAATTGCATTTCTTGTGCCAAGAAACTAATAGAACTTATTTCACTTTTTT TAAAATGTGAATTTAAGTTATATAGTTCAATTTTATGGCCTTACAGATGGCTTTTATTT TGTTTGCAGCTGACACTGCAGTTCCTTTCATGCAAAATACCATAAACTGTTTGATGAAAA TCATGCCCCTAATGGAAACTCTCTAGTTTTTCCATATAACTATCCTACTGTACCTGCCCG GGCGGCCGCTTCGACCAACATGTGGTGAGCATTCCACGGGCGCATGAAGTCTGGGTGCTG TGCTCGAGTCTCTGAATATTTTGATAGGAAAGCGACAAGAAAATTCAA Sequence 410

TTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACAGAAATAAAAATTAGCAAA
CAATTATTCTAGGGATATTTTCAGATTTTACTTCATTTCTTGAAATGCGTGTGCCATATG
CAATTGCATTTCTTGTGCCAAGAAACTAATAGAACTTATTTCACTTTACCTTTTTTTAAA
ATGTGAATTTAGTTATATAGTTCAATTTTATGGCCTTACAGATGGCTTTTATTTTGTTT
GCAGCTGACACTGCAGTTCCTTTCATGCAAAAATACCATAAACTGTTTGATGAAAAATCATG
CCCCTAATGGAAACTCTCTAGTTTTTCCATATAACTATCCTACTGTACCTGCCCGGGCGG
CCGCTTCGACCAACATGTGGTGAGCATTCCACGGGCGCATGAAAGTCTGGGTGCTGTGCT
CGAGTCTCTGAATATTTTGATAGGAAGCGACAAGAAAATTCAAACTGCTCTTTTGCTGACT
ACTGGNAAGTGAAAAAAGATGCTTCAAGGTTTANCCATTCAAAGGAAACCATTAGGCCTTT
TCAAAAAAC

Sequence 411

CCGCGGTGGCGCCCCCGGCAGGTACAGGAGTTTCCCTATTTTGGTGTTCAGCTTGAA
AAAGGACTTGTCAGAATCAACTGTGTCATCAAAATTTAAGTAATGTGCATTGAAAATAAG
GTTGATCATGGGAATATGCAGAATTTCCAATGTATTTTTAAATAACAAATAAAATTGTAAT
TTAGAATTTTTAATCTTAGGTTTCTTGATTAATTTATAAGAGATCAATTATTGTCAGTCT
TTTTTGTATGTTTTTTAAAAACATAGTCCAGAGCATGGCCAGAATTGACACCTCTCTTTT

Table 1

Sequence 412

Sequence 413

Sequence 414

GCGGNGGCGGCCGAGGTACTATGAAAAGTTGATTGTAGCACAACTGTTCAATNAGTAAAA GGTCTTCGGCAAATTCCCTTTAGAGTATACTTTCTATAAACTACATGTTCCACAAAAAGG TCAATTATATACAATTGATTTGTTTTACTTAATCTTATTTGCTCAGATCTTGCAAATG CAATGAGAATATTAAGCCTGAGGCTAGTTCTCAGTGTATAGGTTTAACAAATTAAGGCTC ATTTTCCCAAATCAAAATAGTTTTTAGTTTTCCTTTTAAATTATGAATTACATTCATAGT ACAAGAAGAAATGCTTAAGGAAGAATTTCAAAAGAAATCTGAGCNGTTAAATAAAGAGAT TAATCAACTGAAA

Sequence 415

Sequence 416

Sequence 417

Sequence 418

Sequence 419

Table 1

AACCCTTCAATTATAAGTTAGTNCTTTGGTGGAAGTAAGGATGGTTTGTTAGGACNTTTA
TTAGGTTCTTTAAATTTCATTTGGCCACCAAACCGTGGACTGGTTTGTAAGTCTTAAACC
ACCCCAAAATTAAGTGGTCGTTNGGCCAAATTAACTTTTTTTTAAAAATGGGCTTGNAAN
AACCACCCTTAATAAAATTNGTTNCATTCAGNAAAATTATTCTTTGTTCANCNTGNCTTC
CTGGTTTGCNCAAAATACCNTCTANNNAAATTAGGGAAACTTTTAANNACCGTTTATGNT
TCCTTGAAGGTTCCCCCNTGGGAGGAANCCACCATTGGCCTTAANAANGTTCCCNAATTG
GAAAAAAAAG

Sequence 420

Sequence 421

Sequence 422

Sequence 423

Sequence 424

Sequence 425

Table 1

TAACACTACTTAGGGCAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACTGCG
TGTTCAACCGCAACGAGGATGCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCC
TGGCCTCGGCTTTCTTCTTGGTGGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTG
ACCGCAAGTACTTCCTTTGGCAGACGGCTATTATGTTTTACTTTAGTGCCGTATTGTGGA
TGCCAGAGAACTTGCATTTGCCAGGGAATAATCTCCTGAGATGCTATATTATGAAGTAGA
ATGGTGTAGTCTAATTCAATAAAGTCATCATTTCTTTGCACTTGGTCTTGGACAGTTTGAAT
TTTTACCATTTTATACCATGTGTCTTTCAGTAGGAATTTTGCCATATTATATAACCACAG
GCAACCCAAGCTAAAATGTAGAACGGAGCCGTCATTTCTGGGAGATACATTTCAAA
Sequence 430

Sequence 432

GGGGAGCTCCCCGCGGTGCCGCCCGAGGTACATCGATGTTGATCTTCANGTTTATCTCCC CGCGACTTGTCCACGTAGAGCTCAGGATGCACCTCCGTGGTGAGGTAATACTGCACCTGC

CCGGGCGGCCGAGGTACATGCCTAGACCTGGGCTCCGGCCAGCGCCCAACAGCGTGGATG TCGATGACTTCATCAATACGAGAATACAGGAGGCAGACAATGACCCCACG Sequence 433

ATTGGAGCTCCCGCGGTGGCGGCCGAGGTACATGTATTGCCATTTCTCTGCTATATAGT
AATATTTCTTGACACCAATGGTAATGTGTTTGTTTCTTCTCAGCACCAGATGTGTCCAT
ATGTATTTAAACAGTAGGAGCATTGTTTCTAAATTCATCTATGCTATGACATATATAAAC
CCATTATTATTATGTTTCACTAAAGTTCCAGCACTTTAGAAAAGTTTCAGTTCAAAGTCA
TTTTGGCTCATTCATTTAGATAATACTGACCATTTTGCACTACAATTTCAAAAGGAACAT
GAGAAATTTGGATTTCTTTGAAAGAGTCAAATATGTAATTACAGAATTGAAACACTGNGT
TAATTCCCAAAGGGGGTGGTAATAATTAACATTAA
Sequence 434

Sequence 437

Table 1

Sequence 439

Sequence 440

CCGCGGTGGCGGCCGAGGTACITGGCATATATTANGGCCTTCAAATGATGATGGATGAT AGACAGATAAAAGGCCCAATGAATGATTGTAAATGTGTCTTCTCCTATGTATCCATGATG ATATTGCCTAGTTTTTAATACAAGCTTAAGAATCAATAAAATGATAGATCTGAAATCTGT AGATGCCAGTCTGGCTCAGTATTAATACTGACAGTAGTTTTTTTGTTTTTTAAGAAAGCA AGTATATTAAAATATCTCTGTTAGAAAAGATTACAATTTGAAAGGATCATTCTACAATCT TAGAACTAAAAAGCAATTTAAGGCAAAGAGGTACCTGCCCGGGCGGCCGAGGTCCCCCTT TTTTTNTNTTTNATTTTNCCTNTTTNTCTTTTTCTTNTTTACTGCCCNCNNNAGTTTGGG GTTGGANCCCTTTTTTTAATTTTTNCAACACCCCCCGNCTTTATAANTAACCCTTTTAA

Sequence 441

AGGTACCAGGTTTTATTTTTCACCTTATTCTCTACTTTAAACAAATCATAACTTTCTCTT
TAAGCCTCTGCTATAAATTCTCCTGGCTCTCCTGGGCTTNCATATTTTGGGGGCTTGGGG
TGTCAAAAGTGAGATGAAGTTCTTTAGCTCCAGGTTTTGGGGTAAACCANAGGTAGGTAA
CATTGTTGGGCATTTATTTTGCAANTTAANCAANTACTTTCCTTGNNACTNGGNTGCCGG
GTGGCTCACGTNTTGTAATNCCCAGCACCTNTTGGGGAGGCNTTGAAGACCAGGTNGGG
ATNCAACNNTNNAGGGGTCGGGGTAGGTTTCTNAGGAACCATGGCGCTGNGCCNCAAACN
ATTNAGGCCAAAANACCCCCTTGTNCNTTTTNACTTAAANAANANTNACCAAAAAAAATT
TAANTATTGGGGGNTGGNTTTTTTGGGGCAC

Sequence 442

Sequence 443

Sequence 444

ACACTACTTAGGGCGATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACAGCAGA
AGTTTGCTGTCTCTAGGATTCATATAGCACCCACAGAGCTCCAAGTAACCAAATTCCCCC
AAAGACAGGAGGTGTGGCTGAGGAGGAGTGACCATATTGAGTGTAGCTTTGAACGCCTCC
GTTACTCTTTAGGAGGCGACCGCCCCAGTCAAACTACCCACCACGCACTGTCTCCTTCCC
AGATAAGGGGAACGGGTTAGAAAATCAATTTAGCAAGGGTGGTATTTCAAGGTTGACTCC
ACTAGAACTAAGCGTCCCAGCTTCAAAGTCTTCCACCTATCCTACACATGCTAAACCAAT

Sequence 445
NCTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTCCTTTTTTAAAAACAC

Table 1

Sequence 446

Sequence 447

Sequence 448

CTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACCAAATGAC
CAAAATTTTTATTTGACTAAATTCTATTCATGCATGAGCATGACAGTCTCCCGTTTATT
TGACTTTGGCAATAAAAAAACAAGCAGCCTTGTACTTCATTGTGAGGTGGCTACAACTCT
ATAATATGCACAGTGATTTTAAAATAGGCTTTTTGCATGCCTTGCATGAAAGGTGCTACA
TACAAACCTGTTTTGTGAACTCTTTGGTAACCACCAATTTAAAAATTTGGATGAAAGCAT
TTCCACATGGACAGATCTGAAGCACATTATTGGAGCTCTGAGCCAAAGCTATTACCCTGT
ATATTGATTCTTCAGTTTCCTTGAGGGGTTAGGTGTTGATTTAGAATACAGCCAGATAAT
TTAAAGCATGTCAGGCCCCGGTTAGGAAAATGAAAATG

Sequence 449

CCGCGGTGGCGCCCCCGGCCAGGTACAAAAATAGGAATGGGTTTTTTACCTGTTTAAA GTCACTTTGTGTTTATAACAAAATTACTTTTAGCTGAGGAACAAAGGTGACAAAGATTTC TGTTGGTGGCTGAGAGTCAAAGCAGGCCAATCCACACCATTACCTGAAATATTTTTCAGG CTAATTTATAACTTTATGGATTTCCTCGATACAAGTTTATTAGTTTATTCTCCATATACA AGTTTATTCTCCCAGAATAGCAGCAAATAAAACTTGAATTGGATGTACCTCGGCCGAGGT ACTACGTGCCAGCTCTAGTTTTCAGCCTTGGGAGGTTTTATTC

Sequence 450

Sequence 451

CTACTTAGGGCAATTGGAGCTCCCCGCGGTGGCGGCCCCCGGGCAGGTACTACGTGCCA GCTCTAGTTTTCAGCCTTGGGAGGTTTTATTCTGACTTCCTCTGATTTTGGCATGTGGAG ACACTCCTATAAGGAGAGTTCAAGCCTGTGGGAGTAGAAAAATCTCATTCCCAGAGTCAG AGGAGAAGAGACATGTACCCCACCTCTGAAGATGCTGGGGAGGCAGCTGGGATGGGAGC CAGCCCCATGCCTGTCTGTGACCCCACAGTGGGTGAGAGCCCGTCACAGTCCTGGGGTGT

Table 1

GGCTGCTCTGGAAGAATTAGGAGGCAGCCATAATAAGAGTCTTCAGAGAGATGATGGGAG GGGCCAGTGAGGACAGGAACAGGAGAGTNNGATGTCCTATAATAAAGGGGGC Sequence 452

CTTAGGGCGATTGGAGCTCCCCGCGGTGGCGCCCCCGGGCAGGTACGGAGATGCTGCC
TTGAGACAGCTGAGGTCACCGCGGCGCGCACAGGCCCCGAACGCTCAGGAGTGTGGTTGT
TAGGAGAGCACACAGGTGTTCATACAGTGGCATTTGGGACACAATCGTTGGAACCTGAAG
AATCTGAAGTTTTTTTTACCACCATCTTTTTCTACTCTGTAAGGAAGTAGATCTTTATGG
GGAAAAGAGAATTTGGGGTGTTCTGCAAGCCAGTCAAAGTGGCACAGCAAATCATATAAA
TCGAATTAAATGGACAACACCGTTAGATGTGTATGTAAAAAATTTTCTGTTTCATATTTTT
CCTTTCACTTTCGGTTTAAAACATGCTATATGTACCTCGGCCGCTCTAGAACTAG

Sequence 454

Sequence 456

Sequence 457

Sequence 458

CTCNCCGCGGTGGCGGCCGAGGTNCATTTCCATGGGCCCTGTTCCCATTGATGTATACT

Table 1

GCTTCCTTACTAACAGTGAGGGATGACTTTCATCAGTCTTTTATCACCTGAACAGTCTTC CGGCCATAATGATAGTAACTATAAGCTGATGCAGCTGTGNNGAAAGCTGTAAAACACCTT TTATGGAAGAAAAGANATAAAATGTANTTGTCAAGTCTAAAAAATAGTAGCAACGGGAAT CATAATGAATACATGCAATGAATTTAAAATGNAAAAATGAATTTAAAAAGTAAAAAGGGC TCTGTGGTGTAATTTTTCTTAACTACAA

Sequence 459

CGCGGTGGCGGCCGAGGTACAAGCTCCTAAAAGAAGATTACTGCTGCCAACTTAAGTCAT CTCCATTAACGAAATTGCATTCTTGTGGCAGAGTTAAAACAACAAGAGAAAATTCAGTGTT TGCTGGTTCTGAATGTCATTTTCCTCCCTGGTGTGGTTTTACATTTTCAGCTTCTTTCC CTCTGTGCTTTATTGTTGGAGAATGTGGACAATACAAAGATTTGGGGTGGGGTCATACAG TGTATACAAAACACACACTNTGTGTTTGGACAAATTCGCCTAGCGTGAGAATCATCAG TAGTGAGTTTAAAAGTTTGAAAATCAGACCCAACATTTTGGGGTGNTTAAAATATCTCCC **GCCTTGAA**

Sequence 460

ACTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCTTGACGAAGAATG AAAAGGTTGTATTAAAGAACTATCAGGACATGGTTGTGGAGGGTTGTGGGTGTCGCTAGT ACAGCAAAAAAAAAAACGTCAAGCCAAACACAAACAGCGGAAACGCCTTAAGTCCAGCT **AGTTTATTACCTGCCCG**

Sequence 461

CTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACAATGTTATGTCGGGAACA CGTGCTGCTAACTCACTGGTGAGTTCAATGGCAACGCTTCATTCGGGAGGCTGTTCTGCT TTACGCATCTGAGAACTACATAGGAGAGCAAGTGTCTGCACCTCCTAACTGCAGAAGCTA CCGTCTTCTCAAAGACGAAGGTCTTTGCAAAGTTCAGTGCTCGGTGTTCTCGGCACAACA GCTTTTGAAAAATAAGGCTTTAAGAAGGCTTGTCATTTTAGGGCTAAATTTTAATAGAAT GTGAGTCTGAACTCTTACATTTAGAACAAACAAAACCTTAAAATTNCTGATTGGTTCAAA AAATGGTTTTATGGAAAAATTAATCTGTAACAAAAAGTTGGCATTTGAGTGCGAAGGCTC

Sequence 462

TTTTTTTTTTCCTGTTGCTACTAAGATGTTTCAATTCGCANCGTGTCTCGCTAATT TGACTATGGATTCATCAAAATGCAACTGAGGTTTGCTCAGTTAGGTTACCCCATTCGGAA ATCNCCGTATCATAGTTTATTTCCAACTCCNCGAAGCTTATCGCAGGTAATCGNGTCCTT NATCGACTTTNAACCTGCCCGGCCGCCCCGGCCAGGTCCAAAAACCAACNTGACACA CAGGAAAAATAAAAGTGCAATTTTAATATAGGGAATGNGATNCATGTATAATTCCTCAT AACAAAATGGTCAAAACCTTTAAAAGATCCNCAATAGATTTCTGAAAATCTTAGCAATGC **AAACTTTCAGAGCACANATCATTGGTAATTTT**

Sequence 463

AGGATCTTGGCAGCTTCTTCCTGCTTTGCAGGAAGGACAGAGGTTGAGGTAGGAACTTCA TAAGCAATTTGGAGAGAGGCTCCTCCCATATCCAGTATCCCTACTGTCCTTCTCCGTCCT GCTGCCAATTCCTGGGTAGCCTCAGCATCTGATTCATCCTCGTGGTCGAATCTTCCCAAA ACAAAGTTGATTCCAATCCATGCATAAACCCCTTCCTGCTTCCCAGAGATCACTTCTGCT TGAGACTGTGAAAAGAGGAAGTCAAA

Sequence 464

AGGTACATTTCTTGTTTAGGAGGGTTTTCCTATCTACCTTTCTACTGAAGTAGTTTCTGG AACTITCCTGGTGGATCAGAGTTACGTAATGCAGTCTGAGCCTTCAGACTGCTAGTTAGA ATTGTTTTAGGTGTTCAGAAAGGGCAAAATAGGCTGATGTGGCCTGTCAGAGTGATGTGT TCTCAAAAAGTTCACTTGCACATCTGTGGGCCGCTTTTGTCCTCAGACCCTTAGTGGAC AGACTCCACAAACCCTCTGATGAGACGATTGATGTGGCCAGGGTCCAGTTAGCATCAGTA GAAGGATGTCACTAGGAAAGGCCCAGGTATCTGGTAAGT

Sequence 465

CCGCGGTGGCGGCCGAGGTACCTCAAACTCAGAGTTTCTTCCCTTCTTTGATTTTCTGGA

GGACCTGCAGCTGGCCTTCCTGAGACAGGCTCCATTCCTGTTCCATTTGCCTTCCCGGCA GCCTTCCCTTTAGTGGGTATAGGTTTTGACGTTCTGAGTTACTTTGTATCAAAGAGCTAA TTAAAAATGGTCCTTCAAAAACATAAAGAAAAACAGCTTGAAAAATGTACCTGCCCGGGC GGCCGCCCGGGCAGGTACCAAAAACCAACATGACACACAGGAAAAAATAAAAGTGCAATT TTAATATAGTGAATGTGATACATGTATAATTCCTCATAACAAAATGGGCAAAACCTT Sequence 466

CCGGGCAGGTACCTCAGCTATCAACATTTCTGAGCTACCATTCAATGTTCCTCTGTGTCA
TGGAGTGAAATTCTTGTTTTGTGGGTATTAGGAGTGTGGGAATGTGATAACCTAAACAAC
CTTTGCTCTGAAATTCCATTTTTCCCTCTTTCCCTGAGTTGTATTGACCTACAGAGTTAA
TTTCCTTTGTATTTTTTAAGAAAATATTAAAAATCAACGGTCTCAAAAACCTCGGCCGC
CCGGGCAGGTACTCCAAGATGAGCTTGACGCGGCTGTGCAGCATCTTGATGGCGCTGTGC
TGTGCTATCAGGTGT

Sequence 467

Sequence 468

CCGGGCAGGTACTAGGTTAGAACATTGCTTAATCCTTTTAAAAAANATGCATTNACTGTA
AACACAGAATACTGAAATTGGNGGATTTTTTAACTATNTCTGACATAATTTTATTCATCA
ATTACATTACACATTCATTTANCCCAGATTTCAAATAGGGGGGGAAGAAAGAAACTGTAT
TTCAGAGTAAAATCTCCTAAAGGAAATANAAACACAGAGTTGTAAATNCACATGCTTGCA
AAAACATTAGTCGTGAAATCCCTAGCAACAAGTCACTGGATTTTTCTCTGTCAGCACGCG
TGTCAGCTGCCAAA

Sequence 469

AGGTTTGAGCTCCATAGAGACAGCGCCGGGGCAAGTGAGAGCCGGACGGCACTGGGCGA CTCTGTGCCTCGCTGAGGAAAAATAACTAAACATGGGCAAAGGAGATCCTAAGAAGCCGA GAGGCAAAATGTCATCATATGCATTTTTTGTGCAAACTTGTCGGGAGGAGCATAAGAAGA AGCACCCAGATGCTTCAGTCAACTTCTCAGAGTTTTCTAAGAAGTGCTCAGAGAGGTGGA AGACCATGTCTGCTAAAGAGAAAGGAAAATTTGAAGATATGGCAAAAGCGGACAAGGCCC GTTATGAAAGAGAAATGAAAACCTATATCC

Sequence 471

ACCGCNGTGGCGGCCGANGTACAGGCTGTGATNCGTGTGGCGATCGATCTTCTTAGATTC
ACGGTATCTTCTGAGCAGCCGGCGCAAAATCCTCATTCTCCTNATCCATGTGACCTTNTC
TGGCATTCGGGCATTGGCTGTNCGAATCAAANCACTTACATGAGGGGGCAAAGTCAGAGA
CAGNTGAGGAGCTGAAGAAGGTGGCTCANGAGCTGGAGGAGAAGCTANNCATTCTCAACA
ATAANTATAAGATTCTGCNGGCGGNCCAAGAACTGTGACCACAGGGCANGGCATCCACCA
CCANAGATATGCCTGGCNGGGGCCAGGACAAAATGCAAACTTTNTTTTTTTCTGAGACAG
AGTCTTGCTCTGTCGCCA

Sequence 472

AGGTACAAGCTTACCTTTTAGGGTAGAAAAAGAAAGATCATTTGAAAAATGTATCTAAAA
TAATCCAGAGAACATAATGTTTGTCTTGGTCTGATAATGATAAGAAGTCAAGGATTGGCA
GAGAAAATACTAAACGCCAAGAGTTGAGCCTGTGGGTCTCTCCATAAGAGTTTTAAAACT
CTTGCCAGTTACCACTTTATCCAATTTGCTATCATTTTCGTATTATCAGCTATCGCCCTG
TAAAATATTCAAAACTAGCTATTTNTAAAGTAAACATTTTATCTGTTACTTTTAACCAGA
TAGGTGTCTTTGTCATCCTTCTACTATAAATTGTTCTTTGCCAACCTGTACCTGCCCG
Sequence 473

CCGGNCAGGGCTGGTTTGGGGCACAAGGAAGCCTTAGGGTATGGGGAAAGGCTGTTATTA

Table 1

Sequence 474

Sequence 475

AGGTACTGTTCTATACTATTCAGGTATCTTTTTATTTCTGATAGTTTTATATTATAATAG
AAAGCCAGCCACTGCTTAGCTATCATAGTCACCATTTTCTCACTGTTAACATTAGGAAAA
TCAAGGCTACTATGCTTCAGGATTGTCTGGTTAAATAGGAAAAAAACTGAAGAGT
TTCACATAATTACACACGTGAAATAATTAAAGCTTAAACTGAATTTGTATTTCATTTTAT
TGTCAGATGGTGGTGTTCACCAGCCTGTATCTTGTCTGAGACTGCATTCGTATCTGAGCA
GGTTTTCTATGCCTACTGATGTCAGTATGTTTATACTAACCTTCATGCTTTTTTCCCAGA
ATCCCTCATCTGCCAGAAAACTTGAAAAGTTTATTGCTTGTAGAGTTGTACCTGCCCG
Sequence 477

CCGGGCAGGTACATTCCAGGCAAAAACAGGGATCTCAAGGNGGTCAAGAAGAACATTCTG
GATAGCAAGCCCACTGCAAACAAGAAGTGCGACCTGATCAGCATCCCCAAGAAAACCACA
GACACGGCCAGTGTGCAAAATGAAGCCAAGTTGGATGAGATTTTAAAAGAGATCAAATCT
ATAAAAGACACAATCTGCAATCAAGATGAGCGTATTTCCAAGTTAGAACAGCAGATGGCA
AAGATAGCAGCCTGAAGGTCCCACCCCCACCCCTACAGAAAAAAATGGGAGCAAGAACTTG
TGCTTGGGAGCTGGTTATTGGTGTGGTCCTAGGGAGGGCGGAAAGGGAGGCACTGCCATT
TGGAGACATTCCATTTCAGATTTGTCAACCAGCGATAGGCCACATTCCAGTAAGAACTCA
ATTTGTCTCCCCAAATTTGCAGAAACAAAACGTGATTTAAAAGCTGAGCTTTTTTACAGAA
AGCTTTTTTGATGTTTTAAGTGTTATGTGACTTTGTTGAACTTTTTAAAAAGTGCTNCTTT

Table 1

TAAAATCCCAGATACTCTGAATTTTAGAAAACAAACTAATTCTGATTGNGTCGTGCCCAAGTACCTNGGCCGTCTAGAACTAGTGGATCCCC

Sequence 479

Sequence 481

Sequence 482

Sequence 484

CCGGGCAGGTGGCCTGTTCACTTTCTCTTACTCACTGTCTATTCACTTGTCCTGTTCACT

Table 1

CGTCTGGAAGATCTCAGCCAGCACCATGACTGACAATGAGCTGTCTGCCTTGGTAGTGGA TAATGGGTCAGGGATGTGCAAGGCAGGCTTTGGTGGTGACGATGCCCCCCGGGCTGTGTT CCCCTCCATGATAGGGCGTCCTCGACACCAGGGCGTTATGGTAGGCATGGGCCAGAAGGA CTGCTACGTGGGAGATGAGGCTCAGAGCAAGAGAGGCGTCCTGACCCTGAAGTATCCTAT CGAGCATGGAGTGGTCACCAACTGGGACGATATGGAAAAGATCTGGTACCT Sequence 485

NCGAGGTGGACAANAAACACGNATGGCTAGGANAAACTATCAATGCTGGCAGCCAGNTTG
AATANAATGTGGAAGGAGTGACTTNCAAGGAAANGGCTACCCAACTNGCCTNCATGCGCC
TGCTGGCCAACTATGCCTCTCANAACATCACCTACCACTTGCAAGAACAGCATTGCATAC
ATGGATGAGGAGACTGGCAACCTGAAAAAGGCTGTCATTCTACAGGGCTCTAATGATGTT
GAACTTGTTTGCTGAGGGGCAACAGCAGGTTNCACCTTACACTGTTTCTTTGTAAGATGG
CCTGCTCTAAAAAAGACAAAATGAATNGGGGAAAAGACAACTCATTTGAATACAAANACA
AAAATAAGCCCATCACCGCNCTGCCCTTNCTTGANATTGGCACCCTTTTTGGACATCGGGG
GGTGCCTGACNAAGGAAATTCTTTTGCNGGACATNNGGCCCANTNCCTNGTTNCAAAANA
AAANTGAACCTCAAATCTAAATTAAAAAAAAAGGAAAAAATTTTGNAAAAAAAACTTT
TCCTCTTTTNGCCNAGNGNCCTTNGTTTCNTCCCTTTT
Sequence 486

Sequence 487

Sequence 488

Sequence 489

Sequence 490

Table 1

TCAGATCCAAAGCCAGCACGGCACCGGGTTTCTTGCCTAAGGTCCATGGTGACCACTCCT TGGCTATTGCCAATGTTCACTCAAGGCCCAAGCACTCTTTATTCAGCTGGTGGCAAATCC AGCCAGGCTTGTGTTTTTCCCTTCAGTATGACGAGCTCCCCCTAAGCCCAAGACAAGTCC TAAAATGTCATNTGGGAGCCAGGACCTGGAATCAGGATCCTTAGGAATTTACTTGGTGCT GTATTCTACTATGGCTGAGCTGGCAATCAAAGTGGCAAAGATTAAAGCCCTTTATTTTCT TTGNTCTCCTTTCCTC

Sequence 492

Sequence 493

Sequence 494

ATÁGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACAACTTGAATGATATTTNGA CCACATCCATGCAGGGTGCTNACACTGNGACATNNGGAACTGATATCAGGTCAGCTCTCT GCCTGNCTCANTATGCATCACTATATCTCATCAATATGAATCATATTGATANCNGAAGGN GNTGAAACAAATGAAGCNGGCNTTTATATATTAACTGTGTTNNAGTGCGTATAGAACAT GGGNTCACATTCACTAATATTATGTGTATTCATACACATGCACAAAACCTT Sequence 495

GGTACTTTACCCTTCAACGGGACANGAAACTGCNCCAGAAGTCAACTTCACATTTGAAGG AGAAACGGGAAAGGNTCCANGATTGAAGAAGACAACACATTTTATCAAAGACTTAAGTCC ATGAAAGGAACNCGNTAGAAGCACANAATATTCCAGACAATTTTGGAAATGTATCTCCAG AAATGACGCTCGNNCTACATTTAGCCTGGGNCTGCCTGNGGCTTATATAANATTGGCAAG AAATTCCTACTTGAAGACACAATGGTATAAAAATGGGNNAAAAAATTNAANACTGTCAAG CCAAGGTGGCAAAAGCAAATGANNGACCTTTTATTGGAATTTAAGANTACACCATTCTAC TTTCATTAAAT

Sequence 496

GAGCTCCACCGCNGTGGCGGCCGAGGTACTTTTCTACCTTAAAAAAATCAGTGAGGATAT TTATTTAATGAACATCATTCCTTTTAAATTTTCTTAGAGAAATNGNCTCTGTGGCTCAG

Table 1

TTTTACCACCCATAAAGCGGAGACAGTAATTTATGGTTATTCCTTTCTGACCCACAAAGT ATGAAAAGTTCTTGTAANCTGTAAACTCAGTTCTGNAATCTGCATTATTGAGATGATTAA TATAAAGTTGTATTTTCACTGAAATGANTGTTTTGCTGGTTATGCTTGGTGAATATTTTA GCCGGGCTTATTTTTTTGAAAG

Sequence 498

Sequence 499

GGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACANGAGCTCAGACCCGGGGAGAC
CCTCAACGTCAACTTCCTCCTGCGAATGGACCGCGCCCACGNGGCCNNGATCCGCTACTA
CACCTACCTGATCATGAACAAGGGCAGGCTGTTGAAGGCNGGACGCCAGGTGCGAGAGCC
CGGCCAGGACCTGGTGGTGCTGNCCCTGTCCATCACCACCGACTTNATCCCTTCCTTCCG
CCTGGTGGCGTACCTGCCCGGGCGGCCGAGGTACTTNCTACCACTGCTGCATGAGTATAA
TGCTCCGGAATTATCAGAAAGCATAATGCAGAAATACGAATTANTGGAACTTAATCATGT
GCCANATAAGCTTACCTAACAAACAGTTATATCCCTATTCCTCAACTGAATGCTTTTTAAACATT
AANAACCCTTAATATTTTAACAAAAATTTCTTGATTAGAGGCACAGTGAAAAAAAGAAGTC
NAAA

Sequence 501

Table 1

TACCTGCCCG Sequence 504

AGGTNCATTCAGAATCCCACGAGCAATTCAGATAGACCAGTCACCAGGCCTCTAGCTAAA
AGAGCACTGAAATACACAGATGAAAAAGAGACGGAGGGTTCTAAGCCAACAAAAACTCCT
ACCACTACACCACCTGAAACTCAGCAGTCACCTCATCTTAGCCTGAAGGATATCACCAAT
GTCTCCTTGTATCCTGTTGTGAAAATCAGAAGACTTTCTCTTTCNTCCAAAAAAGAATAA
AGCCAAGCCCAGCAGNGGGCTCTGCCTAAACCGTAGGGGGGGCACAANGCCAGCCGTNGAA
CTATTAAGGGAGGCCCACNCCTTGCTTTTGNAAAACTGAAGAAAAGAGGGGGGGACCCCTT
TTACAGAATTTTGNTGTTTTTTTGGAAATTCTCCCTATTTTTCAAGCANAAAAAAAGGGAT
TTNAGGACCGTTTCTAAAAAAAAAAAGGNATTGAAACCAAAATACC

CTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACATGTNTTTGTCACTTAAA GGTNCTTTCTGTAANCTGCTTCAGATNCTTTNACTATTCAATTTTTAATNCTTAATNTCT GTAAAGAACGTTAATATTCCTCTTTATAATCAATCTTTCCCAGTTNGCCTNAAAAATGTA TTCCCTACTTTTGCTTCAGGAGATCAT

Sequence 506

GCGAATTGGAGCTCCCGCGGTGGCGGCCGCCCGGGCAGGTACAGAGAAGGCACTGAATA
AATTCACAAAGGCCGATTGGTTCACCCATTCTTTTAGNGACAACAGACACGCAATTCTGA
CGAGGACTCCTGTTACTAAAAGACACAGCCTCTGATACAAGAGAGATATCCCTTTGACTA
AAGCATTACCAGGGTCCCCAGGGCCCCCTCCCACTGGGGCGGNAACACTACGGGTCTCCC
CACCATATATTCCATGTCAAAGTATCTACACAAATACAGAGGAAATTAAGCAAGTAAATA
CGGTATGTAATTGTTATCATTTGTATTTCTTTAAGGCATATTTTATAAATATTTTAAAGTA
AACAATATGAGTGAGTGCCTTTCATTAGCTATGATCTTTCATACTGATATAT
Sequence 507

Sequence 509

Sequence 510

Table 1

ACCT

Sequence 511

TTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGNNGNNCNGNTAGCCATNAATCATAN ATATAGGANACAGCANCTATACANCTGACATNACCANTTAATNTTATATNATGAAAGCAN NNCATNTGCNTGTGCATCAAGGCCAGTCCTATTCAACCNANCTNTCGAATGCTGATANCT GGATAGNATGTCATNNTGAAGNTGNCACATAACTTNTCTAAAAAAAAGCANTCTTTGTTG NNTGCTTCTTCCCTACNGATGACTTCTAAAAATATATGACAGGGTATAAAAAAATTAGCT ATACATGATCATATCAACACATGTAACTGCTGAAATGGCATTCTA

Sequence 512

CCGGGCAGGTACAGGTTCAAATGAAATTCAGGTTGTTGCAGGAGACCATGTACATNTTGCAGTATGGGCCGGCGAGTTATGTTAATATGCAAGGTTAAGCAGAAAAAAGCGGANCCGTAGGGAAAACCGAGTNTGAATANGGGCGACTTTAGTATATTGGCATATACCCCCC

Sequence 513

Sequence 515

GCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTCCTCANGCAAAAATTGCACGNGGTTG ATGCCTTACATGAAGTACCAGTGAANAAAGGNGAAGGTGCCGAGCTATAAACCTCCAGAA TATTATTA

Sequence 516

TTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCCCGGCCAGGTACCAGTGGAGGAAG GCCTTCCGGCGGAACATGGCAGTGAACTGCTCCGAGATGCGCTTGAAGAGCTCCTGGATG GCTGTGCTATTGCCAATGAAGGTGACTGCCATCTTGAGGCCACGAGGNGGGATGTCACAG ACTCGGTCCTTGTCGCCTGGAAGGCCCCGCGCGGGAGCGGTCGACCTCGGCCGAGGTAC CCACCACCACTGTATGATGCTCATGAGCTCTGGCNTGCCATGAAGGGAGTAGGCACTGAT GAGAATTGCCTCATTGAAATACTAAGCTTCAAGAACAAATGGAGA Sequence 517

Sequence 518

Sequence 519

Table 1

Sequence 520

Sequence 521

Sequence 522

TATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTGTNCTCGGTAACGGGCCGACTTAATGGGNAGATCAACGCGAAATCCTTGGAAATATATANCAACAGCAAACACAAAAACTGNAGCAATGAGGTTCATGAGATTGGGTAAGTTCTGCCGATAAAAAGCCTCCCGTAAAGCTCCGGACTTTGNCCGTCCTGGTGGCCAACAAATGGAACAGAGCTATGACTGCACCCTCAAACTCAGTACCTGCCCG

Sequence 523

GAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTACAGGGTTGAGTATTCCTAATCTGG
TAATCTGAAATTTCACATGCTCCGAAAATCACAAACTTTTTGAGTGCCAACATGATGCTC
AAAGAAAATGCTCATTGCAGCATTTAAGATTTCAGATTTTTGGGTTAGGAATGTTGAACT
GGTATAATGCAAATACTCCAAAATCTGAAGAAATCCAAAGTCTTAAATACTTCTGGTCCC
AAGCACTTCAGATAAAGGATACTCAATTTGTATTCCTATTTTTGGAGATAAGAGATGGAGA
CTTACAGGCTGGGTTGGTTGGATTGGTTGCCTGTTTTTTTGTTGATGTTGTAGTGGAAGCT
AGGAATGGTTTTTCACATTTTTTAAAGTGTACCTGCCCG

Sequence 524

AGGTACCGGCCATTGGTGCCTTGTGTCAGGTCCCAGAGGGCTGCCTCAATGCCAGCAGCA
ATGCCCTCCACCACCTCCTCACTCAGTACTGGGTCTGGGAGCTCCCGAAGGCTGTGGAGG
CCAGGGCACAGAGTAAAGCTCCTGGGCTAAGCCAGTGGCCAAGCCAGAAAACAATGCTGG
GCAGAAAAGGGTTACAAGGCAGGTAGTCTGGACACTGGATTCAACAGCTTGCCATCAGCC
AGGGAAAGTGAAGCTGAGGATGCATATGGAGCAGGGCCAGGAAGATCAGGAGAGCTGAGG
GAGAACAGGAAAATTGGGAGGAAGGAAGAGCAGCTTANCAGCAAACTCCAGGAGAAATA
ACCAGCAGCCCTCACAGATTTGTGATTGTCTCTTAAAAAGATNTATTTTCTCTTCTTGCC
TGAATGTACCTGCCCG

Sequence 525

CGAATTGGAGCTCCACCGGCGGCCGAGGTACCACCGATAATGCTATTAGCCCAAACCGTG
GGTGTTTTNTAAATATTAATAGGGGGGCTTGATTCAACAAAGCCACAGACTTAACGTTGA
AATTTTCTTNAGGAATTTTCTAGTAACCCAGNTTCTAAAGTAGCTACAGCAAAGGGGGAA
ATATTATGTGTGANCATTTTTCTTCTTATGCTATATCCCCAAGTTTTTTTCAGGACTCAT
TTTAAGTNAAAGGCTAGAGTTGAGTAAAGGAAATAGAGCCCAAATGAGGGTAAGGTTGTC
TGAGCCATTGAAAGTNTTAAATACTGAAAAGAATGGTCCACTTTTTATTTCANNGAAAAT
TA

Sequence 526

TTAGGGCGAATTGGAGCTCCCGCGGTGGCGGCCGAGGTACTTTTTCCACGACAAATTCT TCAGGCTCTGCCTCTTCAACTTTTTTACTCTTTCCATTCTGTTTTTTTCCCATTTTTTGC AATGTAGTTTTGTTGGAGGCCATTTTTTATTGCAGACTTGAAGAGCTATTATTCACCGCC

Table 1

TCCGAGCTGCTCCGACCTGCCCGGCCGGCCGAGGTACTTGTGCCTAGTTTTTCAAGGTAT TGGCTGTTCTATAGATGCAGTGATTGTCCCAGCTAGCTCTGTTACCAGCCTTTTGGTGTG TCTTTATGTTCATTTGGAGAGTCAGGGCC

Sequence 527

Sequence 528

Sequence 529

TGGAGCTCCTCGCGGTGGCGCCCCGGGCAGGGTACAATTCGCCCCGTGAGTCTAGGA AGATTTGNTGAGCGTCTGCCAACTGGCAGATGAGGAACCGAAGTTCAGAGAGTTGAAAGC ACTTGCCCAGGTCA

Sequence 530

Sequence 532

TTAATTGGAGCTCCCCGCGGTGGCGGCCGCCNNGGCAGGTACAATNNTTTATTANGGCAT
TTTTATTGCTCCGAATGAAAAGAGTGGAGCTTTAAGTAAATATGCCAAAAAAATATTCCT
AGCACAAAAGCCTGCACCACTGCTTGAGTCTCCTTTTAAAGATAGAGATCATTTCCAGCT
TGGCACCTTATCTCATACTCTCAACATTAAAGCTACTGGGTACCT
Sequence 533

Sequence 534

Sequence 536

CCCGGGTGGCCGGCCGAGGTACCTTTCTCCCTCTCTACCAGTTTTTCCTCTAACTCTCTC
ACTITCTCTTATTTCTTTCACTTTCTTCTAATGCATTCTGCAAGATCCTGCTTTAGCAC
ATTTATTTCCTCTTCCGTGACCCTCAGCTCGTGGAAATGTGNATAATTAATCCATGCTTT
CAGGTGAGACAAAGACCGAGTTTCATCTGGCTTCTGCACACTAAGGACTTCTTTCATAAG
CCTCCTCGGTATTTGCTCTGAAGTTTCTTTAAAGTTTCTGGGCTGAGGGTCAAGAAGCTG
TTCTCTTGAAATCTCAAGTGGTTGTTTAAAGCATACCAAGTTCTTGCCCTTCGGGGATTG
GAAGTTCCGACCTGTAGCTGGTTTTCTCTCTTTGCTTCAAGAAGCTTCTCTAAATCTCNTT
CTGGNAGGATCTTNGCAAAAATCTCTTNGCAAGTTGGCTGGAAATTCTGACCANTCAATT
GGTCAGGTAGGTAGGAATTTTACCTAAAAGAATGGTAATTAAAAGACAAGGATAGGAAGA
TNGAATTTGGGAAGTCTTGGGGGGAAGAAGGGTTCNACCAAGGTTTTCCCCAAGGGGAT
NGGGGCCCCCAANTTAAAGTTTGGGNGGGAATNGGGTNTGAAGNTNAAAACTTTAGGTN
TTGCTTCCCCCCCTCCTTGGGGGGNAANTTGGGCCCCNGNAAANTAAATCTGGGNAAACC
CCCTAATTTGGGNAAAGGGGA

Sequence 537

Sequence 538

GGTACACTGATCAGGGACTGGAATCTTCTTTCCAATTTCCATGGCATATGCTTTCACTTT
GCTGAGGTTTTTTTTAAGTGCAAGTAGAGCTTATCTTGGTATTCTATAGGACTTGCAGT
TGTCTCTGGAGTTTCTTCCTGGGAGTTTTCTTTAACAGTTTCTGACAAATTCTCTGAGTC
TATATGTATAATATTTGGGTATGAAACTGAAGACTCCCCCAGCTGTGATCTCTCAGNGTC
TGTCTTAAACGGCAGCTTGTCATTTCCTTGGCCAAGTGGGTCTATTTCTGAAAGAGAGT
GCTGGCTGGTATGTCTCCCCTGTTTTCATCTTCGCCGTCATCTGAACCCACACCCTTTGT
GAGCATAGTGTGGAAAGCCAAACTTTTTGACC

Table 1

Sequence 540

GCGATTGGAGCTCCCCGCGGTGGCGCCGAGGTACTGATCTGGGTGGAAGGTGACTCCTG
TGGGCGCGATGATGGGGTGGAGGGTGTCTGATGGAATCCCGTTGGGTCCCGGCTGCCCTA
CGTCACCCTTTTCACCCTTAACTCCGTAGAAACCAAGTCCTCTGTTGCCTTGCTGTCCTT
TTGGTCCAGGGGGTCCAGGTGGTCCTGGTCTCCCTGGAGCTCCAACTGGACCCATCTGTC
CCACATGCCCGGGCGGCCGCCCGGGCAGGTACTCTCAGAGAACAGGAGATATGTGTGCAT
GCCTTAGAAAAAGCCCTTGAGTAGGTAAGGAAGGAAGAAACCTATGGCAGACAGGATTGC
TGCAGCCAAGGGGGCTTCAAGCAGAAATGAAAGAGATGGCTTGTGAAGCTGCCCGTGTCG
TGT

Sequence 542

Sequence 543

Sequence 544

GAANTGAAGCTCCACCGCGGCGGCGGCGCCCCGGGCAGGTACAATTAGAAAACCTGCATC
TTTTAATACAGTGAGATTTNGTATGCATACACTCTGGTGTCTTCATTTTGCAGCCCATTA
TATTGGCTTAAAAGCCANAAAGGTGCTCATGCATGTAATTTATACTTGGAGCAACGAATG
CCANTGTATGTGGNCGCGTNTGTGTGCACNTTTGAAAGGNAGGAGTTTTAGAAGNAATG
AGAAGGAAAATTTNCTTTCTTGGGCATTCATTAAATAATTCAGNGTGAATATCCTTGTAC
NCTTGGCCGNTCTANAAACCAGNTGGATCCCCCGGGGCTGCAAGGAAATTTCGAANTNTT
CAANGGCTTATTTGANNCCCGGCGACCTCCNANGGGGGGGGCNCCGGGTACCCCAANCTT

Sequence 545

CNGCCGGCCGAGGNACCAAAATTTGTGGGAGGGNANTNGAAACCCGGCAGANTTTAANAC CNNATGCCNATAAANGGGGGGNCAGGGGANGAAGACGGGGGGGCCCGGGNGAACAAAACC ACACGGNCTCTANGGAAAANGNGGAGAGAACTGAGAGCGAGGTGNGGCAAGAAGCAGGCT CGGAGCCGGAGGAGGGGGCTANCGGCNNTAATCTCAGGGAGAGATGGCGCNGTGCGGNC AATGATGCAAGCNGGNAAGGGACCNGGCGGGGGAGGGAAAGGGACGAGGGAAG Sequence 547

Table 1

Sequence 549

AGGTCACAGTTATGGCAAAGTAGACAAAGCATTTGTTCATTTGGAGCTTAGAGTCCAGGA GGAATACATTAGATAATGACACAATCAAATATAAATTGCAAGATGTCACAGGTGTGATGA AGGGAGAGTAGGAGACCATGAGTATGTGTAACAGGAGGACACAGCATTATTCTAGTGC TGTACCTGCCCGGGCGGCCGAGGTACCTTACATCAATGGCAAGTTTAAGAAGGATAATTA ATTACACAAACCCTTCACAGACTGCTCTGGTGCCTGGTGGTGCTAGCTCCTCCCACCTCA GCACCTGCTGATTTCTGGGAGCAGC

Sequence 550

CCGCGGTGGCGCCCGCCCGCAGGTACTTGTTATCAACACGTTTGTATCAGAGTTGCTT
TTCTAATCTTGTTAAATTGCTTATTCTAGGTCTGTAATTTATTAACTGGCTACTGGGAAA
TTACTTATTTTCTGGATCTATCTGTATTTTCATTTAACTCAATATCATACTACCGGCTAC
ATCAAATCAGTCCTTTGATTCCATTTGGTGACCATCTGTTTGAGAATATGATCATGTAAA
TGATTATCTCCTTTATAGCCTGTAACCAGATTAAGGAATACAGCTCTTAAAAAAATCAAGA
ACTTCCTGAGTTTCACATATAAAATGGTGACAAACACCTGCTTCTGATAAAGTTTATCCA
ATTTTGTATTTATAGTATTCTATTGTAATAATAGAATTCTATTATGTGCTTCCCTCCTTA
GACATAGTTTTTCTCCTTTTTGTACCT

Sequence 552

Sequence 553

Table 1

CTTCCGTGTGGCTTGTGGCTCAATCATGATGTTGATANGAGAAGGTTTAGTTGTGTCTGC TAGGCTCTGCCTCAGGGATTTTTGGAGTTCTTCTGGTGTTTTGTACCT

Sequence 554

CCGCGGTGGCGCCCGAGGTACCCCGTTCTGCCTGAGCATTTTTTCCTAAAGGAAGAAT
CAATAGTTCTGACTGTTTTAACAGCTGAAAGCTCCAACTGGAGGCAGAAGATGGGATGG
CTTTTCACACACGTGCGTGCAAGTTTAGCCACCTCAAAGGCCTTGTTCTTAAAGCAACAG
TGCTGTTTGCATTATGAAATGTCTCTGGAGTTCCCCTTTGGAAAGGCTGCTGGTGGGCCA
CATGGTCACGATACTTTCAAGTCACACCCTACTTTGTGACCTTATCCTCAGAGTAAAGGC
TTTAGAGGAAAAGGGACCCCACAGTCTCACCCATTACCTGGCTGTCAGCATCTCCATATG
CTCCTGGCTGAGTTTTATTGAGCATCAGCTGGGGATGTGAGCAGAAACCTGAATCCTTGA
GACAGGTGGTTTTCAAAAAAGGAAGCCATAACAATGAGTGGCTTAGTACCTGCCCG
Sequence 555

Sequence 556

Sequence 557

Sequence 559

CTÁTAGGGCGAATTGGANCTCCCCGCGGNGGCGGCCGAGGTACAAGTTGGGGTCATAATT
ATCGAGTCTCTTGATATNATCACAATTACTGTGCCCCCTGCACTTCCTGCTGCAATGACT
GCTGGTATTGNGTATGCTCAGAGAGAGACTGAAAAAAAACGGTATTTTNTGTATCAGTCCT
NNAAGAATAAATATTTGNGGNCAGNTCAATCTTGNNTGNTTNGACAAGACTGGAACTCTA
ACTGAAGATGGTATTACATCTTTGGGGGGANNCAACGAGNGGAAAANGCNCCGATTTCTTT
NACCANAAGAAAATGTGTNCCATGCTGNNNNTGGTNAAACCCCAGCCNGTTGCTAGCANG
GCTACTCCCCATTCACTTACAAAA

Sequence 560

NCTACTATAGGGCGAATTGGAGCTCNCCGCGGTGGCGGCCCCCGGGCAGGTACCTGAAA CTGCCGCCACATGCACTCCTCCACCGCTGAGAGTTGAATAGCTTTTCTTCTGCAATGGGA

GTTGGGAGTGATGCGTTTGATTCTGCCCACAGGGCCTGTGCCAAGGCAATCAGATCTTTA TGAGAGCAGTATTTTCTGTGTTTTTTAATTTACCTTCAGTCAACTTTACCAAGAAG TCCTGGATTTCCAAGATCCGCGTCTGAAAGTGCAGTACCT

Sequence 561

Sequence 562

Sequence 563

Sequence 564

AGGGCGAATTGGAGCTCNCCGCGGTGGCGGCCGCCCGGGCAGGTACTGGGGATACAGGAG
AGAANCNANCGNNTTTGTCTTTGATCNNAANGAATCCGCATNGTANAAAGTGGAANATGN
NATGNGATGNACACATTAATTATNATCATNCCCTTNNNCTACCTAAAATACTCGCAGTGG
CTCNACCTTACGCATATAAAAAACTNCGCATTCCAGCCCACCGCCTTCA
Sequence 566

Sequence 567

Sequence 568

Sequence 569

CTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGGGCGGACCTCATCCGCCTCCT

Table 1

GCTGAAGCACGGGGCCAACGCAGGTGCCAGGAACGCAGACCAAGCCGTCCCGCTCCACCT GGCCTGCCAGCAGGGCCACTTTCAGGTGGTGAAGTGTCTGTTAGATTCGAATGCAAAACC CAATAAGAAGGACCTCAGTGGAAACACGCCCCTCATTTACGCCTGCTCCGGTGGCCATCA CGAGCTTGTGGCACTGCTGCTACAGCACGGGGCCTCCATTAACGCTTCTAACAATAAGGG CAACACAGCGCTGCACGAGGCTGTGATTGAAAAGCACGTCTTCGTGGTAGAGCTGCTTCT GCTCCACGGGAGCGGTCAGTTCAGGTGCTGAACAAGCGGCAGCGCACGGCTGTAGGACTG TGCTGAACAGAATTCAAAAATAATGGAATTGCTTCAAGGNGGTACCTCGCCCGAGGGCTC CTTCCTTATGACTCCATTCAAATTTACGGGNTATTAAAGCAGGGGCTTCAGTGGCCCGGG GTCCCT

Sequence 570

Sequence 571

Sequence 572

Sequence 573

Sequence 574

Sequence 575

CTATAGGGCGAATTGGAGCTCNCCGCGGTGGCGGCCGAGGTACACAAGGGAGAGGCTCCT GGGCAGTGACGGTGGAAGCTCCACTACCTCTGGGATTAGGGGCACTGTTTCCAGAGTCTG TAAGGTCGTGAGGATGTCACTTATGCTGTGCTCCTGTGGCTGGTTCTCCCCTCCAGGGAG TCTTTCCCCAGCCTCAGCTGGTTCCTGCCCAGCCTCAACCCCAGGCTTGCCTTCAGCACC

Sequence 577

Sequence 579

Sequence 580

ACTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACAACATCTTTGAAGG
GATGGAGCTGCGCGGGGCTCCTCTGGTTGTCATCTGCCAGGGCAAGATCATGCTGGAAGA
TGGCAACCTGCACGTGACCCAGGGGGCTGGCCGCTTCATACCCTGCAGCCCGTTCTCCGA
CTATGTCTACAAGCGCATTAAAGCACGGAGGAAGATGGCAGACCTGCATGCCGTCCCAAG
GGGCATGTACCTGCCCGGGCGGCCGCCCGGGCAGGTACCAAAAACCAACATGACACACA
GAAAAAATAAAAGTGCAATTTTAATATAGTGAATGTGATACATGTATAATTCCTCATAAC
AAATGGTCAAAACCTTTAAAAGATCCACAATAGATATCTGAAAATCTTAGCAATGCTGT
ATATATTTTTGAGGACTAAATGATGAATTTATTCAAAATTGGTCAAATATATT

Sequence 582

Table 1

ACTATAGGGCGAATCGGATCTCCCCGCGGNGGCGGNCGCCCGGGCAGGTACCACTTCTGA TGATGGAAGCAGTGACCTGGATCCCATAGAACACAGCTCAGAGTCTGATAACAGTGTCCT TGAAATTCCAGATGCTTTCGATAGAACAGAGAACATGTTATCTATGCAGAAAAATGAAAA GATAAAGTATTCTAGGTTTGCTGCCACAAACACTAGGGTAAAAGCAAAACAGAAGCCTCT CATTAGTAACTCACATACAGACCACTTAATGGGTTGTACCT Sequence 584

CTÁCTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACACAACATCCTTTCAA
ATATTCTTCTTTATTCTCCAATTCACTTTTCAGGAGAATAGATAACCTCAATCATATTG
ATTCTCAGCCTAATGGTCTCCCTTACATAAATTATAATGACATAAGCATTTTGTATCACT
TTATTGTTACCATCGACCTCCTACAGTTTGGGGGAACCCCAATCATTCTTTAAAACATTAG
AATGACAACTCCAGTTGATTTGGCATATTGTATAGGTGAGTGGGGAAAGACTTGTCAAAT
CCCAGAAAGGGGGCGTGGCACCAGCACCCCCAACCAGAAGAAAAATCTCTCTTTGGTGC
TAGTGTCATAGCTCCCTATCTGTTCCGCTAACCCATTAAATGATGTGGTGGAGGAGGATC
CTTTCACAATCTTTGTTCATTTTTTTACAGAGCAATGGGAAGTNNTACCTAACCTTTTAC
NAAATTCATTTTTTGGGT

Sequence 586

NCGGGGGGGGCCGGCCGGCCGGGCCTTNAAAAANTNGAGGAANTTNTTAATGGNT CCCANTAGGGCNTTTNAAANCTNCAANCGGCTTTCTTTNTTNAATTNNAANGCTAATNCT CTNGCAAATCCAATAAAATCGGNCNTTTNNTATNCATTCCNGCTTTATATTTTNATATTT NAAANGANGCCNCCNGTAAATNCTATTTTNTTTGGCAAAATACCAAAAGGGNCAAAAAAC CTTTAAAAATTNCNGTAAANCATAANGTAGTTCTNAGGGGGAAANGTTATCATTCCCAAN GTCCTNGNGTNGTTCCTTCCTTAAT

Sequence 587

Table 1

CCGGGCAGGTACAGGACAGCCAGCGTCATCATTGCTTTGACTGATGGAGAACTCCATGAA GATCTCTTTTTCTATTCAGAGAGGGAGGCTAATAGGTCTCGAGATCTTGGTGCAATTGTT TACTGTGTTGGTGAAAGATTTCAATGAGACACAGCTGGCCCGGATTGCGGACAGTAAG GATCATGTGTTCCCGTGAATGACGGCTTTCAGGCTCTGCAAGGCATCATCCACTCAATT TTGAAGAAGTCCTGCATCGAAATTCTAGCAGCTGAACCATCCACCATATGTGCAGGAGAG TCATTTCAAGTTGTCGTGAGAGGAAACGGCTTCCGACATGCCCGCAACGTGGACA

Sequence 591

CCGGGCAGGTACACGGAAATCTGGACAGTGCTCCACAGATTGATACATTAGCCTTTGCTT
TTTCTCTTTCCGGATAACCTTGTAACATATTGAAACCTTTTAAGGATGCCAAGAATGCAT
TATTCCACAAAAAAACAGCAGACCAACATATAGAGTGTTTAAAATAGCATTTCTGGGCAA
ATTCAAACTCTTGTGGTTCTAGGACTCACATCTGTTTCAGTTTTTCCTCAGTTGTATATT
GACCAGTGTTCTTTATTGCAAAAACATATACCCGATTTAGCAGTGTCAGCGTATTTTTC
TTCTCATCCTGGAGCGTATTCAAGATCTTCCCAATACAAGAAAA

Sequence 592

Seauence 593

CCGCGGTGGCGGNCCNCCCGGNNTTNNAAANNNGGGGNNNTNTACATAGAGGTGAGGGT CATGCCCGTGTTTCAGCTCATNCAGTNCAGGGACTTCGCCTTGCCCCACCCATNATGGGT NAGGCCGGGAAGGGGCCATTTTGGAAGCCAAG

Sequence 594

Sequence 595

CCGGGCAGGTACCGTCGCCCGGCTCTCCGCCGCTCTCCCNGGGGTTTCGGGGCACTTGNG GTCCCCACAGTCTNGGTCCTGCTTCACCTTTCCCCTTGACCTGAGTAGTCGCCATGGCAC AGGTTCTCAGAGGCACTGTGACTGACTTCCCTGGATTTGATGAGCGGGCTGATGCAGAAA CTCTTCGGAAGGCTATGAAAGGCTTTGGGCACAGATGAGGAGAGCATCCTTGACTTTTGT TGACATCCCGAAGTAATTGCTTCAAGCNCCCAGGAAAATCTTTTTGCAAGCTTTTTAAAG AACTNTTGTTTGGCAGGGGATCNTTNTGGGNTGACCTTGAAATCAAGAAANTAACCTGGG

Sequence 596

GGAGATTATGTCTACTTTGAGAATTCCTCCAGCAACCCATACCTAATAAGAAGGATAGAA GAACTCAACAAGACTGCAAGTGGCAACCGTGGAAGCAAAAGTAGTATGCTTTTATAGACG ACGTGATATTTCCAACACACTTATAATGCTCGCANATAAGCATACTAAAGAAATTGAGGA AGAATCTGAAACAACAGTTGAGGCTGACTTGACCGATAAGCAGAAACATCAGGTTGAAACA TAGGGAACTCTTTTTGTCACGCCAGTATGAATCTCTGCCCGCAACACATATCAAGGGGAA

Sequence 597

TATTCATAAGGTTATTTCAAAGTTAATAAAGACAAAGTGGCAACTGTAGAAAGTGTTGCC
TCCAATCTTGGTCCGTATTTCCAAAGC

Sequence 598

NCGGNGGCGGCCGAGGNNNNNNNNNNTGGTTGAGGGGGAGAAAAACCCGCCACCCNNGC GGGAGNGCAGNAGCACGACCNCANTTTACNGCAACCGGCAGCNCCCNCNCANAANAGANN CNCCNGCCNCAGCCNCCCAAGNAGCNGGGANNACAGGCANGCGCCANCACACCCANTTAA NNTTTNTNTTCCCAGGGGNGAGGGGGCCCCACCAAGAAGGCCAGAATGNANNTGNNCCCC NGACCGCAAGGGANACACCCACCNCAGCCNCCCAAAGGGCNGGGANNACAGGNGNGAGCC ACCGNGC

Sequence 599

CCGGGCAGGTACAAAGCTATAAAGGAACGTTTTTAGAGAAAGCACTGAAGACACACATTT TGCTGACCTAAAAGATTTTAAAATGAATTAGAATAATTTACATCATATAAAGAGGTATTT AGTCTTTAAGTGGAGAAAGT

Sequence 600

NGNGGCGGCCGAGGNACNNCANAANTNNNTTCGGGGGNCANAAAAACCCCCCACNCCCCC
NNNCNAGGACACCNCGNGGAAGTTTTTNAAAAGCCNCAGGGGGGGGGACCCAANAAAGNG
AAGNGACCGNCNCNNCCAAGGGCCNCCAANANGNCCGANGNGANGGCAGCNGCNNTNNAA
GANGANTNNTTNTNNNGCGGGGGGNAACGNCCCCNANAAAAGAGGGACCNGANCGGNCNCC
CCGCCCGGCGAAGCACGAGGAGNNCNGNGNCCCCACGNCCACGGNNCCCGCNACNGNGN
CCAACAANGNGNNNNNANCCGANNNCAGCANCAGGGANCNGCAGNCCAACGNGGAGCACC
NGA

Sequence 601

CCGGGCAGGTACTGGTCTACAGGGACAAGCAGTCTTTAAAACGAAACTCACCTTCAGACC
TCACTCTACGGACAGTGCCACACATAGAAAGATGACTCTGTCACTTGCAGATAGGTGTTC
AAAGACACATGAAGATTAGAATCTTGCCAATGGCTGGTCGTGACCCTGAATGCCAACGCA
CAGAAATGATTAAGAAAGAAGAAGAACGTTTGAGGGCTTCCATACGTAGGGAATCTCAGC
AGCGCCGAATGAGAGAAGAACACCACCAGCGGGGGCTGAGCGCCAGTTACCTGGAACCTG
ATCGATACGATGAGGAGGAGGAAGGCGAGGAGTCCATCAGCTTGGCTGCCATTAAAAA
Sequence 602

Sequence 604

CCGGGCAGGTACAGGCACAGCATATATTTGAGAAAACATCTTACAAATTTCATTTACTAT AGGTTTCTCAATAATCTTTACATTTAATCAATGAGAAAAGTGATTCAGTCTCTTGAATTT TAAGTTAAAAAAATTAAAAAGTATTTCCAGGGACTCTTAAAGCTCTCTCCCAAAGTATAA AATATTATGTACTGTGGGGTCAGATTCAGCATACTTGAGGGAACGAAAGACTTTTCGTTG GGGCGTGACCCGTTTGATGTTTGGATGATCTTCAAGTGTTAGCAGCCCCGCTTTCTGTTT TTCTTTTATCTGAA

Sequence 605

Sequence 606

CCGGGCAGGTACATATGATCCTTAGCCACCAGGGCACAAGCTTACCAGTAGACAATACAG ACAGAGCTTTTGTTGAGCTGTAACTGAGCTATGGAATAGCTTCTTTGATGTACCTCGGCC GCCCGGGCAGGTACCTTAACATTCACATGGAAGTAGTAAAAATAAGATTCTGGGTGCAGT TCTCCAATGACAGGAAAAAAAACAAAGAGAATTTGAAGAATACCGTCAGAGACAAATACA TTACAACCAAAATTGACTTCAAGGCACTTTTGAAGGAGATCAAATTTATAACAAAATAAT TTAGTGAAAGTGAAAGCTT

Sequence 607

CCGGGCAGGTACCTGGACCTGCTGTCCCAGCCCTGCCGCGCTGTTTACATCTTTGCCAAG
AAGAACGACATTCCCTTCGAGCTGCGCATCGTGGATCTGATTAAAGGTCAGCACTTAAGC
GATGCCTTTGCCCAGGTGAACCCCCTCAAGAAGGTGCCAGCCTTGAAGGACGGGGACTTC
ACCTTGACGGAGAGTGTGGCCATCCTGCTCTACCTGACGCGCAAATATAAGGTCCCTGAC
TACTGGTGCGCGCACCCTTCAGGGTCTTGAGATTGAGCTGCAGTCACAGCTGAGCATGA
AAGCTGCCTTGGAAGACACACTGGC

Sequence 608

CCACCGCGGTGGCGGCCGAGGTACCCAGGATGNTTTCTGGCAGGAGGGAGCNTGTGTTCC
TGTGACCTGTGACCCACCACACATTNCATGGGCTCTACCAGTGTACCTGCCCGGA
CTTCCTCTCCTACCTACAGTCCCTGCTCCTATTCCCACCTCAGCAACTGAAGCCGCCCC
AGAGCTCTGCCTTGAGGATATAAACACATTTAAATTACTGTCATATGCTTCCTATTGCAT
TGAGCATGGTGATCTGGAGCTAGCAGCAAAGTTTGTCAATCAGCTGAAGGGGGAATCCAG
ACGAGTGGCACAGGACTGGCTGAAGGAAGCCCGAATGACCCTAGAAACGAAACAGATAG
Sequence 609

Sequence 610

Sequence 611

AGGTTTTGCAGCTCGTGCCATCATTTCAGAGCTGGTGAGCATTTCAGAACTAGCTCAACC
ACTAGAAAGTGGCACCCATTTTCCTCTTCCTACTTTGTCTTCAGCAGTTAGCTAAATT
ACAAGATCGAGAATGGTTAACAGAACTTTTTCAACAAAGCAAGGTCAATATGCAGAAAAT
GCTCCCAGGTAAGAGAATGCTGACTTGTTTGTTTTTTTAATATTATATCTAGAGA
TTTCAGGTACCTGCCCG

Sequence 612

CCGGGCAGGTACANATGNGNNGTGTCTNNCAACTTTCATNAGAAAANGCCATATCTATAC CATATTTTATTCGGAGTCACTGANGATGTAATGATATATCTTTTTCATTATTATAGCAGA ATATTTTTATGGCANGATATTTAGANGNCTTGANCATNCCTATTAAAATANTGCCAAACA CCAAATATGAATTTTNTGATGTGCNN

Sequence 613

AGGTACAGAACTTGGTCATAATATCTTGCATTTTATAGATTTATTAAAGATTAGTTTCAA
GTTCACATTCGCTATTCAGTTGTAAACCGAATGGATGGGAGGGGAGAAAATATAAGCTCT
CCACACAGGTATGCTCCTCTCTTTTCTGAGAGAGAAGGCATGGGATTTTCAGCATAAATT
CCATGTTATGTGAGTGCTGTTTGAGTTCTGAAGTTCCTATCAATATCTGTTCCTGCAAGT
GATCTCTGTAAGACCACCTTACATGCTGGTCTTAGTTATTGTTAAAATTGCAAGGTTTCT
TCACACCCTCTTTGATAAGAAGTGTTTAGCTGGCAGAGC

Sequence 614

CCGGGCAGGTACCTCTTGAGTGTCCCTTGAATTGGTAACCGGTTTGTTGTCATTATTTTC
TAAGCGAATATGCCGTAATTGGTTATTGGGAACATCTTTGACAAAGATCCATTTAACTTC
AAATTTGCCCTTCCACTTATCCTGAGACCAGACACCAGCATACGCATTATAGTCCACAAC
AGACTTCATTTCAGCCACTCACAAAAATGTCCACTGCCATTCACACTGAAGAGTAAATA

GAGTGGGCCTTTCCCATTCAGGGAACGGTAAGCTGCATCCAAACGCTTATTACCATGCTC AGTACCT

Sequence 615

CCGGGCAGGTACTTTTGATTGTGCACGCTTTTAAATAGAGAGCAGAGTTGCCCACTTGAA ACTACTCTCTTGCATGGGATATTTCAAGCTGTTTTACTATGGGCAAGGAGCAGGACCAA AATGCTGCCAGGGCTTAAAAAGAGCCGTGATCAGATTAAACAGAAGTTGGAGAAGTGGAG GGATGTGGGCCACACACGAGAAGAAATTCAGGAAGTAAGAAGTAAGAGTGACCCTATTAT GCTTCTCAAGGACAGGATGGTGAACAGCAATCTTGCCAGTGTGGGAAGAACTAAAGGAAA TTGATGTGGAAGTGAGGAAGGAGATTGAGGATGCTGCCCAGTTTGCCAC

Sequence 616

Sequence 617

CCGGGCAGGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTG
ATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAG
GTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTT
CCAGTCGGTACCTCGGCCGCCCGGGCAGGTACCCAAGGGATGTTTCCAAGCTTCTTGATC
TTTAATCTTTTAGCAACCTTCTGATACTGGATTTACCTTCCTAGGTGTGGTGCCCTCCTT
CTGGAATTTAGATCTCTGGGGCAAACCCTGTCAGGAT

Sequence 618

CCGGGCAGGTACCCTGTGGCAAAATTAGTCACTGGTAATGAGAAAGATATCACTGAAAGC CTCAAGTGCCTGAGAAACAGTTTACTCATCCATGGGATCTCGCCAATTGTGAGGAAACAG CTCAATGGCCATTTCCAGTTATAAGCAGCTTATTTTTACTGATTGGACCTGGTTACCTAT CATTTCTAAAAATAACTTCTGATACAATTTGTACTTCCAATTTATAATGAATACTTTCTT AGATTTTAGGTAGGAGGGAGCAGAGGAATTATGAACTGGGGTAAACCCATTTTGAATAT TAGCATTGCCAATATCCTGTATTCTTGNTTTACAT

Sequence 619

GGCGGCCGAGGTACTCAANACATCTTTCAATAAAAATGGGGNTCGGCTTCTCTGGAGTCA CGGACAGTTGTTAAGGGCACCCCAAAANAGTTACTCTNCCAGGTTGCCTTTGNGGTGGAT GGCCGNGTTTGGGCTTTGGTTTATTAGNGTTCCTCCTTAGGCTGCGAAGAATATTCCTC NCTCCGAGGGTCTTCGNCTGTTTCGTATGGAATGACAGCATTGTCCCCTTTATAACCCTG GGATGCCTGATCCTNCTCTTTCTTNCGGATGGGCCCCAGCTCATCATCACTCC

ACTATAGGGCGAATTGGAGCTCACCGCGGTGGCGGCCGCCCGGGCAGGTACTGAACAAAG GCATAGCCCTTGTGCACAGAACAGCCGGCCACACGGCCATACTTAGAGAAGATGGTCTCC ACATCTGATTTCTTCACCAGAGCTGTGTTGAGGTTTCCAATGAAGACTCGAGAGTTGATG GACTTGGGGTCATTCTTGTTGGTTACATTGCTTGCCTGAAGCTTCAAGGACATGGTGCCC ACTTAACAAACATTTCTTGAGTGTCCTCCTCTGTGCTGGCACTGTGGAGATGCTGGGAAA CACCGTGCTCACCAGTCTTCTGCTCTACTTGCTTTTCAAGAAGCCCCCTCTCTGGGAACC AGTAACAATGATGAGCCTAGCCAGCTGTTTCCTCCT

Sequence 622

CGACTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCAGGAGAGCACA ATTGGAGCGGCCTTCCTCACACAGACTGTCTGCCTGGATGACACAACAGTCAAGTTTGAG ATCTGGGACACAGCTGGACAGGAGCGGTATCACAGCCTGGCCCCCATGTACCTGCCCG Sequence 623

Sequence 624

TACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACAACGCCNNNAATGACA ACACTTAATTCCAGCTATACGNGGCAAAAGATGTTATGGNAGGGAANAGAGAGGTTNAAA TACANATGAAATAAAGGGTCACCATCTCCTCA

Sequence 626

CTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACACAAAAAA AACATTTGGTATCAATAATTTGGTTGTGCATTCATTTATTCAGTCAACAAATATTTAGCT GAGCACTGGCTAGC IGCCAGGTATTGCACTAAGGACCCAAAGATGATGAGGAAGAAGATGATGTCC CTGCCCTCATGGAGCTTGCAGTCGTGTTGAGCAGACTGTCAAACAGATTTAGGTAAGGCA ATGTGACCAGTGCTATGATACAAACAGGATGCTACAAGAGTACCT Sequence 627

GGGCGAATGGACTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACATTTCGAGCAGCGGAAG
AAGGAGGAAGAGAGCTGGTTGCCTTGAAGGAGCGCATTGAGCGGCGCCCCGGTCAGAGAGA
GCCGAGCAACAGCCGCTTNAGAACTGAGAAGGAACCGCGAACGTCAGGCTAAGCTGGCGG
AAGGAGAAGATGAGGAAGGAAGAAGGAAGAGGCNCAATGAAGCCGGTGCAAGAGGATTGA
TGCCAAGAAAAAAGAAAGGGTGCTTGTCCAACATGGGNGGGGCCCTATTTTGGGCCGGCT
ACCCTNGGTTCAAGNGCAGTAACCAGTAAAGCCNTGGNTAAAGGCGGTCAAGACCGGGGG
GCCGGGTAGATTNAAAGGGTGCCGCATTCCCTTCTTTCCCGGAGCCGTTAANNAAAGCCC
TTCTGGGACCATTTGGACTTACCATTGGGGGGGGAAAGCCAGGCTTTCNCGGGGG
ANGAAAAAGCCCCCAAG

Sequence 628

GAACCGCCAGGAGCCAGAAGGCGAGCTTGGCGAGTTTTGTGNGCTTTTGACCTGCCCGGGCGGCCGAGGTACTTGTTATCAACACATTTGTATCAGAGTTGCTTTTCTAATCTTGTTAAACTGCTTATTCTAGGTCTGTAATTTTTTAACTGGCTACTGGGGAAATTTACCTNAATTTTTCTGGATCTAATCTGNNATTTTTTCATTTNAACCTCCA

Sequence 629

ACTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGNACCANNTNCTTNTTNG AGNNNCNTACNAGNTGTACNNATCGCNGNNCNTAAAGANNTNCCCNNACCACNTCCTNTT GNGCTTNTTTATTNGNATTGTTNGAACANTCTNNNNTNTGNGANTCNTTACATTGAATCA TCTNGNCNANTTNATCCNANNCTTNACTGACTCANACTCNTTATGCTGAACTNNTNAATN CAAAATCNCTATTGCTTTAGGACTCTGGGAAGCNGNTGATAAAAAGATAACACGAGCTAC TGATATGGGCAGGANATGTTNCTAANCAAATTGGAGAAATATAAACATGAAATGTGGCA ATGATCC

Sequence 630

Sequence 631

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Table 1

Sequence 632 ATCGATAAAAGAGGCAAAGTAAAAGGGACCCAAGAGATGAAGAATAATTACAATATCATG GAAATCAGGACAGTGGCAGTTGGAATTGTGGCAATCAAAGGGGTGGAAAGTGAATTCTAT TTCAAAGAACTAATTCTGGAAAACCATTACAACACATATGCATCAGCTAAATGGACACAC AACGGAGGGAAATGTTTGTTGCCTTAAATCAAAAGGGGGATTCCTGTAAGAGGAAAAAA AAACGAAGAAAGAACAAAAAACAGCCCACTTTCTTCCTATGGCAATAACTTAATTGCTTA TGGGATATAAAGAACCAGTTCCAGCAGGGAGATTTTTTTAAGTGGACTGNTTTCTTTCTT CTCAAAATTTTCTTTCCTTT Sequence 633 CTACTTAGGGCGAATTGGAGCTCNCCGCGGTGGCGGCCGAGGTCGGGACCGGGGCCGCTG AAAAAAAAAAGGAGGGGGACCTGCCCG Sequence 634 NNNAAATTANAANAAAAAANTNAAAANCCCCCCCCANNCCCGGGGGGGGGCCCCCCC CCAAAANNTNNNTTCCCCATAAGAAANNNNNAAAAAAAACCNCCCCCNGGGGGGAAAA AAAANGGAAAAAACNNNTTNTCNNGNGNGAAAAAAAAGGGNTTANNNCCCCANAAAA NNGGGGGGNNCCCCCAAAAAGGNGGGCCANCNCCCCNNNNCNAAAAATTTGGGG Sequence 635 CACTACTATAGGGCAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTCTAGTCGGTTAA TTTACACTTTATTTTTTAAAAAGTTGATTTAAAAAAGAAACAACACAAGTTTAGAATCC ATAAAATGTCAGCAATGCTGATGTGCACTGGACTGAAACATCTTGATCATCTTCTGATAG GCTTGCTTTCTTTGAGCAATAAAGGGGTACCTGCCCGGGCGGCCGCTCTAGAACTAnnnn nnnnnnnnnnnnnnnnnnnnnnnnnnGAGGGTTAATTGCGCGCTTNGGCCGTAA TCATGGGTATTAGCTGTTTCCTGTGTGAAAATTGT TTTTNCCAAANNNNAAAAAAAANCCCCCCNCCCNTTTTTNANTTTTTTNAAAAAAATCCCG GNCNTNNNAAAACAAANCGGAAGGNTNNAAANTNCCCCCTTTNACNTTTCCNAANAAAAA AAAACNCCCCCCANAAAAAAAAAAAAAANNGGGGNNATAAANNTTTTTTACNCCCAAAA Sequence 637 ACTTAGGGCAATTGGAGCTCCCGCGGTGGCGGCCGCCCGGGCAGGTACTAAACACAGAT GGGCACACTCTAGATATAGAACACGTTTCTTGCTGTGGTTGTGTGACAAATGGCTAGAAT TTTAGGAGGCTCTGGGACTGCACACTGTATATGCAATCCATCTCAGACTTTGGGATGGGA ATCCATTTCATCATCCAGCATGGCGAAACTTGGTTCATTCGCCCCAATGTGAGTCCTTCC TGGGTAAAATTAAAGGCAGACCGGNTGGGTGCTAAGGATCCCTTGGTGTGGAGAGGCCAT TTCCGTTGAGCAGCTGGACTGTGAAATCAATACCAAAGGGGATGGTGGGGGTCTGGGCGTT

GGGGAATTCTTTGACAACTTTCTTGTCCTTCCTTAACCATGGGCTGTATCCCCNGGAGGG TCTTTCCGGCTTGTGGTTCTTGGGCCCTTGGGGGGGTC

AGGGCGAATTGGAGCTCCCGCGGTGGCGGCCGAGGTCGCCGCTGGGCCTGCAGGTCTCT GTCGAGCAGCGGACGCCGGTCTCTGTTCCGCAGGATGGGGTTTGTTAAAGTTGTTAAGAA TAAGGCCTACTTTAAGAGATACCAAGTGAAATTTAGAAGACGACGAGAGGGTAAAACTGA TTATTATGCTCGGAAACGCTTGGTGATACAAGATAAAAATAAAATACAACACACCCAAATA CAGGATGATAGTTCGTGTGACAAACAGAGATATCATTTGTCAGATTGCTTATGCCCGTAT

AGAGGGGGATATGATANGTTTGCGCAAGGGTNTGCACACAAACTGCCAAATNTGGGNGAA AAGNTTGCCCTAACAANTTTTGCNGAANATTTTGTCCCTGNCCGGGNGGGCCNTTTTAAA AAACTAGGGGGGCCCCCCGGGGCNGGNGGNAATTTTNAANANAAANTTTTANNNGNCCC CCCNCCCCCTNGGGG

Sequence 639

Sequence 640

GGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTCCGAGAAAAGAGCTAGGGTAGGC
AACTAAAACTTACACAGTGCCAGTCTCAGGAGGTCAGTAGCTCACAGAACTCAACAGATA
AACTGGATTAAAACTTAAAAGTCTTCTTTCTATTTGAGCCCATAATGACTATTTTGAACA
TGGCTCTTTTGCTGCTGCCTATATATAAATTTTTTATTAATTTTCTTGTATTGGGAAGAT
CTTGAATACGCTCCAGGATGAGAAGAAAAAATACGCTGACACTGCTAAATCGGGTATATG
TTTTTGCAATAAAGAACACTGGTCAATATACAACTGAGGAAAAACTGAAACAGATGTGAG
TCCTAGAACCACAAGAGTTTGAATTTGCCCAGAAATGCTATTTTAAACACTCTATATGGT
TGGNCTGCTGTTTTTTTTGNGGGAATAATGCATTCTTGGCATTCTTAAAA
Sequence 641

ACTATAGGGCGAATTGGAGCTCNCCGCGGTGGCGGCCGAGGTACCTCAGGGGTGGTCTGT GGAAGCCTTAAACTCTCCACACTCAGAGTCCTTTGTTTCCCCAGAGGCTGTTGCAGAACC TCCTCAGCCAACGGCAGGTATGTCTCCCTGCAACACAGCTGTTGTACCTGCCCG Sequence 642

TACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGNCAGGNACAAGCTNTNT
TTTTTTTTTTTTTTTTTTTCGGAACCGTACCAGAAAATTTATTAAAAAAATTAAAA
CTATT

Sequence 643

Sequence 645

CTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTCACGCAGCAACGCGGAGGAACGGGAGGAACGGGAGTGAACGGAGAGCGTAGTGACCATCATGAGCCTCCTCAACAAGCCCAAGAGTGAGATGACCCCAGAGGAGCTGCAGAAGCGAGAGGAGGAGGAATTTAACACCGGTCCACTCTCTGTGCTCACCACGTCCAGTCAAGAACAATACCCAAGTGCTCATCAACTGCCGCAACAATAGGAAACTCCTGGGCCGCGTGAAGGCCTTCGATAGGCACTGCAACATGGTGCTGGAGAA

Table 1

CGTGAAGGAGATGTGGACTGAGGTACCTGCCGGGCGGCCGAGGTACCTGCAGAAGGCCT ACAGGGTGCCAGGCACTTCTTTAATGTGTTCTTTCTTTATGTGATTATTTGATTAATCTC TGCCTCCCCACTAGGACTGTAAGCTCCCTGAAGGCAAGAATCCTGTGCTTATGCTCAAT ATTAGCTCNTCCCTTGGCACAGAGTAGGCACTTCAACAAATGCTCCCCA Sequence 646

CTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACTGGGATTACAG GCGTGAGCCACCATGCCTGGCCAGAAATCTATGTTTTCTTAGAACATGTGGAAGAAGGAA AAAGACAAAAAAGGAAGTCTGGATTCTGAGGACCACGTCTCACCCAGGGTGACATCAGGA ATGGGTGCTAGCCTCTGCAACACGACACCCAGTCTGAAGAAGCTCTATACAGGGTACCCT NGGNCCGTTTTAGAAACTTAGGTGGGATCCCCCGGGCTTGCAGGAAATTCGAATATCAAA GCTTAATCGATACCGTCGAACCTCGAGGGGGGGCCCGGTANCCCAGCTTTTTGTTTCCC TTTAGGG

Sequence 648

Sequence 649

Sequence 650

Sequence 651

TGATAAAGGAATATCTACCAAAACACCTATTAGCTAACATCACACTTGATGAAAAACT Sequence 652

TTAGGGCGAATTGGAGCTNACCGCGGTGGCGGCCGCCCGGGCAGGGTACTTTTAGTAGAG ACAGGGTTTTACCGTGTTAGCCAGGATAGTCTCGATCTCCTGACCTCGTGAGCCGCCTGC CTCGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCGTGCCTGGCCACGTCCCTA TTTAGAAATGAGAGGAGTGACTGCACATAGGAAAAATGCCACTTTTAGCAATTCAAAGT GGAAAAACTTCTTTTATATAAAAAATTATCCCAACTCCCACCCCTTGGCTCTCAGTGTTGC ATCTCCCACAGAGGTAAAGTTGTGCCATTTTCCCACGGCTTTAAACAAAGCAAAAACCCACCAATCCTAATAACCCC

Sequence 653

Sequence 654

CTACTATAGGGCGAATTTAGCTCCCCGCGGTGGCGGCCGAGGTACACGGAGCTTGAAGCC
GAAAAGGGTGAGGATCACTTCTACAGAGAAGGAGCCTCGGTCCACAAAGTCACCATTAAA
TATATAGGGGTTGGTCTCCGAGGGTAAACCGTTGAGCTCGAATATGTTGAGGAGGTCATA
GAACTGGCCATGGGTGTCCCCACATACTGTAATCTTCTCTGTCTCTTTTGAGTGTGGTTTC
CACGAGCGTGCTCAGCTTGGAGAGGACCTCTTTGACCTGTACTGAGTTTTATTATCTCCA
ATAATAATGGTCTGGAACTCAGGAGGATCATAGTAAAACCTCCAGTGAAGGTTAAAATTC
AGGCCTGTTGATTTTTCTTCGTTTTATGTTTTCCAGCAAGGATATCATAAGGACCAACT
AAT

Sequence 656

ACTATAGGGCGAATTGGAGCTCNCCGCGGTGGCGGCCCCCGGNCAAGGTACTCTCCCAC TGGAACTCTGGGGCCCACTGAGGCACCATTATTGGGGATTTCAGGGTGGGCTGGGCACTG CA

Sequence 657

Sequence 658

Sequence 659

Table 1

CGTGAGCTATCGAAAAGAACGGCAGTTTGGGAGTTCTGCAGGGAGTTGACCACÀNAAGTG GGAGAGTGAAGGGAAGAAGTGTGTCGTGAATAAAGCTTGGCTGGTTTTCANATAAAAGGT CTTGCCGAGTGGCCAGGTGTGGTGGCTCACTCCTGTCACGTCCCANCACTTTGGGAGGCC AAGGCGGCGGCTCATGAGGTCAGGAGTTTCGAGACCAGCCTGGCCAACATAGTGAAACC CCGTNTTTACTAAAAATGCAAAAAAT

Sequence 660

Sequence 661

Sequence 662

Sequence 663

Sequence 664

ACTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTTTCAGTTTCATAT TACTCTAAATCCATTACAAATCTGCTTAGCTTCTAAATATTTCATCAATGAGGAAATCCC AGCCCTACAACTTCGGAACAGTGAAATATTTAGTCCAGGGATCCAGTGAGAGACACAGAAG TGCTAGAAGCCAGTGCTCGTGAACTAAGGAGAAAAAGAACAGACAAGGGAACAGTCTGGA CATGGCATCAGAGATCCACATGACAGGCCCAATGTGCCTCATTGAGAACACTAATGGGCG ACTGATGGCGAATCCAGAAGCTCTGGAAGATCCTTTCTGCCATTACACAGCCTATGGTGG GGGGGTGGCAAATTGTGGGCCTCTACCGCACAGGCAAATCCTACCTGATGAACAAGCTGG CTGGAAAGAAA

Sequence 665

TAGGGCGAATTGGAGCTCACCGCGGTGGCGGCCCGCCCGGGCAGGTACACNGTGGATGGGCCAGTCGGTCTTNTCTGGCAGGTTGTTTCTNTCGGTAGTGTCCGGCGAGATGACCTCCTGCTGCTGGGCCTGGATGGCCCCCAGGATTCCCCAGAGCAGGAGCACGAGCAGGTGCCCTGGAGCATCTTGGCAGCACCTGTGGCCCTGAAGTCCTGGTCCCGAGGAGCACCTSequence 666

GAGGCTG

Sequence 667

Sequence 668

Sequence 669

Sequence 671

GCTNCTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTGGCCTGCACCAG
AAGATGTCTGCATTACTCATTGCTAAAAATGTGTAGCACAGAACTGCACTAGGATTAATT
TGTTTACAAGAAGAAATTTAAACTCTACGTTTGGTTTTCACATACAGCAGCTCTATTGAA
TAACATGCATCTGAATTTTAAGTTGCAAAGGTATCTGAATAATTTTTCATGTGCATCTTT
TGTCGAATGTTTTGGTTCAAGAAAGAATGTTTAAAGCTTTTTAAAAGACTTCAGTTCTTA
ATGTAACTGTACAAAATTAGTTGTAAAAAATAACATAATTTACCAGTAAACCCACTCATA
TAGAAATGTGCAAAGCCTTTTGATATAAAAAGGTTTGTACCTGCCCGGGCGGCCGCTCTA
GAACTAG

Sequence 672

AGGTACTGAAGCCAGCCACGCTGCGCCCGGCCCTGCCCCGGGCCTTCCTCGTGCCTGGGA GGTCGTTCTAGGGATGCTCCTGACCTCCGTCTCTTGGACCTAAGATGGAATGTGTCCCCA GCTCAGGGATTGCCTGAACCAAGAGGCCAGGAGCCCCCATGGGCCGCCCAGTACCTGCCC GGGCGGCCGCCCGGGCAGGTACAAAGTGCTGCAGTAGCCGGTGAGCAAACTCATGTGTGG CTCCATCTCGGCTCCCTGTTCTTCCTCAGGAATCCACACAGCTTCCCAAAGCACTGTTGA TGCAGGAAATCTAACCTGCCTATTCAGCCCATC

Sequence 673

Sequence 674

TCTTGNATTCTTTTTC

Sequence 675

Sequence 676

Sequence 677

Sequence 679

Sequence 680

AGGTACAAACTATTTCATTATCAGCAAAAATTAACATCGACTGGACCGAGAAATGACTCC
TTTTTACAAACGGGGAAAGAAACGGAGACTCCTGGAGGAAAGCTGCTTCTGCTGGACATG
TTCTCCCGCGTACCTGCCCG

Sequence 682

AGGTACTACTGGCACTGAGCCAATGTATCCTATCAAGGAAAGCTTTATCTGTCACTGAGC

Sequence 685

AGGTACCTCCTGCCTTGAGTGATTTAAAGCATTTTAAGATATGCTTTGCTGCCTCTAGAT ATTTCTCTGGTTAGATCCCCACAAAGATACTGTAACATTAAGTTCTGGGACCATTTGAGA ACAAACTAGCTGCTCACAGATTCCTGAAAGAAATGCAAAACCTTTTCTCTGGCCCCAAGT ACCTGCCG

Sequence 686

Sequence 690

AGGTACCACTTGTGATGTTTTAATAAATTCTGTGTGGTTTTTACATAGCCCTGAGAGGT AAGCAATGAGTCAGGAGTTTCCTCCAAGCACCTGTTAAGTGGCATCATATAAATAGCAAT GTCAGGAAATCAGGTACCTGCCCG

Sequence 691

CCGGGCAGGTACTGGAATGAAAATACAGGTAAAGCATTTGAAAATTATTTTTCTGGCTTA GACTGTTTACTGGCTCGATTCTAGCTCTGTCCTGGTAAAGGCCTCCAGAACCTTCACCTA CTATTATCAAGTCTGGCCTCATAGGGAGGGACTTTTACTGTACCTCGGC Sequence 692

GAATTTCCATCGGTTTGCTGAGAAGCACAACTTTGCAAAACCCAATGACAGCCGTGCTCT CCAGCTGATGACCAAATGTGCGCAGACTGTGATGGAAGAACTAGAGGATATTGTGATCGC GTATGGACAGAGTGATGAGTACCTGCCCG

Sequence 693

Sequence 694

TATAGGGCGAATTGGAGCTCCCCGCGGTGGCAGCCGCCCGGGCAGGTACAACAAAG TTCATCCTAGTAATTCTTAAAGCTCTTCAATTCCTATAGAGTTTAGCCTTTGTCAATAGC CAAAATATGTGCTTGAAAAAATAACTTCTTTGAGTTTCAAAGCAAATGAAAACATAAAACA

AGCAAAAAGGCTTTTTTGTTGGTGNTTTTCTCTGCATATCTAGGGTTTGTTTCTTCATT CATAAATACGGTTTTCAAAAAGCATTGCCTCAGCCAAAATTATTGCCCTTTTTAAAAATG CTTTTCATGTATACACTTTCTACATAACTGCTTTTCTTTACAC

Sequence 695

AGGTACATGAAGGCCCCCAGTTCCCCCATGCTAGACACGTCCCCAGAAGCAGCACCTAAT GGGCAACACTGCGGAATCATTTTCCACCCAGATCAGGGGCATCCCACGGACACTTATTCC AGAAAACTGAAGCTGGGCCACAAAGAAGGCTCCCATCCTTGCTGCTATTTGCCCTGGACC ACTTCAAAATGTGACACATCGGGCTGCAGTGAGCTGAGATCGTGCCACTGTACCTGCCCG GGCGGCCG

Sequence 696

CCGCGGTGGCGGCCGAGGTACTGAACATGTTCTAAACTCAGATAGTGATGACTGCACAAC TCTGCGAATACACAAAAAAACATCCTCGGAGGGAGTCTGAAGGTATGTAAATTACATCTC AGTAAAGCTGAAAAACTGCTTTGGCTAAAGTGGCTATCCCTCCATGGTGCTGGGACCTGC CCG

Sequence 697

Sequence 699

Sequence 700

Sequence 701

Sequence 702

AGGTACCTGCAATGAAGGAGAGGAGGAGGACAGGGAGCCAGATTTCCAAGGACGAGAGGAT GGATGCGGAGCAGGTTTTCTGTAGCATGTGGAGGAGGGTAGGAGGTGGCATGTGATGACC TCGTGCTCCAAGAATAGTGCTCAGTACCTGCCCGGGCGGCCG

Sequence 703

Sequence 704

GCGGTGCCAGGCGAGGTACGTGACAAATGTCATCTAATAACCCTGGGAGGGCTGGGTCCA CCAGGCTGTCCCAGTATCCACCACCCTCTTCCTATCCTCAGGGTGCAAAGGCCAATTCAC TCCCTCTCCCGTTTCCTTTCATTCTTTCAGTGTTGCTGTATTATGTAGTACCTGCCCG

Sequence 705

GCTNATTGGAGCCTCCACCGCGGTGGCGGCCGAGGTACGATGCAAACCAGCAAGCCAGGA AGCACCTCCTTCCCGTCACCACAGCAGGCCTGAGCAGGAGCGTCACCGGAGCCCAC TGGAGAAGCCCCACAACGGNCTNCTCTTCCCCCAGCACCGGGGACTATCAGTACCTGCCC G

Sequence 706

CCGGGCAGGTACCCTCCAGGCCCTGTGTATTATTAAGATCTTTTAGTAGCGAGTTGCTCT TTCTCTGGGAAATCGGCTGTTAAAGTCAGAGGGAGCTCTTAATAGTTTGCATGGTATTTG ATTAAATGGAACAGTTGGATCAGTACCT

Sequence 707

ATTGGAGCCTCCACCGCGGTGGCGGCCGCCCGGGCAGGACGCGCTCTCCTTCGAAGTCCG GAGGAGTTTCCTGGATTTGGCACTCTCGTGCAAAGCGGTCATATGCTGCAGAGTGTCTCC TCTGCAGAAGTCTGAGATAGTGGATGTGGTGAAGAAGCNGGGTGAAGGCCATCACCCTCG CCATCGGGAGACGGNGCCAACGATT

Sequence 708

Sequence 709

AGGTACAGCATCGCTGGTGGTTTCAAAAAACGTAGTCATTCCTCTCACTGCAACAATGTA
AGATAAGCAGAGTAGATCTGTTATTTCCAAATTAAAGGTGATTAAGATATATGGAGAGAG
AACATGGCATGTGAGGTTTATAGGGCTAGAAACTGCAGAACCATGTAGAACCCACATTTA
ACTACAGTACCTGCCCGGGCGGCCGCTCGA

Sequence 710

AGGTACATTTGAGATGGTCTCACGTGAGACATCAATACGGCTTGCTGGGGGGCACAGGTT TAGGGCAGATGAAACTCACAGGAGGGCGGGTCTGGGTTAACTGAGCTAAAGAGCTTTTCA AGCCACTAGAGCAACANAGCTGCCCACAGTTGAGTCAGATTAACCTGGGAAGCCTCCAAG TGAATTGGNTACCAGCACCACATTCACAGATCTCAAAATTTATTGAAACTGATTGAGAGG NTGGATTTTGATAACTAAGA

Sequence 711

ACCCCCTATAGGGCGAATNNTGGNAAAACCGCCCCGGCGCCGAGGNACCCAAACCTNTN CATGGNCAAGAGAAAACCNTTTGTGAGGGAAANNTNTTAAAANNANGACATGAAAATGGA GACGGANATTAAGAGAAACAAAAAGACTCNNCNAGACCAGCATGGACAGNACCTGCCCGG GCGCGT

Sequence 712

Sequence 713

Sequence 714

TCTAAAGAACGTGTGTCGAAAAGCATGTCAGTGAGTAGCCATAACCTTCAGAGGGGATCT ATGCCTGGCTCTAAAACTAGNGGATCCCCCCGGGCTGNGANGAATTCGATATCAAAGCTT ATCGATCCCNCGCCTCGGNGGGGGGGCCCGGGNCCCANCTTTTGGTCCCTTTAAGG Sequence 715

Sequence 716

Sequence 717

TTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTTAATTTAATGTTTAATAATATTAAATAT CTTTAATATTAACGAAGTGATCTTTTAAGAGATATTGGTATTGCAAATGTTTACAAATAG TTTCTTAGTTGAATCAAGATTGGTATGAGTTGTAATTGTGGAGCTGGGTGATAGATCATG ATAATTCATCATCATCTCTCAGTTTATATTTGAAATTGTATATTAAACTTGAAAAGACACT TTAATTTGAATTACTATTTTATCTTTTAAATGTGGTATTTCTCCTTAATTTACCCTAAGA AAACACTATAATTTTATCACAGTACCT

Sequence 718

Sequence 719

GGAGCTCCCGCGGTGGCGGCCGAGGTACCCTTGGTTTCTCAAACAACTCACTGATTTAT GGTCTTGAGACCATAAACTCATTTTCCTTATATGAATGACATTTCCACATCCACAACANT ACCACCAAATATATGTATCTAGTTCTTACTAACTGCAAATCCTCAAAGTGAACTGCGTGC ATTTTAATGTTGCGTAGTTTGCTGATTTATGATTACCCTTAATGTACCT Sequence 720

Sequence 721

Sequence 722

TGTAGCTCNCCGCGGTGGCAGCGGCCGCCCGGGCAGGTACTCTTGTTTAACCATCAGAGG

Sequence 724

GGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTGCAGTTAGAGCTTCAATCTCC AGTGTGATGGTATTAGGGTTAGATCTTCAATCTCCAGTGTGATGGTATCAGGGTTAGAGC TTCAGCCTCCAGTGTGATGGTATCAGGGTTAGAGCTTCAGCCTCCAGTGTGATGGTATCG GGGTTAGATCTTCAATCCCCAGTGGTGGTGGTTAGAGCTTCAATCTCCAGTGTGATGGTA TTGGGGTTAGAGCTTCAATCTCCAGTCTGATGGTGTTTCGGGATGGGGCTTTTAAAGATG TAATTAGGGTTTAAAGATCATAAGGGGACCTGGTCTGATGGGGATTAAGTAGGCTTATAT TGAAAGAAGACACAAGAGGG

Sequence 725

AGGTACTTTTTTTTTTTTTCACGTGGTCCCAGCTTGAGTTTACTGAGCCTCCTCCAGG CTCAGATATGTGCTTGCCTGGAGAAACTGNTTCCAAAGGCCAAGCAGCCCTTGCCTTTGG AGAGCTGCTTTTTGTAACTTACAATAGTGTTTCCCAGAGTGCATNCCATGAAAATATTAG TTCTTTCAACATGCTGAACAATGAAAGAATCCATGGTCAAATCCTGAGAACNTATTGTCC CTNTTTTAGAGATTCATAAGGTACCTGCCCG

Sequence 726

AGCTCCCCGCGGTGGCGCCCGAGGTACAGAACTCCAAAAGAAAATCAGGCCTCATTGC CAAAGCTCAGGGATAAGTCTAAACAGAAAGGCATTTATACAGCAACAAGAAAGTTACTGG GGGCTGGGGATGAGGGAGGGCTGGGGTAGGAGGATACTAAAATATTTTCTGAGGTGCCCA ACTGCTTGTCTTAGAAGAGGCTAAACTGAGCCAAGCGTCTCTGTTTGTCTCCTCCACCCC CTCCTCTACAGCTTTACAATGTTCTCTAGCAGAAGCAAAAACAGGGTCACTGCCATCATA GATAAAAGGATG

Sequence 727

CGAGGTACCAGATCAAAACCTGGGAACTTCGTATTTGTCCTTTTCTCTCTGCCAGGAATA
TCGTCCTCTCCATTTGCCCAATGAGCCCCACCTNCTCAACATTTTTACCTNTGTGGAAAT
CCCTTCCTTCCAGAAGCCTCCACTCGCTTTNTGCCAAGGAGCTTCTGCGGCGCCCTGCAC
GCACCTTTACAGATGCAGGTGGCTGTTTCCTGTGTCAGACTGCAAGCTCCCCCCGCGTAC
CTGCCCGGGCGC

Sequence 729

AGGTACTCCACAAGCTTGCCTGCCATGGGCTGTCGGGATGTCCACGCAGCCACAGTCCTT TCCTTCCTGTGTGGAATCGCCTCAGTAGCAGGCCTCTTTGCAGGGACCCTGCTTCCCAAC TGGAGAAAATTACGACTGACCATTCAACAGAAACGAGAAGAACCTGACTGTTTACACAGG CCTGTGGGTGAAATGTGCCCGGTATGACGGGAGCAGTGACTGCCTGATGTACCTGCCCG Sequence 730

CTÁCTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTGATCCAACTGTTCC
ATTTAATCAAATACCATGCAAACTATTAAGAGCTCCCTCTGACTTTAACAGCCGATTTCC
CAGAGAAAGGGCAACTCGCTACTAAAAGATCTTAATAATACACAGGGCCTGGAGAGTACC
TGCCCG

Sequence 731

ATTGGAGCTCCCGCGGTGGCGGCCGAAACTTTATAATCTTTTAACTAAATGTAATTGTC ACCATAATCTTATAGACAAAGCATTGAGGTTATTGAGCTAATGCTGAAGGTAGTAAGTG GAGGAGCCAGGATGAGGTCAGAATCTGAGATTTTAACCATGCCTATGCTGTCACTTCTTA CACTTTAGAATACCTCCATGCTCATGTGGACACCTAGGAACAAATGAATATTTCTATTCT

TCTCCCAGAATTITAAAACATTAAACATGTTAAACTGTATTTTTGTTTACCATAAAGCCT TCCNAGGAGGAACAAGCACTAAACACAGTCTCTGGCTTAAGGATTTTGGATGAACATATT TCAAAAGCCATCTGCTTCNCAGCAATTCATAATCCATACCCCTTTTCCTTTTTGGCCACT TATTCACCAAGAATCTNCANTAGTTCCCTCGGGCCGCTNTANAAACTNANTGGGATCCCC CGG

Sequence 732

Sequence 733

Sequence 734

CTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACCTTATACA
ACGATGCTATAAATATTTGTATGCATAATTCAACAGTAATCAGTGGTGTTTATCTAAACT
AACTGATAATCTACAGATTGCAGTGCATTTATGATTTCAATGGAATTAATCTAATTCTCC
ACACTTAATTGTGAGAATAGCTATAAACAGATTGTCAAGAGGAGCCTTTTAGTGCCAATG
CTTTACTTGAGGAAAAAAATTTCTTTTTGGGCAAACCCATCTTTATTCATTGCAGAATACA
ACGATTCTCAAAAGTAGCTTAACAACCCCAACTCCGCTGGGTAAGTGTGGCGGCACACGC
CTGTAATCCCAGCTACTTGGGAGGCTGAAGAGGGAAGGCTGCTTGGGGCCAGGGAGTTTG
AAACCAGCCTAGACAACATAACAAGAGTCTGTCGCGAAAAA

Sequence 735

Sequence 736

GCGAATTGGAGCTCCCCGCGGTGGCCGCCCGGGCAGGTACCACCATCCTGTCATAAT
TCTTTTTTTTGGCCAGGGGAGACAAGGGTCTCACTCTCTTGCCCAGCATAAAGTCCTTT
TTAAAACTGTAAAATAGTTTATACATTTGAGCATTATTATTATAAGCTTTTGTTTCTTAC
CTCAGAAGAATATATTTTCAAATGATAGACTTCTGGGACTTTTTGGTACCT

CCGCGGTGCCGCCGAGGGTACCACCCATGTGGAGGAGACTGCAAGGAAGCTGTTATTC
AAAGTAGAACAGTCAGCCTTGTGCTTGAGTCCTGCTTTATGCTTGCGTGTTTCATAACAA
AACACAAAGGCAAGTCTTCATATCAGCACTTAGTCTTGATTCAAGTAGCTGACTACTGTA
CCTGCCCG

Sequence 739

TTCTTTTAGCAAAACAGAATCATCCCATAAACTATAAGGTCGATGGTATCAGCGGGTCCC CAAACTGACTGCACATCTGAGTCATGTTAACAAACACATTCCAGGCCCCACCTGAGCCCT CTGAATCAGAATCCCTGTAAGGAGGACGATGAACTTGAATTTGCACTGACTTTCCCAGCT GTTTCTTACTCTGATCAACTTGGGGATAGGGACCCATTTGAGCTGCATCACATCATTCCA AAGCCAAAACACAACAGCAGGACAAGAATATTTTCAAGGCAGTCTCTAAAGCAGAGGAGA AACTGTTGAGGGAACCTAGAAAGTAAAAGGAGATCTGGCTTGCTGGGCTCCATTTGAAC Sequence 740

Sequence 741

Sequence 742

AATANCCCGAATTGGAGCTTTNCGCGGTGGCGGCCGAGGTACCTTCATGCTCTAAATCAT NATGATCTACTATCTGAAAAGGAAACGACAAATTTTTNAACAAAAGAATTTCACAACAGA TAGGCAGTTGATAGCATGAGGCACTAACATTAAACCCAAGTCTTTCAATGGCACTTGGAG TCCCAGGGCCTGCCCG

Sequence 743

Sequence 744

Sequence 745

GCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACAACCTGATTACCTGAAA CAGCAGCNNAGNCATGCAGAGGAGGATCAGCAGCAAGAAGGGGTGAGCCATGAGTTCCTG AAGCCAGGAGGGCTCCATTCTTCTCAGAGGTCCTGAGCTCTGGAAAGCCTGAGAGAACTC CCCGCGTCCT

Sequence 746

GGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCTCTCCCACACTCTTCCTGACAA AGCAGNTGAGGGACTTTCTCTGCCAAAATGAGAGAGTAAACTTAAAAAGAAGACAAGGTG GGATATTGCAAACAAGAGATACAACACAGGAGGGAGCCGAAGAGAATCCCTTGATTTGAG GTGAAGCAGCTGTACCTGCCCG

Sequence 747

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Table 1

NATTGGAGCTCCCGCGGTGGCGGCCGAGGTACTCTAACCTGGGCGACAGAGTGGGACCC TGTCTCAAAAAAAATAAATAAATAAAAGAAAGAAAGAAATGATCTCTCCTCATAGTTTG TGTGTAGGAAAAGAAGTGATAAAACTGACCTAATTGAACTTCACCTTTTGCTCAGTGACA GATAAAGCTTTCCTTGATAGCATACATTGGCTCAGTGCCAGTAGTACCTGCCCG Sequence 749

ANGGCGAATTGGAGCTTNCCGCGGTGGCGGCNCGCCCGGGCAGGTACAGTAGTCAGCTAC TTGGATATCAAGACTAAGTGCTGATATGAATACTTGCCTTTGTGTTTTGTTATGAAACAC GCAAGCATAAAGCAGGACTCAAGCACAAGGCTGACTGTTCTACTTTGAATAACAGTTCCT TGCAGTCTCCTCCACATGGGTGGTACCT

Sequence 750

GCTNCCCGCGGTGGCGCCCCCGGGCNGGTACCCACCGTTCATCTGTAACATGGCTGTA
ATAATGGCACCTACTCGTTGCTGTTAGCATTGAAGGAGCCAACGTATGCAAGCCAATCAC
TTAACAAATGTCCATTGTTCTGCTTGTCATTTCTTTGCTTATACTTCCTGACAACAAGCA
GAAACCTTAGAAGAGTGGTCTGTTCACTTTAGGGAAGGCTAAGTCAGCATTAGGTGTCTT
CCATCTTAAAGCACACAANACAGACTGGGTAGAGCAGCANCGTCACTGATCGCCACTCTA
ATAGCTCTCTGGCTAAGTTTCTCA

Sequence 751

GCGGTGGCTTTCGCCCGGGCAGGTACTCGGGCCTAGAAATTATTTAANNTGGCGACTGAT ACGTCTCATGGTGAACTCGTTTNTNCTAAGGCACTCCCACTTATAGTAGGAGCTCAGCTG ATCCACGCGGACAAGTTAGGTGAGGAGGGGCTGACATATTCTTGANTCACTCTTGGATCA ATCCCTGACTTCAGGCCCTGCTGGGTCCTTCTTGGTACCT

Sequence 752

CCGCGGTGGCGCCCGAGGTACAATATAGGCAGACAGTTTGCCTTCAGAAATTCAGAAAT GCAGCTTTTGAGGGAGGTCAGCATCATTGGTCTCAGCTACTAGAGTTGAAGATGATTCAG CCACTTTTATTCCAGCCACTCCATTTCTAGCATACACTAAGAGAAGTGTATATTTAAAGA GGCCATTTTCCTGCAGGATGTTTATAAATAGTTCCTGGCCCCGCGTACCTGCCCGGGCG GCCGCTCG

Sequence 753

Sequence 754

Sequence 755

CGAGGTACTGTAATTTTGGGGAGCAAGCTAACACATTTGACTTGCGGCTGAGCTCTTAAC
TAAGCAATACCTCAGTATGCTCCTTCGGGAAAAATTAAAGGTTCAGTAGTCAAATACTTT
TGGAAATGCTGGGCCATTATGCACAGAGAAGGCCGCAGTAAGGAACATTTTAAATTTGAA
CAGAGAACATCCAAATCTAATTCATCTTAGAATCCATTTGCTATGGAATGTACCTGCCCG

Sequence 756

Sequence 757

CGAGGTACTGCGGGCNCTCTTGATTCCAGTCTACTGGACTGCTTGTTGCTTTGGGTATTT
GAGTATTTATGTGTTTCTTTTGGCTCCTGTTTGCATGGTCACTGGCTGTCATAGGGAATG
GTGATCGGCTTTTCCAGTTGCTCAGGNCACAAAAGAGGTTGGCTGGTGTCATGGACAGCA
CATGGGATTTGGAGTTAGAAGGTCTCAAGTTAAAAACCCTCAGGCCCCTGCATTCTAGCT
GGGGGACCCTCGGGCAGGTTGCTTGAACCTCTCACCTTGACTGGTTTGTTGAACTTGCAG
AGTGCTAGCAGCACCTGCCCCCAGCGTGGGGGAGTGGTTTTGCAGATTAAAAGTGNTGTG
AATGCACTTCCTCGATGGAGGGCCTCTANCACCATGGTTTCGTCATCCTGTATCTGTCAC
TCACCCTGTANGTNAAGGGGTTTTTCACATTTGNNGCATCAAAAAAAGACCCCTA
Sequence 758

GCGGCCGAGGTACATGGTGGCTACCACATCCTGNTGTTTGTCTATACTGGGAGAATCAGG CNTTCCNAGTCATCTTGGCTGCCCTAGCTCTGAGCTTCAGGGGGATATATGACTCAGAAAT GCTATGCTTTCTGGAATTTTGGATATTTCATTTTTATTGTTCTTGGTAAATTCTCTTTTGA CTTAGGAGAAGCTAACTATTTGGAAAGGTCTCTCAGAACTCTAATTACAAATATATGGTA CCTGCCCGGGCGGCCGCTCG

Sequence 759

CGNCCGAGGNACTGGNTTGACANTGTGTTTAAAGTCAAAAGATTAGGCTTGAGATCTCTT
TCTAGTGNGATGGTTTTACAAGTATATACCGTATGTTAATGNTTAAAAATTTCACACCCC
AAAAATGTGCAGNATACCAGATGTTAATTATATCTCATAAAGCTATTAAAATTTTATCTC
AAAATTATAGCTTTATTGCATTTAGGGCATTATCCAATTTTGAATCTAGTCCAGTTATCA
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GGAACCAATTTTGCCATCTATATTAGNNACCTTGGGCTGCNATAATGAAGTACCCTCGGC
CCGCTCTAGAACTAGNNGGGATCCCCCCGGGCTGCAAGGGAATTCCNATATCAAGCTTAA
TCGATACCCGNCGACCCTCGAGGGGGG

Sequence 760

CGCCCGGGCAGGTACTTGTAGCAGTCCACAAAGAGAACAGCCAGAACATTCTCTATGCCA CTGCCTGCTTCTGGGTGAATCCCAGGTGTGAGTAATGAGGCTCACATGAGTGGGTATATC ACTAACACGGCTTAGGAGCCCCATCTCNAGTCATTATTTTGCTTGACAACCATGAGCTTC CAGGATCCCGACAAGGCACATGGCAAATTACAGGAGTCCTCACACTAAGAGAAGCCCTAA GCTATGGCCAGCACAGGTATTTATAGTTCCTCCCAGTCCTTTCGCAGTTTACCAGTGGGT CATTTTTACCATAAGCAGTGTTGCCTAGTAACATAGCTGACATTCTGCCTGTATGGTTTC CACGGGAACAGAGCTGATAGCTGGGTTAAACTGAATCCAAGCCCAA Sequence 761

TGGCGCCCGCCGGGCAGGTACACTTTTTTGGCTTATGGGTATCTTAGTTTAACCTTTT CTNTTTGAGNGAACTGTGTCATTTCAAAAGCCTGAAGACATTGTGATGACTGCCTCC ATAATGGCTACATTCTAGGGGCTTTGCCCTGAATCGAATATTAACTCAAAAAGCAAACAG TACCT

Sequence 762

CTCCTATTTGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACAGAGCCACACAAA TCTGGGAGAAGACTATTTCAGGAAAGGAGGAGGAAATTTGAAGACCTGGGGCTAGAATGA GCTCAACATATTCTAAGATCGGCAAGTTTAGTGTGGCTGGAAAAGAATGAGTAAAACAGA GAAACCTGANATAAGATGAGGTCACGGAGAAATGCATGGGTCAGACCACGTATAACCTTG CAGGTCATGGTAAAGGCATCTGGACTTTATACTGAGTACCTGCCCG Sequence 763

Sequence 764

CCGCCAGGTACATTCAAATTTTTGTTATCCTCTTCAAGAAAGTNACCTNGGTAGANTNCA TATATATCCCAACATNNTAGGAACTCATAAAATGCATACTTTTTTGGTGTGATCAGAGAT GGGTAACTCCTTATTACTTGTGGGTAGATAGTTTTGGAAATAGCCTGGAGTCATTGAGAG CCAATCCTTATCAACAAAATGGCATAAATGGACAGGAATGGGTTCTTCTTCACTTTAGAG ATAGCTCTGAAGACATGTCTCAANTGGGATNAGTTCAGNTGCATATATGAATAGCAGTC Sequence 766

Sequence 767

Sequence 768

TTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTTACATGGGGACCGCCAGG GGCCTCNAGAATCGGTATCCTGAGTCCTCTTGAAGAGCAGTAGAGGTTGTTTCATTAAGT GCAAACACATTGTTCTTAATTTGAAAACTGTGGGCAGAAACAGAAGCCCGAGACTAATTT TTCCATTT

Sequence 769

TTAGGGCNAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACAGCTTAATGGCAAAAGAGA
ATCTTAATCCCTAAGAGCTTTTTCTAATTGATGGACATCATTTTCCAATTGAACAAATTG
GAATTTATTAGTGGTGACTGTGGCTTTGAATCTGAGCTAGTTTATTCTTGCAGTCACAGA
GAGTGTCCTTATAGAAAATAAAAAGGGAAAAGCTCAGTTCTGCTGAATATAATCAATATA
CACAATCAATTGATAATTCACAACTACCTCCTTTGCCTTCTTGCACACTCTTCCTGCCAC
TCAGAAACATCCATACTTACTCTTCAGGATGGGTTTTTTGAGCCTGAATTATCCAGATGG
GCTGTTTCAACTTTTCAGCCATACCTTAAAAGTTGAAAAGGGATGGCCCTAATTTCCAC
CTCTAATTCCCCTTCCAATTTCTGGGTTTGAAGCAAGACTNGAGAACTTGGG
Sequence 770

TTAGGGCGAATTGGAGCTCNCCGCGGTGGCGGCCGCCCGGGCAGGTACCTGATTTCCTGA CATTGCTATTTATATGATGCCACTTAACAGGTGCTTGGAGGAAACTCCTGACTCATTGCT TACCTCTCAGGGCTATGTAAAAACCACACAGAATTTATTAAACACATCACAAGTGGTACC

Sequence 771

TNCTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCCCTGCGCCAATCAT CACAGCCTGGTTGTATCAAGTGTGCCAAACTGCCTGCGCTAACAACCAAATGCAAATG TCATACGTCTCTGTCACTAGCAGCATAGTTGCTAGAGAGACACGTGTGAGCCACACCTCA AAGACAAGCCTTCATCATCTTTTCCTGGAGATAGCTGACTAGCAATCAGATGTTCAAATA AAGCTACTTTCTTGTACCTGCCCG

Sequence 772

CCGGGCAGGTACTGNTTGTGATCCAGCTACTGAGGTCTTGAACCGAACAGACCTGGGAAG
NGTCTCANAGCTGTCTCTCAGGCTCTGAGAGAAAGTAGCCAACACTACAGTAGACAGAGA
GAGACAGAGATCAAGACAGGAGACAGAGACAGCATAAGACAAAAATACTTTATGAAATTG
CCAAGTCCTCAAGACAATTCTAGNTAACNTCTTTTCAGCNAAANTGGNTGGAACCCAGGG
CTTTTAACCTCCAAAGGTNNCACAAANNAAATNAAAACTAAATNANNAANAATNGCTTCN
CTNNGGGCGCGNCTTCTTATGTAAACNTATNGNGGGGNTATACCCCNCCCGTGNGCCNTG

Table 1

GCCATGGGGAAATTTTCCGCAATTTTCCANAGGCCTTTTATTANTGNATNATCCCCGNTGCANAAACANCTANTNNAGGGGGGNGG

Sequence 773

Sequence 774

Sequence 778

Sequence 779

CGACTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTGTTATTCCAGT
TTTGCAGATGAAGAAGCTGGGATTTAGTGAAGTTAAATAACTAGTAAATAGAGAGGGCTA
TGTTCCATCCTAAGTTGCTTTTGATTCCAAGACTGCTATGGTATTTTGAGACGGCTGATT
TGGTACCTGCCCG

Sequence 780

CTATANGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGGGTTTGTAGATG
GAAGGAAGAACTTGTGTGCTTAGACCTGACGCTGGGAGGAGATGCTGCCACCTAGGTTAC
TTGTAGGACCCTATACNGCAACCTCCTTTGCCAGGAACTATTTATAAACATCCTGCAGGA
AAATGGTAGCTGAGACCAATGATGCCGACCTCCCTCAAAAGCTGCATTTCTGAATTTCTG

Sequence 782

Sequence 783

CCGCGGTGGCGCCGAGGTACGCGGGATGTGACAACCCTGCTGAAGTGCCACCTACTATA
TTTGGTCTCAGCGATTAAACGAAAAGAGATGGTAAGGCAACAAAAATTATCAGCATATAT
TTTCAGCTTCTTTGAGTTTTGCAGATTAGTATAGTTCAAAGGATAGACAAATTCACTTGT
TTTCATTTTGTCTTTAAGATAAATTATTTGGTACCTGCCCG
Sequence 785

Sequence 786

GACTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCCCCGGGCAGGTACTGGGAT
TATAAGCATATAAGCCACTGCGCCTGGCCCTATATACCTTCTTTATTCCTTTATTTTAGT
GGCATTTCAAGAGTGTTGAAAACATATGTTAGATCTGGCATGTTTAAATAGAAATCCTTC
TGAGCCCTACTTTGGGGGCAAAGGGAGCCGGCCCATTTATAGAGCTCTTATGATGTGGTA
GACAGCGGCAGTACCT

Sequence 787

AGGTCTTGAGTCGACCCACGCGTCCGTGCCTTACAACTGGATCTCATGAGACATTTCCTC
AACTGTGGCTTATAGTCTCTGATGAATCTANGTTTGTGCCAAAGTTAATACAAAATCAGC
CAATATGCCTGGATTTTAAAAGTAATCTATTTAGGCTTTACTTTTTGATATTTTGACCTG
CCCGGCGGCCGCCAC

Sequence 789

AGGTACTTATATGCTAGGAGCCTGGGACATACTTTTATTATTTCATAATTTTACATCTTT
AAATCTTAAAGAAACATCGGTAATATCTGCATGAATCAGAATTCAAACGCAGCCTTGCTT
TCACAATCATAGATTTTCAGGATCAGAAATTTATTCTGTCAAGAAGAAGAAGGATGACCAAAA
ATGCCGGACGCGTGGATCGACTCAAGACCTGCCGGGCGGCCCGCCAC
Sequence 790

Sequence 791

Sequence 792

Sequence 793

AGGTACCCTCGGTTGCAAGCACAAGCAAATGTGCCAGGGTGGTTGATGCAGCTGTGGTCA CAGGTCCTATCCAAAGAGCACTCGTCCACATCTTGGCAAGACTTCTCATCTGTTAATAAT TTAAATCCTTTCTT

Sequence 794

CGAGCGGCCGCCGGGCAGGTACATCATGCCTCCAGTTCTGGAGCTAACACAGATTTCTC
CAATTTCATCTGTTTTGCAGAGCTGGGGAGGTCCATCTGGTTTCACAATGCACATCATCC
CACCAGGCATTACATGCCCTACATCCTGGACCGTCAGTGCTGAATTTTTATCTTCAGTAT
TGACCCGTATTACCCCATAGCTCAATCCATTCATTGAGAGAATGGCTCTTCCTGGCAAAG
GGGCTCCTGGAACTCCAGGCCTGCGGATTGCTACAGTCATGGCTTCAGCAGACGTGGCGC
ACGGTCAGATGGCCTCAGGCTTCAGTCCATGACTTTGGAACAG
Sequence 795

AGGTACCCTCGGTTGCAAGCACAAGCAAATGTGCCAGGGTGGTTGATGCAGCTGTGGTCA CAGGTCCTATCCAAAGAGCACTCATCCACATCTTGGCAAGACTTCTCATCTGTTAATAAT TTAAATCCTTTCTT

Sequence 796

CCGCGGTGGCGCCCCGGGCAGGTACAGGGCAATCAGAGGGTGAATGATACGCACACC TGTGTATCTCCCATATTCTGCAACTTCTGTTTTTATTAGAAGTGTAGAATAAGTTCCCAT CTTGTCTTCTAAGCTTTCAGGTTCCCAGGGTGTACCTCGG

Sequence 797

Sequence 798

CCCTTAGCGTGGTCGCGGCCGAGGTACTTTATCATCCATAATATCTTACTCTCTAATCCA

Sequence 799

CCGGGCAGGTACTACCCAAGGTCCTCTGTGACTCGCCGCCCACTACCCAAGTGAATGAGT CTCCCCTAGAGCTTTGCTACTCAGAGGGGTCTGAGGACAACAGCATGGGCCAACACGTGC ACTCGAGCTGCCTGGAGATCTTGTTCAAAGGCAGATTCTGAATGAGTAGGTCTGGGTTGG AGCCTGAGAGTCTGTACCT

Sequence 801

Sequence 802

AGGTACCAGGACCTCTAACTCCCCCTGACACAGAGCAATTAGACTCCCATAACAATGGTA
TCAATTATACCACTCCATTGGAGGGACTTCCTTTATGTGTCACCCAGGATACATTGCTCA
ACTGCAGTTGCCTTGCAGTTTGATCCCAAGCATGGTTGAGTTACCATAAAAAAATTATGT
ACCTGCCCG

Sequence 803

CCGGGCAGGTACCTGCTAAGTGCTGGACAGCCTTTCTCACATTTCCTCCCAGCAATCCTA GAGGCAGGCCTGGTTGCCTTTGTGAAGCTCAGAGTGGTTAAGTAACTTGCTCAAAATCAC AGAGCTACTAAGTGGTACCT

Sequence 804

CCGGGCAGGTCTTCCCAGGGATAGTTTTCCATTTGATTAAAGTTTTGTTCTTATGTTACT
TTTTACTGTTGTTTTTTGCAGTTTACCTAATGCTAATAGGGTCTCAGGAACTGTATTTGAT
GTTAAAGTGTGGTTTTTCCAGAAGATGACAGATAATTGGTGGTCTCCCCTTTTCCTCAGC
AACATAGTTTGTACAGCATACTGACTCAATTCTTAAGTCTGATTTGTGCAAATTTTTATC
GTACTTGAGAGTTACAAAGCAAGTGAGAACTTGAGGGATCAAGATCCTGGAGAGAAAACCTTAAAAGGGTAAACCCAACATTTGGCTCTACTTTTCCCCTTGAGGTAT

Sequence 805

CCGGGCAGGTACAAACCCCAAGTGATTATAGAAAAATCAATGTGGCAGCTACACTAGAGA TGTCCAACCCCAAGGCTATGGGCCGTTGCTCCCTCTTTCCCCCCAATCCCAATCCCGCGT ACGCGGGCCTCTTTTCCGTGGCGCCTCGGAGGCGTTCAGCTGCTTCAAGATGAAGCTGA ACATCTCCTTCCCAGCCACTGGCTGCCAGAAACTCATTGAAGTGGACGATGAACGCAAAC TTCGTACCT

Sequence 806

AGGTACCCTAAGTGGGAACCTACCAGGACATTCAAAGCAAGAGCAGTAAGTTCTGAATG
TTCTGGGACAACCTGGGTGATATGCATGGATATGGGCTGTGGAGGCTGAGCATTTTAATG
ATAACTTAGGGAAACGAGGCATGGCCATGGTGTAAAACTCTCAAATCCCAAGCCCTAATC
CAACCTTAAAATCCGAGTCTTCTAAAGGGCTGTTTTAACCATGAAAGGACCATAAGAAAG
GCAATTCACAGAAAATGAAGCCATGTGGCCAAGAAATATAAGAAAAACAGTAAAAGCCCT

TAATCTCAATAGCAATAGAGTGGATGCAAATGAATATAAT

Sequence 807

Sequence 808

AGGTACTGAATTCTACCCTGGAAAAACAAAACCCAGGTGTCTCCTCAGCTTCAAAAACTC TCAGGGAATGAATCCCTGTGTCCTACACCCAAGTATGTGGAATTTAAGAACCTGCTGTGG ACCTACCTATTTTCTTAGAAATATGCAGCTGAATATAACCATTTTTGGATATTTGAGATC ATTATGTACCTGCCCG

Sequence 809

AGGTACCAAATAATGGAGCTAGAATTCCTATCAAAATAATGGAGCTAGAATTTCCATCAA CATATAAAGTCCATATGTGAGCCTCATATAAGGCAAACTGTAAAATCAGTCAAGGTTCTA AGTCTTTCCTCCAAGATCTGGAAAGAGTGATTGAGCATTCGTTATTTTAAATTACGGACT ATTTTTTCCATACAAGGAAGTTAACATCTAGAGCGATCATTCTCAAACTTTATTGTATA CCAGAATCATTTGGAGGATTTATTAAAACACAAAGTGCTGGGCCTTACTCCTGAGTTTCT AATTCTGTACACTCTGCCCCCATCCCGGGATGAGCT

Sequence 810

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Sequence 811

Sequence 812

AGGTACTTTATTCTCTTATCCAGGACTGGATCAAATGATTTATGGCATTGTGCTGTTTTA
ATGTTCTCATCACAGGGTCGATTCCAATAACTTGAAGCCCCAAGCCGCCCTAGAGGTTC
AGTTAACAGCCCACCACCACCACCACGCCAACGAAGATCTTCATCCCCAACAAAGGTTTTTN
CTGGCTGGTGATTTAGGGAATTTGTTTTCAGAAGATTGTCCCTAATTAAAATGNCACCCC
TCNAGGTCATTNCATNGGAAATNGAAGAGGNGCATATACTCCCTTGGTTCATNCCCACCA
TTTGTGNAGCCANGGCCCAAGAAAGGTT

Sequence 813

Sequence 815

CAAGAAGAAGGTGAAAGTAGAGCTATGTGCCCAAGAAAAACTTGTAGAGATGAATAAGA ACTGAAACAATAGTAGAAACACTTGCCCTGAAGAAAAAGGATGGAAAAATGAAATAGATT GATTTTTAGCTGGTAGGGAAGAAAGTTAACATAGTCTTAGTCGGTTGTTTTTCTCAAGG AACTGAGAAGCAGGATTAGTTTTTAGAAATTTGAANAAGGTAGTGAGAGGTGAAGCCCAG CTGGGTCGAGTGGGGACTTGGAAAACTTTTNTGTCGTACCTGCAGGCCTNCTACACCTAC CTTTTTTTTGGGC

Sequence 816

Sequence 818

Sequence 819

CTÁCTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACTTTGTAAA GAGGTGCAAGAAAACCAAAAACATAGGCATCCAAGGTAGAAGGCGTATCTCCAAAGAAAA CTGAGATGTTCCCAATCTGTTTGATAGAAGATTTAGGCACTCCTTGGCATCTCTGTATAT CTGTGCTTCCACTTCTCGGAGGTGGTAGAGGGGAGGCTGTCCTCTGGTCAGGAGAATCCT ATTCAGTGCTCCCTTAGACATTCTCCAGGCAGGATCAAACTCAAAGGAAGAGAATTTG TGAAGCAA

Sequence 820

Sequence 821

CCGCGGTGGCGCCGAGGTACTGTGGGATTTGTCTTTTATGAGTTACCACGTTCAGAGAC
TAGTTCATCTTTGGTTGTATAGGATGTTAGGATCTCAGTTGGCATTCACAGTTAAATCAT
GCACCTTCAGGAACTGGGAGCATTTTGATCCAGAGTCACAATCATTCCTTTCTTATCTTC
ATCCCTATGGTATGTGTTCTGAAGTTTAACTGACAGATGGCAGCTGGTACCTGCAGGC
CTCCTACACCTACCTCTCTCTGGGCTTCTATTTCGACCGCGATGA*GTGGCTCTCTGGAAGG
CGTGAGCCACTTCTTCCGCGAATTGGCCGAGGAGAAGCGCGAGGGCTACGAGCGTCTCCT
GAAGATGCAAAACCAG

Sequence 822

AGGGCGAATTGGAGCTCCCCGCGGTGGCGGCNCGAGGTCACTGACTTACNCCCTTCCCAC AGCTACAGATAAGGGCTCGCAAAGTTGGCCTCAGAGACACATCANGAACCAAGGTGGACC AGCAGGTGCCGAGCCTGTGTATCTGCTTGGAGGAGACGTTCCAATGTGCTGCTTGTTCAG AGATGGTGAGTTGCAAGAAACAGAAACCCACCACAATTTCTNAGGCAAAAAGGGAGTTAA

Table 1

TTATAAGGACATAAGAGCACAAAGTTCCAGTGCAAGAGATACATCCAGGCTGCACAAGCT CCGGGAGTGGGGCCTGGCAAGCCAAAAGAAACCAAAGTTTGTCTTGCCTTCTGTTCCTCT TTCTGAAGCCACATAACCCTTTATTGACCNGNGTNTCTTTGCATCGCTTTTGTTTTCTTT TTATG

Sequence 823

NCGCCCGGGCAGGTACCACAAGAACTATGAGCTGGTTATCCACTTCATGTGGAATCATAA GCGTCCCAAAGTGACAATACATATAGATTGCCAGGCAGTGAAACAGTTAAGATGCCACCA TAGCTTTCTTTTCAACATCTTTCTAAATTACCTTACTATTTCTTTTGTTCCAAGTTTGTA CCT

Sequence 824

GGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACAAAGAGAAGCAGCTGA AGTTTCAGAACATGCTGTTATGCTTGCTAAGGATAGCAGAAGAAGAGTTGACTCCAGATGC TAACATCAGAGAAGTTGGCCTTGAGGGGGGCATTGTTGATCTTACTAGACAAGGAGACAGA TGAGAGATTATGCCATGATATCAAAGAGACTTTAAATTATATGCTTACATCTATGGCAGT GGAAAAACTCTCCCTGTGGTTAAAGCTTTGTAAAGACGTACCTCGGCCCGCTCTAGAACT AGTN

Sequence 826

TAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACAATAGCATGGGAA CCATTAACCAGCAGGCCATGGACCAACTGCAGTATCCTTTGTGACCCAGAACAGCACCAA GGTCAGAGGGCACCTGTATTCATAAACCAGCTGCCTGACTGTGAATCCTGATGAATCAAG CTCAAAAGGAGAAAACATAAAATNCATAAAGTACCTN Sequence 828

Sequence 829

CAGACTCATGTCAAAAAATATGATCTTATTACTTGAGTAGTTAAATTTAAGAAATTTAAGA TGACACATCGAGTGAAGAAGGGATGATGAATGGAACAGTCTGAAGGCATTAACTGTAAAG AAGTTGAAGTGGAGTTTAGAGAATGTCATCTTAACAGTTACTCTAATTCACCCCTGT Sequence 830

Sequence 831

Sequence 832

Sequence 833

NGGCGAATTGGAGCTCCCCGCGGTGGCGGCCCGAGGGTACGCGGGACAAATAAGAAGGC
TTCCTGAAAGCACTGCTGCTTGGCATACTTCTTGTAGTAACCCTGTCACCGTCTGCTTTT
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GGATATTGCCTCATTTTCCACATATATTCCTTATTCTGAAGACTACTTTGAGGTCAACAT
TCCAACAGACCTACGAGCAAAACATTCTGGGGAAATAAGTGAGAGAAAGGAAATTGAAGA
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ATGTGAGAATCCTGGTGAAATATTCATAATTTTGAGAGATGAAGTAATTGGTGATACTGT
AGAGGTTGAATTTACATCAAGTAATAAGCGCATTAAAACACGGCCAGCCCGTTGGAATAA
GAAAGTCTGGTGCATGAAAGCTTAAAGGTTTNCTGCTGGTTCAAGTCCATGTCAATGTCT
ACTGTGATGGAATCGTTAAAAGCTACAACCAAAATTAAGTACCTGCC
Sequence 835

GGAGCTCCCGGGGTGGCGGCCGCCCGGGCAGGTACTCAAGGCCCTAATCTCAATACCAT CACATTGGTGGTTAGGGCTGTAACATTGGGATATGGGGCAAGACAACATTCAATCCA AAGCAAGCATGTCCACACTGTTGGGACTCCAATCCCACTTTTGCATTGAGTCATTATTTA ACCACTGTACCT

Sequence 837

GGGCGAATTGGAGCTCCCCGCGGTGGCGGCCCGAGGTACAATTTAATTTACAACTGTTG
GAAATAAAAATCACTTAATTTTTTTCCAGTGCTTCTCCCTCATCTGGTTATTCAAGAAAA
CAAAACAGTCTCTGAGATATTTAGCTTTTCAAACTGTAAATAGATGCTCTAGTGTTATTT
ATTTTTAATCCCACTTGTATTATTTTACCTCTAGAGCATCTTGTATTAGGACATGTTAT
ATTTATGCCAGTGGGAAATAAGTTATGGCCAAGTTTTGCAAAAACAGGAAGCAGTGAGAT
ACTTGTTTTTTCTCCTCACTAAATATCAGTAATTGTCAGGAATGGTATTACCTATTTTC

ATTTCCTCTTTTCAGCTTTAAGCTTTGNTGGATTGGGACACTAAAACTGATGTATACCTG AGGGAAAAATAGAATGTGCTCATGGTTAGGGAAAATTATATTTTTTAAT TTGTTTTTTAACCAAGTAGGAATTTGGGTGTATGGATAAGANGCCAATCTGCTTCTGTAG GCTATAGAAGAAAACCAGTTGTATTTTATGGNCATAAT Sequence 838

Sequence 839

nnnnnnnCGGANNGCGGAANGGGGCGGCACAAANCCGCANACACGCGNAACAGANNNGC NGGAGCACGGACGNAACGGCAGNGGCGAGCGGAACAGCNAACTCAAAAGGCGGGAAAAAC GGGNGAGCCACAGAAANNAGGGGGAAAAACGGCAGGAAAAAGAAAANGGGGAAGCAAAAN GGCCAGCAAAAAGGCCAAGGAAACCGAAAAA

Sequence 840

TNGGAGCTCCCGCGGTGGCGGCCCGCCCGGGCAGGTACGGGGGCCAGTTATTATACTGC

Sequence 841

Sequence 842

TACCAGTGGCCCTGGTGGATGCACCATAGATGAGGAGCCTGGGAGCCTGGCCAGGTTTCT
GCTGGTACCTGCCCG

Sequence 843

Sequence 844

Sequence 845

TAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGTCTACGAAGTCCCATGGCTTTTCCAG TTCTCTCTTGCCTTGAGGCTCAAGAACAGTTTGTTTTAACTGAGAGTCTGGGAGGAACTA CAGTTTTCCCCAGAGTAGTCTTGGCGGACTACTGGAAGTCACAGCCAAAGAAACTCTGTG ATTACTGCAAGTGCTGGATAGCAGACAATAGGCCTAGTGTTGAATTTCATGAAAGAGGAA

AGAATCATAAGGAAAATGTGGCAAAAAGGATCAGTGANATTAAACAAAAAAAGCNTGGAT
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AANTTTTTNGGGNCCCCAGCCTTTTNANCCCCTTGTAANCCCNNGTCTTTTTTTCCCCCN
CNTNCCCTTGGNATTTTTNNAANTTCCCCNNGGGGGG

ACTTAGGGCGAATTGGAGCTCNCCGCGGTGGCGGCCGAGGTACATTTCCTAAGTATCACA
TGACTTAACAGGTGCAAGCTGGCAGGCATCGGACTTGGTATCCGTAAGACCTGTTGCCCC
TTTGCCTTCTGCCATGATTGTAAGTTTCCCGAGGCCTCCACAGAAGCTGAACAGATGCCA
GTATCATGCTTCCTGTATAGCCTGTCGCCTTTGGGCAGCTGGACACCTCACCCACGCTTC
AGGCTGGAGCCTTCCTCATCTTTATTAGGTGTCTTAGAGGCAAGTGCCGGAGGTAACATC
CTCCTCTGCATTTCCTACACTGACAAGGAGAATGCTGTGGCTCTACGCAGTCATCCTTTT
ACAACTTTTTTGCCAGGGAGCAAAAAGTCTTGNCACATNAAGTCGAATGAAGTACCTTGC
CCCGGGGCGGGCCGCTTNTANAAACTAAGTGGGGATTCCCCCCGGGGCTTGGCAGGAA
ATTTTCGAATTNTTNAAAAGCNTTTAATTNGATNACCCGGTTCNAACCTTCTAAGGGGGG
GGGGGCC

Sequence 847

GGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACTGCTGTAGCAAAC
AGCCCTAAACCAAGTGACTTAAAACAACCATTTTCTTTGTTACAGTTTTGCTTTCCTGGG
TTGGGCTCAGTTGGGCGGGTTTTGCTGGTGATCACTCTAATGGCTGCTTTTCTCCCAAG
TAGCCTTTCCAGCAGAGTTGCTGGCCTTACCTGGTAGCTGATGGCTTAGGGCTCACAAGA
GTACCT

Sequence 848

CCGCGGTGGCGGCCGAGGTACGCGGGGTCGGCAACTTTGGGAACCACCAGTAGGATGTGG
TTAAGATTCAGTTCTTGCTGAGCTAAGGAAGCATTTCTCACTTCTTTTTAATTGTCTGGC
TCACTTCTAGTCCCTAACTAAATGCTCACTCAAGAGTTTTAGCTTGAATGTCAAATGTCA
AAAAATTAATTGGGTGATCTTTCTCCATTTCTAGGATAAGAAGAAAAGAAAAGAAAAGAAATGAAG
TGACCATCCAGCCTTTCCCAATTAGACTTCCTCTCCTTCCACCCCTCATTTCCTTTTTTGC
ACACATTACAGGTGGTGTTCTGTGATAATGAAAAGCATCAGAAAAGCTTTTGTACCTG
CCCG

Sequence 849

CACTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTTTGGCCTCTCTG GGATAGAAGTTATTCAGCAGGCACACAACAGAGGCAGTTCCAGATTTCAACTGCTCATCA GATGGCGGGAAGATGAAGACAGATGGTGCAGCCACAGTTCGTTTGATTTCCACCTTGGTC

nnnnnnCGCGCTTGGCCGTAATCATGGGTCATAAGCTGTTTCCTGTGTGAAAATTGTTT
ATCCGCTCACAATTCCCACACCAACATACCGAAGCCCGGGGNAGC
Sequence 851

Sequence 852

ACGACTNCTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCAGGCAAAGT

Table 1

CCGCGGTGGCGCCCCGGGCAGGTACCAAATGGCTCACAAAGCCCAAAATATTTACTA
TTTGCCTCTTTACAGATAGTTTGCTGACACCTGACATATAGGAATGGGGACATTGCTTC
TCACCACCCCCAGCTCTCTCACTGGATGGTCCATGTATACAAAGTAGAGCCCTTATTAAA
TGCAAAGATGTTGGTCTAAACCCTGCTTGATAGGATGATTGAGTAAATTCAAGAAAGTGG
TAATGAGGGCTGGGTTGCCGGTGGCTCACTCCTATAATCTCATTACCTTGGAGGCCAAAG
GNTGGGCAGATCGCCTTAGATCAGGAGTTT
Sequence 854

Sequence 857

Sequence 859

Sequence 860

Sequence 861

Sequence 862

Sequence 863

Sequence 866

Sequence 867

Sequence 868

Table 1

Sequence 871

Sequence 869

Sequence 872

Sequence 873

TACTTAGGGCAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCAGTCAGGTTGTTCATT
TGAGCCAACAACAGATTTCTTGGTTATTGTGCTATTGCCACACCTGGGTTGGTGGTTTTA
TAGCCATTTCCATCATCAGTTTCCTGTCTCTGCTGGGGGTTATCTTAGTGCCTCTCACGA
ATCGGGTGTTTTTCAAATTTCTCCTGAGTTTCCTTGTGGCACTGGCCGTTGGGACTTTGA
GTGGTTCGAGCGGCCGCCCGGGCAGGTACTCATCACTCTGTCCATACGCGATCACAATAT
CCTCTAGTTCTTCCATCACAGTCTGCGCACATTTTGGTCATCAGCTGGGAGAGCACGGCT
GTCATTTGGGGTTTTTTGCAAAAGTTGTGCTTCTCAAGCAAACCGATGGG
Sequence 875

Sequence 877

TAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTTCTTTGCAGTATACAAGGA CTAACAGTTAATATTGACCCAATCTTATATACGTGGCTCATCTATCAGCCTCAGAAACGA ACAAGTAGACATATGCAACAGCAGCCTGTGGTAGCTGTTCCTCTTGTTATGCCAGTTTGT AGAAGGAAAGAGGATGAGGTGTCTATTGGAAGTGCCCCCTTGGCAAAGCAACAATCATAT CAGGCCTCTGAATATGCCAGCAGCCCTGTAAAAAACAAAAACGGTAACAGGTTGAAGAAAG TTCTCCTGGATAATATCCTGAAGACTATTTTCCAACCTTGGTTCCATTTTTCCANGGTCA

Sequence 879

CTTTTCA

Sequence 880

GACTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTTAGTGAAATATT CTTGGTAATATCATTCAGGTGGACTTTGGCATCATAATCAAATAATTTGATTTCTACTAA CTGTTGAAGAACTTTGTTAGCCACTTTGCTTATTCATTACATTTTGGGTGATCTTAAGCG CACATTAATTACCCTGTCTGTTTAGCATGTCTTGCTGTTCATCTTGGAATTATTTGTTGT

Sequence 881

Sequence 882

Sequence 883

Sequence 884

TCGACTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCCGCCCGGGCAGGTACTCTG
GAGTCAAAACGAATCAGTTTTATATAATCAATTATTTTAGACTATCCGAAGCATAATGCT
TAAGTTTAAAAGAGGAGACAAAAATAGGAGGACAAGATACTTGAGAGGCTGTGGCACTAG
GACTGCTTGAGAGCCCAGGAGTTGGAGGCCAGCCTGGACAACATAGCAAGACCTCATCTC
TGGTCAGACATGATGACGGTGGCTTCACCCGGGGGTCTCCCCACAGCAGCAGCCTCGGGT
AAGCAGAACCTCGCTCCGGGGGTTTACAAATCCTTCTCCCTTCCCCACAGCACAACACCCG
CGGCTCCCCGCGTACCTCGGCCGCTCTAGAACTAGGTGGGATCCCCCGGGCTGCAGGGAA
TTTCGATTATCAAAGCTTTATCG

Sequence 885

Sequence 886

ACTNCTATAGGGCGAATTGGAGCTCCCCGCGGTGGCCGAGCGGCCGCCCGGGCAGGTACA
TAATGCAGGATCTGATGTCCTCCTCTGGTAAGCAGCATGCACCGCATAAACAGGTCCTTC
ATGGCCTTGAAGATGCACTGCTTTTAAAAGCTGATTATCCTCTATTTCCCAGTGAATCAC
TTGATTATCAGATCCTTCCAGAAAACTAATTCAAGTAGAAGGGGGAGCCATCCTGTTTAC
AAATCCACTGTATGCAATTGACTCGGGCCGGTGTGACCATTCAAGTTGGTAACAACAACC
CTTTTCAGGGGGTCATAGAGCACCACGGAGCAGGGACGTGCCAAAGGCCCAGAAAGTCCT
CCCCCGCGTACCCTCGGCCGCTCTAGAACTAGGTG

AGAAACATTACTGTCCATTTGTCTAAAATAATCTATAACAACCCAAACCCAATCAAAATG

AATTCAACATTTATTTTCCCC

Sequence 887

TAAACAATNTTGGCCTTCTCGATGATTTTATTCATGTTGCTCCAAAGTTAAAACCCTGTA GAACTAAGTAGGTGAAGAGATATTTTGTATAAGTGCCACAGAAGAGAAAATATAATNAAT TGAAATGATCACCTAAGATATACATGCTCCAACCATATTGATTTAGAACAAAACACAGC AGCCCATAACAGTTTGTGGCCTCTACTAACTGTCCTCTGCTGTCCCATCTAGAGGGTTAT GTTTCTCTATTTTTAAAATAAAATGTAGTTAAATTAGCCTGACGGGATGTTTCCTCTCT

Sequence 888

CCTATAGGGCTNTTTGGNGCANACCCCGGTGGCGGCCGGCCCGGGCTGGTACTTCCTT TTTTATGACTAAATNCTACTCTATTGTATGGACATGACACATTTTGTTTAAATTGTATAG GTATGCCATACTTTAAGTTTGTTCCATAAATCACTTCATTAACATTTGGGTTGCTTCCAC TTTTTGGGTAATTAATTAATTAATTTATTTATTTTGAGATGGAAGTCTCGAAAAA AAAAAAAAAAGAATGTGTATCTACCCGCAGTTGTCAGGCGCAGTATCCATATATGTCATT TAGGTCAAGTTTGTTGNTTTTCAACTCTTCTGTATTTTTACTGACTTTTTTGGTCTAAGT TGTTTAATCATTCACTGAGACAGGTGTGTTAAATCTCTCATTGGGGTGATGATTTATCTA GTTCCCATTTTAATT

Sequence 889

AGGTACCTGCAGGCCTCCTACACCTACCTCTCTGGGCTTCTATTTCGACCGCGATGAT GTGGCTCTGGAAGGCGTGAGCCACTTCTTCCGCGAATTGGCCGAGGAGAAGCGCGAGGGC TACGAGCGTNTCCTGAAGTATTGCAAAACCAAGCNGTGGGCGGCNCGNTCTTAGAAACTA GTTGGNATCCCCGGGGCCTGCCANGGAAATTTCCGAATAATTCAAAGNCCTTTATTCNG GATTACCCGGTTCGNACTCTTNGTAAGGGGGNGGNGCNCCCCGGGNTTACCCCCAAGCNT TNTNTTTGGTTTTCCCCCCTTTNTAGGTTNGNAGGGGGGTTTTAAAATTNTGGCNGCCCG NCNTTTNGGGTCGGNTNAAATTNCAATTGGGGGATNCNANTAAGGCNTTGGTTTNNTCCC CTTGGGTGGGTTGNAAAAAATTTTGGTTTTTAATTCCCCAGCNTTTCCAANCCAAAATTT TTCCCAACCAANCCAANACCNATTTAACCCGGTAAGGNCNCCCGNGGGGAAAGNNCCAAT TTA

Sequence 890

GGCCGCCGGGCAGGTCGCTCGTGATCTAGATAGTGAGCGGACGCGTGGGTCGACTCAAG ACTITTAAAGATITATCAAAATTTGGTGAGCCGAATCTCAGAAAATTGGTGAATTCGGTT AGTTCCCAATAGGCCGCAGTAGTAATAAGTGGAGTGTTCGGGATATAGAAAAATTTTCAC GAATGGAATTAAAATTTCTAGGCGAATTCAGTGAGTTCCCAATGGGACATGATTGTATGA GTGAGCTTTTCAATATATAGCAACATTTTAGGTTCAAGAAACTTAAGTATCATGGTGAAT TCAGTAGGTTCCCAATAGGATTCGCATGTAATAAG

Sequence 891

CCCTTTCGAGCGGCCGCCCGGGCAGGTACAAACATGTGCCACGTCACCACACAAAACCAA AGTCTGCTCAGAGAGGTGGGCTATGGTGTGCAGGCTGCAACCTTTCTCTGCAATTGTTAA GTCTTCAAAAATCTGAGTTCCTCACATAAAATTCTGTGCTGTGGCCAGAGCTCGTTTTAC CATTTTCTTAGATTGGATCACTTTTAGGATCAGCTTCGTTGTTCTTTGCGTAGACAAATG ACTCTCACAGCTTTCTCCAAGTGTNCCAGAAGCACTAACTTACTGAAAATAGAATCTCAT CAAAGCTTAACATATTCACTCTGAAAACAGCGGANCTGCTGGGTCGCTTAAGGAAAGCTG ANAACCTNAAACCTGTGGAAGGAAAACCAGTGACCACTTGGGGCCTTATAAAAGTTTGAT TGGCAGGTGANGAAGGGGATCTCAAGAGGAGAATCCCNAATTTCAAAAGACATGGGAGAT TTTGTCCCTAAATGTTTTATACTAGTGCTCTTGNNAAATGGAAAACCCT

Sequence 892

CCGGGCAGGTACAAACATCCACACCAGAAGAGCAAGACTTAGAAATGGCATCAGAGGGAG AGCAAAAGAGGCTTGAAGAATATGAAAATAACCAGCCACAGGGAGAGAATGGGTCATAAA ATCAACCCAACTGGCTATCAAGAGAATTATACCTTGCAGAATGGCACCTTTGGTATTAGC **GTACCT**

Sequence 893

AGCTTCTATTTTGTCAAACTCCTTTGGACAAATATTCAACATTCAACAACAAGCTTTGTA AACCTAACGCTAAACAAGTCATGGCAAGCAAACTGGATTTTCTTAAGAAATGAGGAAAAG

TGCAAGTGATCTCAGTACCTGCCCG

Sequence 894

AGGTACTTCTTTGCAGTATACAAGGACTAGCAGTTAATATTGACCCAATCTTATATACGT
GGCTCATCTATCAGCCTCAGAAACGAACGAGTAGACATATGCAACAGCAGCCTGTGGTAG
CTGTTCCTCTTGTTATGCCAGTTTGTAGANGGAAAGAGGATGAGGTGTCTATTGGAAGTG
CCCCCTTGGCAAAGCAGCAATCATATCAGGCCTCTGAATATGCCAGCAGCCCTGTAAAAA
CAAAAACGGTAACAGAATCCCGTCCATTGTCAGTTCCTGTTAAAGCCATGTTGAATATAT
CTGAAAGCTGTAGAAGTCCTGAAGAAAGAATGAAGGAATTTATTGGA
Sequence 895

Sequence 897

Sequence 899

AGGTACGCGGGGGTGGCGCCAGGGATTTGAACCGCGCTGACGAAGTTTGGTGATCCATCT TCCGAGTATCGCCGGGATTTCGAATCGCGATGATCATCCCCTCTCTAGAGGAGCTGGACT CCCTCAAGTACCTGCCCG

Sequence 901

Sequence 902

ATGACATGGNTCAGCTTCGGTTTAAAAAAGGTCAGTGTCTATCTGGAAATTTCTACGTGA GAGGTGATAGGAACCAGAGTTTACTTCTTCACACAAGAGGAACTGGACACGCATTTTCAC CACTTGCTGGAC

Sequence 903

AGGTACGGCCACAAGAGGGTAAGAAATTATCGCATGGTCTAATACCAAATTTTCCCCCAA ATAGAACCTACCAAGAGATCGAGCAATCAAAGCGTTATCTGTCAAAGCAATTCGCTTCTT ATTGATTTTGCCATAACCACGCTTGTAGATTAGTTCATTTACTGACTTCAGATTGGGGTA

Table 1

CCTGCCCG

Sequence 904

GCCGAGGNACGNNACNCCTCGTTCAGGGGANAAAAACCCANGCGNCCCACGCCCNAACA NGNNCCANAAGCTGTCCNCCANGCNCCCAGGCNGCCNCACNGNACAACGANNNCNCAGCC CNGGANNGNNCNNCCACAGANCNGGCNCANCAACNCNGGCNCCNGACCCNCNCTCCTTTGT GACCCNAGCCCANNCCCACCCCNGCGAAAGNGACCACAGCNNCCACCANGGCAAGGGGN NAGGAAGGNCCAAAGGGCNCNNCAGNGGGNACGNNCAGCNGGAGNGGCANCGAANNGNGN GCCNNCNCAGNANNGGGCAAGGNAAAGAGC

Sequence 905

CCGGGCAGGTACTCCCTCCAGACATCCGTATATTGGCCTGGGCCCCTGTAGAACCAAGCT TCAGTGCTAGGTTCAGCTGCCTTGAGCGGACTTACCGCTATTTTTTCCCTCGTGCTGATT TAGATATTGTAACCATGGATTATGCAGCTCAGAAGTATTGTTGGCACCCATGATTTCAGG AACTTGTGTAAAATGGATGTAGCCAACGGTGTGATTAATTTTCAGAGGACTATTCTTATC TTGCTTCAAAGTACCTCGGCCGGCTNTAGAAACTAAGTGGGATCCCCCGGGGCTGCAGGN ATTTCGATATCAAGCTTTATCNGATACCCGTCCNACCCTCGAGGGGGGGG Sequence 906

Sequence 907

CCGGGCAGGTACAAAGTGAGGAGGCAAGACAGGTGCACAGAGCATAGCTTTGTCCCATCT CAGGAACCCTGGGTTCCACCCCAGCTCCTGATCCCAAGAGATACGTTTCCCGGGACTCCA AGGGAGAGCTGAAACACTGGTCAAGCTCAGAGCCCTGAAGCTCTTTCCCACTCCCGCGT ACCTN

Sequence 908

Sequence 909

Sequence 911

AGGTACCAACTGGCCTCATCCTATATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAA ACNGAACTGGNGGCTTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTNTGA AAATCTGGGAACTGGTCACTNGTTGTGTGCCCTTGCTGG

Sequence 912

AGGTACCACCCATGTGNAGGAGACTGCAAGNGAAGCTGTTATTCAAAGTAAGAACAGTCA GCCTTGTGCTTGAGTCCTGTTTTATGCTTGCGTGTTTCATACCAAAACACAAAGGCAAGT CTTCATATCAGCACTTTAGTCTTTGATATCCAAGTTAGCTNGACTACTNGTACCTNGNCC GGGCGGCCGCTNTAGANNTAGTGGATN

Sequence 913

CCGGGCAGGTACTATAGCTGTAAGGAGAAGCTGAGAAATGATACCCAGGAGCAGCAGGCT

Sequence 914

Sequence 915

AGGTACCATCGATCCTAGTGGGACGCGATCCAAAAATATGCCTATTAAAGATAATTGCTT TGGTTATGTTTAATGGGAAAGNCTATCTGTTTGGCTTAAAAAGGGGACAGATGTTCTGCC ATCACAAATTGACCAACANAATTNTTGTTTCTCCTGNNACTCCAGTAAGAAAAGACNCGT TTACAGACAGTGGGGTTCAAGGNNCAGNCACAGAA

Sequence 916

ACCGCGGTGGCGGCCGAGGTACAAAGTGTCTTTNTGTCCTGTGTTTNANCCNTTTAACAT ACAGAACCTAATTTTACTGGCATTTTAATGTTAATTCTCCACTCGAAGGTGAACATGGGA TGTTTGTAACACATATGTTTTGNTTATCAAGCACACATATGACCCCCTTTTCATGAATAT TCATAGGTTCCC

Sequence 917

ACCGNGGTGGCGGCCGAGGTACACTTTGCCTGCTCCAGCCCTGGAATCAGCCATTGCTGC TGTGCTATCCTTGACAGAACTATAACCTGAATTTAACAAGGAGGAAATATCAGGCAAACA CAAATGGAGTGACATTCTANTAAACAACTTGATCAGCACTCTTTAAAAAATGAAAGACAAA AGAATGACTTGAGGAATGAGTTTC

Sequence 918

Sequence 920

AGGTACGCGGGGCCGTAACTTTTCTATCCGTNCGCGTCAGCGCCTTGCCACCCTCATCTC CAATATGNCGTGGTCCGACCCCCAGTGGCACTAACGTTGGGANCCTTCAGGGCGCTCTTC CCAAG

Sequence 921

AGGTACTTTTTTCCTTTTTTTTTTTTTTTTAAGTGCGTTCATTCTCACTGCTGTTATTGT TTTCTGACAGCATGTCTGAACCAGCTAAGTCAGCTCCTGCTCCGAAGAAGGGTTCCAAGA AGGCTGTGACCAAGGCGCAGAAGAAGGATGGCAAGAAGCGCAAGCGCAGTCGTAAGGAGA GCTACTCCGTGTATGTGTACCTGCCCG

Sequence 922

CCGGGCAGGTACCCAGTTCCAGGCCTTGACTCTTGGATGGCATTTCTGGACTTGCCCTGG GCCAGAAGGAAGCTCACTGCCCTGAATGGAGAGTTCCAGGCCTGGCAGCATTCACCACAA ACTGACTAAAGAGGCCCTGGGCCTGAAGTGAACATCAGTGGTAGTCTGGCAGTATTCCTT ATGGACCTGTGGTGGTGGTGGCCATAAGGGTGAGGCTCCTCTGCCAGTGGAAGGGGGAGG GAAGAGTAGGAAGGACTGCATCTTGTNAGTTTAAGGTTCCAGCTCAGATGCAGTAAANTA GAGCATGNCCGGNNGATTTCTAATATTTTTTACTTNNAGTCCCTGGCTCCTGGAAA Sequence 923

Sequence 924

AGGTACATATCACAGGATTAAAACTCCAGTTAAGCAACTGAGCTAATCATTGAAGTAAAT
TAAAAATACCAAGCTTCTTTAACCTATCAATGCTGTTTTAGAAGCATCATCCGAACAAAT
AGAGATTTAGTTATAAATTGCTGGGCTACATTCTGTGATGAGGAATTTTGCTTAGTACCAC
TAGAGGAAGAGAGACTAGAGGCCCAAGAAGANGGTGAAAGTAGAGCTATGTGCCCAAGAA
AAACTTGTAGAGATGGAATAAGAACTGAAACAATAGTAGAAACACTTGCCCTGAAGAAAA
AGGATGGAAAAATGAAATAGATTGATTTTTAGCTGGTAGGGAAGAAAGTTAACATAGTCT
TAGTCGGTTGTGTTTTCTCAAGGAACTGAGAAGCAGGATTAGTTTTAGAAAATTTGAAGA
AGGTAGTGAGAGGATGAAGCCAGCTGGGTCGAGTGAGGNCTTGGANAACTTTTTTNTCGN
ACCTGCANGCCCTTCTTANACCCTACCTTTTTTTTNGG
Sequence 925

Sequence 926

GGCGGCCGCCGGGCAGGTACTACGAGTGAGTGAGGCTGGGAGGAACACCAACCTAAGCC
AGGGTAATGAGGGGGGACTCTTTACCCAGGACCCTGCCCACTGGCCTTCCTCTCCAA
ACACAGGTTCCGGCATACCCAGGTGTGCAAGGCCTCAGCACTGAAGCATGGNGGGGATCT
GGCACAAGACCCAGCCTGGACAGAGATCTTTGGTGTTCTCTCTGNGGCCACCATCAAGTT
TTGAGATGCTGAGCACAGAGCCCCACAGAGTCAGCTCTTCCTGGCTCTGGCTGACAGCAGTA
TCTCCACGAAGGGCACAAAGAGNGGCACCTTTGTCATGTATAATTGTGC
Sequence 927

CCGGGCAGGTACTACGAGTGAGTGAGGCTGGGAGGAACACCAACCTAAGCCAGGGTAATG
AGGGGGACTCTTTACCCAGGACCCTGCCCACTGGCCTTCCTCTCTCCAAACACAGGTT
CCGGCATACCCAGGTGTGCAAGGCTCAGCACTGAAGCATGGTGGGGATCTGGCACAAGAC
CCAGCCTGGACAGAGACCTTTTGGTGTTCTNTCTGTGGCCACCATCAAGTTTGAGATGCTG
AGCACAGCCCCACAGAGTCAGCTCTTCCTGGCTCTGGCTGACAGCAGCACTCTTTGAG
GGCACAAAGAGTGGCACCTTTGTCATGTATAATTGTGCCCGTCTTGCCACACTCTTTGAG
AGTTACAAGTGTAGTATGGAACAAGGTCTGTCCT

ATTITTTTTTTTTTTTTTTTTTGGCNGCTTTTCCTGATTTTTTAACTACTCATACAATA
GTCTGGTAACTGGTNTTCTTTTTAAGCAGGGAACTCCNGGATTCAAATNCCTGATAATTA
AAGGATCTTTTGATATTTTGGCAGTTNCTCTCACTAAAAGAAGTTNCATTCANCAGATTA
NAATGATTCATGAGAAATTCTTGGNTAGTAAATATTTAATCCAGATTTTATAATTGCCTA
AATCTCTTTATAGGTTATTTCTTGCAATATTTCAAGATCCTGAGTCAGCCATGCTTATAC
AAGCAAACTTTTATTTA

Sequence 929

Sequence 930

GTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACCAGATTCT GATTCACTGATAATCGACTCATCTGTTACTAATACTTCCCCATCTGGCTTTCTGCGCAGC ACCTTTCTCTCATCACTGGCTTTCGGAGTCTTTGGGGAGGGCCTCAGAGACTGTTTCTG AAGGGACATTACTTTCTACATGTGGGTACCT Sequence 932

TTAGGGCGAATTGGAGCTCCCGCGGTGGCGGCCGCCCGGGCAGGTACTGTGCAATGCCT CAGGTTGCACCTGACTTATATGCTGAACTACAGAAGGCACATTTAGTTTTATTCAAGGGT GATTTGAATTACAGGAAGTTGACAGGTGACAGAAAAATGGGAGTTTTTCTGTTCCATTTC ATCAGGCTCTGAATGGCTTCCATCCTGCACCACTCTGTACCT

Sequence 933

Sequence 934

AGCTTTACCGCGGTGGCGGCCGCCCGGGCAGGTNCTTTCAAACAACGCGGTAGGCCTTCC CTTTNGGGTCTGCCATGACAACGATACCCCAGGTGGCAATGCTTGAAGCCGATGACCATC TGCGTAATGGNCCATTGGACTNTGGGGGGTATTCCATCTTTAAATGGGCCTTTNCGTGCC ACCCATTACCTTNGGCCCGCTTTAAAAACTAAGTTGGGATCCCCCCGGGCTTTCAANGGA AATTTTNGAATATTAAAAGCTTTATTNCGAATTCCCCGGTCGGAACCCTTTTNAAAGGGG GGGGGG

Sequence 935

TAGGGCGAATTGTAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACTGTGTATCATCGC AGTCTTGCTTTTTTGAGTAATGGATTCCTAGATTCTATGAGGATACCACAACCACTTTTA AAGAGGTTTCTAAGGCCAGGTGCANTGCTTACGCCTGGGAGACCAANGTGGGAGGATCAC TTGAGCTCAGGAGTTTGAGACCAACTTGTACCT

Sequence 936

NCACTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCACAAACACGAT CGCAGATCCAGGTTTCTCAAACTGGAGCATCTGCTTAATTTTCCCATAAAATCAGTCTTA TTCTTTCTGACAGCTCTGAGACTCCTCCGGCCACGACTAGGTGCTGTCCTGGAGGAAACG GTGGAGGA

Sequence 937

AGGTACGGGAGACTCATAACTCTCCAGGCCCAGTGCTGGGGGAACCCCTCATGGGAGC
AGCTGTAATGAGGCCTGGAAACTGGACACTGCTGAGCCCTGACATCCAGACCTCAATGCC
CTGACTCAGCCCATGGCAGCGACCCCTTCAAACAGGCTCCATGTGGGCCTGTAATCAGGA
AAGACTAGAGCATCCAGGAGTGGAGATTTGATTCTGAGATGCTGGGAGTTGTTCCTGGTT
CTTGCTCCTGTCTGGCTGGTGCTGACAGCCAAAAGCGGGGAGTTGTGAGCTTTGTCCT
TCAGCACTAGAGGCTTCACTCAACCCATGAGAAGGGGATGCCCCAGGCTTGCCCATCACA
AGCACTGGCCAAGCTGACTTCCCGCTGCTGAGGGAAAGA

GTGGNAGTGGCGGTGGCACACACTACGCATACTTC
Sequence 939

Sequence 940

AGGCGAATTGGAGCTCCCGCGGTGGCGCCCGCCCGGGCAGGTACCTGAGACAATAGC

ACCAAATTCAACAGAGAAAAGAATGAGTGAGAGAGCACTTTACACCAAGGCTCTGCACA TAATTGGTGCAATTTGAAATTGAATGGCTCAGAAGACTGCTCTGTGAGGAGCAGATTGGA GAGGATANACTCATCTTGCCGCGTACCT

Sequence 942

CGCCCGGGCAGGTACTCCCCTCCCCAAATAGAAACCTCAAAGACTGATCCATTTCCCCTA GGGCCTGGGCCAGGAGTAGCTCACTGCTCACTGCTGAGGAGAAAGGCACAAGATATAATG TCATAAGAGCAGGACAGTGGCTCACCTACAGAGTTCCCTATAGGGGAAAGAAGGCAGGAA ATAGGCGCAGGGTCTGGTCCTGTCCCTGCACCACCCTGAGCAGCTAGTCTTGGGAAGGGA TTACAGGCCCTGGGCCATAGGCTGCTCGCCATTCTGCTTTCCTATCCTGTTTCTCTCCCT GTGCTGCTCCCTTTTAGCCAGGGCTGAGAAATGTTCAGCACCTGAGGCAAAAACTGCCAT AATACCT

Sequence 943

Sequence 944

Sequence 945

CTACTTAGGGCGAATTGGAGCTCNCCGCGGTGGCGGCCGAGGTACAAGTTTACACCGTAA GAGGCAACATGGTCAGCCACAATGTCTTCACCTCCACAAGGGCTCATNACGGTGGTCAGG GCGAGGGCCCCCAGCATCAGAGCTTTGTTTAGGATCATNCTCTTTCCAAGGCAGCCTCAN CAGTTGCTGTTNTGAGCTGNAGAGCAATTGNNCCCGCGTACCTGCCCG Sequence 946

AGGGCNAATTGGAGCTCNCCGCGGTGGCGGCCGAGGTACCTGCCTGGAGCCTGGTAGACT TGCTGGGTGGCTAGATTCAGAAGAGAGAGAGCAATCACTACAGCTCAGCTCTCAGGAAGC CACATCCATAGGAAAAGGGAGAGAGTACCTGCCCG

Sequence 947

Sequence 948

GCTCCCGCGGTGGCGGCCGAGGTACTACTCAGCTGATCACAAGCTGCTTGATGGGAACC TACTAGATGGACAGGCTGATGATGGCAGTGATGATGACCACATTCAGTTTGTGCAGA AAAAGCCACCACGTGAGAATGGCCATAAGCAGATAAGTAGCAGTTCAACTGGATGTCTCT CTTCTCCAAATGCTACAGTACCTGCCCGGGCGGCCGCTCGATATTATTCTTCAATTCAGC TTGTTAAACCTCCTTCAGGATTCTAAAACCTTTTAGACTCTTAAATTGCAGCCTTCCATG TCCCTTGTCCTGCCTCCAGCACACTCTTCAGTAAACAAAAGTCAACAGCACCAGGGCA

Table 1

Sequence 950

ACAACTTTGGATTGTCAATGAAAGCTTGNTTGTGGATACTNATCAAACNNTTTTTNGTCT ATTTANTCCTTGNTGAAGCTAAAAAGGAAAGAGAGAGAGGGCAAAGAAAGACAAAGG AGGAAAGACCTGCCCGGCGGCGTCA

Sequence 953

Sequence 955

CCGCGGTGGCGCCCGAGGTCAACGGCCAGCCAATCACCAAAATGGCCTGTGGGGCTGAA TTCAGTATGATAATGGACTGCAAAGGAAACCTCTATTCCTTTGGGTGCCCTGAATATGGT CAGCTGGGACACAACTCAGATGGGAAGTTCACCGCCGGGCACAGCGAAGAGTACCTGCCC GGGCGGC

Sequence 956

Sequence 957

Sequence 958

GTGTGCCACCGCCACTACCACTGATTGCCGAGACCCACTCCAGCCCCTTCCTGGAGTCTG GCGGACCCAATTCATGACATAATTATCAAAAGTGAATCCAGAGGCTGTACCT Sequence 959

Sequence 960

CCGGGCAGGTACTCATCAGATGGAATGTTTTACCCTGCCGAGGTTNTAGTCATGATGTGC TGAGCTCTCTGNGTCTGACGTGACTGACTGGTANCTGGGCGTTGGCNNGACCCTCCTTTN NCTNTANNANCACATNATGNAGAATTTNNCACCTATGGGAAAATTAAANTGATNGACATG CCCNNNGAAAGGATGCATNCCCATCTGNNCAAAGGCTATGCGTACCTCGGCCGCTNTAGA NCTANT

Sequence 961

AGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACCTGGTTTTAACTTC
ATGTGTCTGAAAGCAGCACTGAAGAGGTTAGAAAAGACCATCTTGATCTGAGGATGCCAC
CCCTCTCCCATCTCCCAGCAGCAGCCACCGTGGCATGGAGAGAATCTGTGTGCTAGGGAG
AGGGACAGCACAGTGATTGTGAGATACTGCTTTGAACTCAGTGCTGCCCTGTCACAGCTG
AAAGCAAAACTGGGCTGAACTCAGCCAGCACCCATCCACACAGGGAGCATTTAGATGAGC
TCTAGCCAGAGAGGAATCGCCCATCCCAGCAGTCTGAATATGAGTTCCAGCAAGCCCCGT
CACTGTGGGCTAAATTGGTCCAAGACCTTAAATAAACTTGAAAGGGCAGTCTAGGCCATA
AAGACT

Sequence 962

CCGGGCAGGTACTCCGCCATTTTACGTGAGAGACTTGAGCATTCTTGGATTTGGTATCCT CAGGAGTCCGGGAACCAGTCCTCCATGGATATCAAGGGATGACTGTTTGCCCGTGTTTTT AGCCTTTGTATCTTTGCTCAAGAAATCCCTAAAACCTGGAGTACCT Sequence 964

Sequence 966

AATTGGAGCTCCCGCGGTGGCGGNCGAGGTACCAATAAGCATATTGCTTTGGCAATGCA TCTCCAGAGCANGTGACCCTGGCCGTCTGTCCTGGGGACACTGAC Sequence 968

ATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTCCTAATGAAACCCGTCTTTGG CCTGTGGCTGAGACGCCATCTGTAGGCGGTGAAATCTTTCCAGCCTATGTGACGAGGGTC ATGCCACAGGGTGCGCACCTGAAGGAAAAGGAAAAGGAAAGGTTGAAACACAGCTCCTTC AGGGCTTNTTCTTACCTGGCCAGGGGTGTTTCCTGTGTGCCACAGGGCGTTCCGCAGGTG CTCGCCAGGCCCTGTGGTGGAGTTTACAACTTTCACAGAAAGGCCCGAGTATCCCTGAGC CCTCGTGGGGTTGGTGCCCAGTAGGACTGGGTGACTTGCTTCACATCACAACATAAAAG

Table 1

CGGCTGCTGGACTGGTAGCCAAAAGACAAATNCAGCATAGTCATCGTCCCTTTTCGGTGT
TGATGAAGAAGGTGCCACTTGAAGTCCACAGCATTAAACTCATCATAACCTGGAAGAAGA
ACCCAGAGCCAGGTTAAAACCTGCAGCCTTCAGAAAGGTTCTTCCGTCATGTTTCCTAGA
CATTCCTCAACACCCACAGGGGATAGGTACCCTGNCCCGGGCCGGCCGCTTNTAGAACTA
AGTGGAATCCCCCCGGGCTGCAGGAAATTCNATATTAAGGCTTTATTGATACCCGTCNA
CCTTNAAGGGGGGGCCCGGGACCCCAACTTTTTG

Sequence 969

Sequence 970

Sequence 971

Sequence 973

Sequence 974

CCGCGGTGGCGGCCGAGGTACTCAGAAGTGTCTCTAGGAGGCTGGGCCAGTTTCCTCTCT
TTTCTGCAGGCGTCTCCAGAGCACCCTCTCACCAGCTGTATCTACTCACAATCGTCTGGC
ATTTGGAATCTGGTTGAGTTTGGGTCCTCAATACCCAGAAAATAGAGCCTCCAGGACCCG
CCCCTAAGCAGGAATTTTTCAGATCTCCCTTCTGGGTCCTTTTGGTCCCTAAGTCTCTGGC
TTTGGCATTCCTGGTGGGAATCCTTGCGGAGAGCCATCCTGGTACCTGCCCG

CGAATTGGAGCTCCCGCGGTGGCGGCCCGCCCGGCCNGGTACANTTNAATACATTANTG
TAGTAAGNTATTAANTGGTGCCCCTATGATCTNCGAGAGGTAATACACTATCACGTGTTC
CAAATTTTNACAGGAAAAGAATCATAGANTCCTATANCTGAAGGGGGCTNTACCGGGNTC
TACAAANGCCTGCCAGGTGCTNGGATNTCCTNCATCACATNCANCCATGANAAGTTACTT
GTGTCATGGTACCT

Table 1

Sequence 976

Sequence 977

Sequence 978

GAATNGGAGCTTTTCGCNGTGGCGGCCCGAGGTACAATAACTNGCCTGAANTTCTATGGC AACAGGCATTTANTNAGCGAGCGGTTTTATGGNCTCATCTGTATCTGGGATGCAAAGAA ATGGGAATGCCTGANGTCAATTAAAGCTCACAAAGGACAGGTGCCTTCCTTTCTATTCAC CCTTGGCAAGTNGGCCCTGTCAAGTTGGTACCTGCCCG Sequence 981

TAÁAAATCACGTCACTATATAGGCACTGCTGTATGGAAAACGCATTTTGTGTTTCTACAA ATTGTAAGCGGAAATGCCTTTTGAGTACGCGGGATTTGGATGATNGACATAAGGTTTTTA GCATGTNCCTCCTTTTCTTCACCCNCCCCTTTTTTCTTCTATTAATCANGAGAAACTTCA AAGTTAATGGGATGGCCGGATCTCACAGGCTGANAACTCGTTCACCTCCAAGCATTTCAT GAAAAAGCTGCTTCTTATTAACCATACAAACTCTCACCATGATGTGAAGAGGTTTCACAAA TCCCTCAAAATAAAA

Sequence 982

TATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACACGCCTTGCCAGACCAGA GTCAGTTGTATCATCCTGGGGCAAGTATGAGGAGAAGCTCACGATTACCAGGCACCTCAT TGTGAACATGCTTTCTGCAACGCCTGCATCACCCAGTGGTTCTCTCAGCAACAGACATGT CCAGTGGACCGTAGTGTTGTGACGGTCGCCCATNTGCGCCCAGTACCTGCCCG Sequence 983

Sequence 984

TCGAATTGGAGCTCCCCGCGGTGGGCGGCCGAGGNCAGAGCCGCCAGGCGACTCAATTCACGCGCTCCTTTTCTGGGGATGAAAAGGTNCTCACCANATCTTTCTATGCAACTGAGAGCT

CCTAAATCAAGTCAAAGGGGACCATCGTACCTGCCCGGGCGCGTCTAGAACTAGTGGAT

Sequence 985

Sequence 986

ATTGGAGCTCNCCGCGGTGGCGGCCGCCCGGGCATGGTACGCGGGGGAGACCAAGGGCTA ANGCTGGGAGGTGAGTCTGTCACCTTGAGCCGGGCGAGCGCTGTGGGCCAAGCAGGGGTT GCAGGCAGTAGGAGTGCAGACTGAAAAAAATGCAGACCGCCGGGGCATTATTCATTTCTC CAGCTCTGATCCGCTGTTGTACCT

Sequence 987

TATTTAGGGCGAATTGGAGCTCNCCGCGGTGGCGGCCCCCGGGCATGGTACAAGCACCA GCACCAAGGGATAATCAATGGGTGGCCACCACGCATTCACAAGTATGCCTAGGTTTGAAG CTGTGGAACCTTTTAGCTCCAAGTTCTCTGCATGGGTATTGGGGCAACCTAAACTCCTAA TCTAGGAGAGTGAGTACCT

Sequence 988

Sequence 989

Sequence 990

Sequence 991

Sequence 992

CTACTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGGAATTTCCATCGGTTTGC TGAGAAGCACAACTTTGCAAAACCCAATGACAGCCGTGCTCTCCAGCTGATGACCAAATG TGCGCAGACTGTGATGGAAGAACTAGAAGGATATTGTGATCGCGTATGGACAGAGTGATG AGTACCTGCCCGGGC

Sequence 993

Sequence 994

GCGAATTGGAGCTCCCCGCGGTGGCCGCCGGCAGGTACTTTTCTAGAAAAGCCTACA TGTATATACTTAGTTACAGCTGCACTTCCCCATTACTTATTTTTAGGAAGGTTATAGAGA

Sequence 995

GAATTGGAGCTTTCCGCGGTGGCGCCGCCCGGGCAGGTACGCGGGGTTTTTAGCTTTTT
AAATCTGCTTTGGTATACTCCATANNNTTTGTGCCATTGGATTATTCTGTTCCTATAGAA
ATCCCCACTATAAAATGTAAACCAGACAAACTTCCATTATTCAAACGGCAGTATGAAACC
ACATATTTGTTGGCTCAAAAACTGCAGATCCTTGCTGTTACGGTCACACCCAGTTTCATC
TGTTACCTGACAAATTAAGAAGGGAAAGGCTTTTTGAGACAAAACTGTGCTGATCAGATAG
AAGTTGTTTTTAGAGCTAATGCTACTGCAAGCCTTTTTGCTTGGACTGGAGCACAAGCTA
TGTATCAAGGATTCTGGAGTGAAACCAGATGTTACTCGACCTTTTTGTCTCCCAGGCTGTG
ATCACAGATGGAAAATGCTTTTCCTTTTTCTGCTACCAGCTAAATACTTTGGCACTGACT
ACACAAGCTGATCAAAATAACCCTCGT

Sequence 996

CCCGCGCTGCCCCCCCGGCCAGGTTCACCGTGTCAGCATTTGTTGAATTNGCACTT ATTGTTNAATTTAGCTCTGGAACAATGCAGGGAATTTGAAGTTTCTTGTAAATAACCACA ATTAGGAAAAAACCATACAGCTCAAGGAAAATCCACTAGTATANCCAAGATACCCTAAGT TCTTCAAGAGACACAGANGGGAGAATTATGCCAAAGGTAACTATCACCACCAGAACGCGG CCATCCACGTACCTCGGN

Sequence 997

CCGCGGTGGCGCCGAGGTACGCGGGGGACGTTAGGTGTCCGCCGGAGGTGTCGTTGGTG TGTTGCGCGACTGGCCTTGAGGGAGAGCTGGGGCCTGCTCCCGGAGAGATACCGGCTATG TCGATCGAAATCGAATCTTCGGATGTGATCCGCCTTATTATGCAGTACCTGCCCG Sequence 998

GGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTNCCAACAGAAACCTGGCCAGGCTC CCAGGCTCCTCANCTATGATGCATNCAACAGGGCCACTGGCATNCCAGCC Sequence 999

Sequence 1000

Sequence 1001

Sequence 1003

Table 1

Sequence 1004

Sequence 1005

Sequence 1006

Sequence 1007

Sequence 1008

Sequence 1010

Sequence 1011

Sequence 1013

CCGCGGTGGCGCCGAGGTACACCAAGGCGACCACAGCAGCTGCAACCTCAGCAATGAAG
ATGAGGAGGAGGATGAAGAAGAACGTCACGAGGGCACACTTGCTCTCAGTCTTAGCACCA
TAGCAGCCCAGGAAACCAAGAGCAAAGACCACAACGCCGGCTGCGATGAGGAAGTAGCCC
ACGTTGACAAACTGCATGGCACTGGACGACAGTGGCCCGAAGATCTTCAGAAAGGATGCC
CCATCGATTGACACCCAGATGCCCACTTGCCAACAGGGCTTGCACCACACAGGAAAGATG
AAGCCAAATTGAAGAAGGATCATCATTGGGTCTTTAATGAAAGCCTGGAAGNCACNTGCC
ATGGGTGGGCTCCCTGTTTCAGGG

Sequence 1014

TTCGAATTCAAGAAGGCCAGCAGAGGATGAACACAAAACCTTAGGTCACTGGGTGA
CAATCAGNTGACACAANAAAAGTAGGCACAGCACNTGACNNGNTGTATTTGACNNCACTT
TGCAAGAAACACTGACTTGANNTCANCTTTNAAANGTNTAGCAGTTNCCTATAATNANAT
GGCCANTACCCTNTTCCATCCCCTCTNCTTAGGANCANTATTCCCNTTTCCACNCANTAN
AGGTAAGGANCAATTCCTNATTTTTNTTAAAAAGGGGNCAAANNAACCTTGGGNTCCNCA
ANANANAANCNGGTTNTCTCGNTTGNTCNANTTTCTTAGTTNCCAAACGTTNCTTTCCNG
ATNGGTTATGNTTTTTNTAAACCNAAANAAANAANANTTTCCGGTNGGGGTTTCTTTCTT
TNTTAATTN

Sequence 1016

Table 1

AATTCTTTTGACGACCCTAAGGTCCTGGACTGCCTTGGGGACATTGCCAGGGACTTTGTA
TATTGAGGTATACCATTTGGGGGAGAAAGAAGAAAGTTTTA

Sequence 1017

Sequence 1019

TGAGGATCCTGTGCGCGATCGCAATGGACAGCTACTAATGGTCACAACGACCTCTTTCTC
TAATCCTTACTTTATACATCAACCTTCAGGTGGCTCCCCAAAATGTTATACCAAATCTGT
AAAATGCAAATAAAACAAAAGACAAATCTCCATCACGTACAACATGAACTGAACAGCCAT
TTAAAAATTCAATGGGTGAGAACTTCTTGGACCTCATTGGCTAGATTCCTTTCTTAAAAT
CCATACACCCGNAATTTAACAGGGAAGGTTCCCCATTCCTTGGAAGGAGCAAACTTTCAG
NATGGTACCAAGACCTTGGAGNTGAAAATTATTTT

Sequence 1020

Sequence 1021

Sequence 1022

Table 1

Sequence 1023

Sequence 1024

Sequence 1025

Sequence 1026

Table 1

Sequence 1030

Sequence 1032

Table 1

Sequence 1034

Sequence 1035

Sequence 1036

Sequence 1037

AGGTACAAAAATTAGCTGGGCATGGTGGCGCACAACTGTAGTTCCAGCTACTCAGGAGGA

Table 1

CGACTACTTAGGGCGAATTGGAGCTCCCCGCGGTGCCGCCCCCGGGCAGGTACTGAGA CCGGGAGGTGTCTCTTTTTCTGGGAGCATGTGGCAGAACCATATGGAAGCTGGGCCTTC ATGTGGCAGCAAGTTTTCGAGCCCACCTGGAAACACATTGGGGATGGCTGCTGCCTCACC AGAGAGACCTGGAAGGATCTTGAGAACGCCCAGTTCTCCGAAATCCAAATGGAACGACAG CCCCCTCCCTTGAAGTGGCTACCTGTTGGGCCCCACATCATGGGAAAGGCTGTCAAATAA TCTTTCCCAAGCTCCAAGGCACTCATTTGCTCCTTCCCCAGCCTCCAATTAGAAACAAGC CATCCACCAGCCTATCT

Sequence 1040

Sequence 1041

Sequence 1043

GNGGCAGCAGTCACTGTGGCNTAAATTTCTAAACTTACATANCNNATCNTGTAATAGCAA ACCTTAAAAAGGGCAAGGNANAGAGGACTTAAAAATGAANAANAAAAGNGATAGGGAGAA TGAAGAATTTTTTTAAAAGCTGTTTTAGATCAGGGTAAGACCGNAGGCTTAAACAAAAAA AAAAAATAAAAANGTNCCT

Sequence 1045

Sequence 1046

Sequence 1047

Sequence 1048

AGGTGTCGACCCACNCGTCCGGCTACTTACTGGCTTGCTTTTTTTTTGCCCTGCCTTGCTC
AGCTTGCTTTTTTATAGAACCCAAGACTACCAGCCTAGGGCTGGCACCATCCACAATGGG
CCCTCCCACCTTTTGATCACTAATTTGAANAAAATGCCNTTACAGCNTGGATTCTCATGA
AGGCATTTCCTCAAGGGGAGGCTCNCTTTTTGAAAGAAC
Sequence 1050

AGGTACGTTTTCAGAGATGTGTTGACTGAAGTAACCTTCAGCGGGCCTGAGTAAACCCAC
AGCCAGTATCCAGCCCTGCCTGGGAGTCCCTGAACTGGGAAANTATNNTGTGATTTCTTT
CACCTGGTGGCTTTTAGNTTATTTAAGGCCGTTNTTGGGAGGAAGGGCNCATTGGCCTNA
NNCCATCTTTAAAAGAAAGTTTCTTTTCTCCCCTTTTAACNCCANCAATTANAAGGGTAT
TTTCCTNNTGGTAGNNCCANGNAACCNCANCNCCCCCTTTCTTTTGGNAAGAAACNTTTT
NCAACCCNTTCCCAATTTTTTTTTTTNGGAANCCAAAACCANCCTCTAACNCCGGGGNGNN
CNAANGTAANNCAAAAATTCTGGGGGTTNTTAATTTGGGTTTTTAAAGGGGGTTCCTTTC
TTTTCCANTNGGNGGNAAGATTTTTTGGGGGNGGGNNAAAAGGTAANANTTTTANGGAAA

Δ

Sequence 1051

ACACTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCCCAACATATAT
TTTTACGAGGGTTATTTTGATCAGCTTGTGTAGTCAGTGCCAAAGTATTTAGCTGGTAGC
AGAAAAAGGAAAAGTATTCTCCATCTGTGATCACAGCCTGGGAGACAAAAGGTCGAGTAA
CATCTGCTTCACTCCCGCGTACCTGCCC

Sequence 1052

Sequence 1053

Sequence 1054

GGCCGCCCGGGCAGGTCGCTCGTGATCTAGATAGTGAGCGGACGCGTGGGTCGACTCAAG ACTTTTAAAGATTTATCAAAATTTGGTGAGCCGAATCTCAGAAAATTGGTGAATTCGGTT AGTTCCCAATAGGCCGCAGTAGTAATAAGTGGAGTGTTCGGGATATANAAAAATTTTCAC GAATGGAATNAAAATTTCTAGGCGAATTCAGTGAGTTCCCAATGGGACATGATTGTATGA GTGAGCTTTTTCAATATATAGCAACATTTTTAGGTTCANAAAACTTAAAG Sequence 1055

AGGTACCATGTTTCACGTTAAAATGCCAAAATGTGGTGCCTTCAAAGAAACAGTCAATGA
AACAGAAAGCAAAAATAAGCAGAAAATTAGAAACGTTATTTGGCATCATGAAGGGCAACA
CCAAATTTCACTACTAACTGCAAGGATTGATAAACACCATGATTTCAGATTTGAAAAAAA
ATGGAAAACTGCTAATGCACAATGTTAAGAGATCTCCATGAGAACCAGGCATTAATCCCA
TATAGCAATGTTAATATTGTTACCAATTTCAGGAAAATGATTTTTTGATAAATGGGCT
ATTGTAAGATATACCTTTTTATTTCTTAGGAGCATGTGACCTGCATACGTAAACAG
Sequence 1057

AGGTACAGAGCCAGCCAGTGTTGGGCAGCAGGCTCACAGCCTCAATAGGGAGAAAAGACA
AAGGCCTCAAAATGACAGGCAGCCTGACAGAGGAAGGAGTCTGACACCTCAGCTTGAGGC
GTCTTTGGAATTCCTAGCTCATCTCAGAATTATATCTTAGAGTGATAATATGGGGTGGTA
GCCAGTGGCCAAACAGCAAGAACTAAGAGTGGGCCCTTGCAAAAAAAGGTTGGGAAAGCT
GGGCCCATATTGCCTGGTAAACCCTTGAGCCTGATGCTCATACAGCTGTCCCTTGTTTTA
GCCAGGTCTTGACAGAAGGGTTACCAGCA

Sequence 1058

Sequence 1059

CCGGGCAGGTACTCAGTATAAAGTCCAGATGCCTTTACCATGACCTGCAAGGTTATACGT GGTCTGACCCATGCATTTCTCCGTGACCTCATCTTATACTCCAGGTTTCTCTGTTTTACT CATTCTTTTCCAGCCACACTAAACTTGCCGATCTTAGAATATGTTGAGTTCATTCTAGCC

CCAGGTCTTCAAATTTCCTCCTCTTTCCTGAAATAGTCTTCTCCCAGATTTTGGTGTGG CTCTGTACCT

Sequence 1060

Sequence 1061

CGAGGTACCTTCATGCTCTAAATCAGATGATCTACTATCTGAAAAGGAAACGACAAATCT GACAACAAANGAATTTCACAACAGATAGGCAGTTGATAGCATGAGGCACTAACATTAAAC CCAAGTCTTTCAATGGCACTTGGAGTCCCAGGGTCTGCCCG

Sequence 1062

Sequence 1063

Sequence 1064

Sequence 1065

CCGCGGTGGCGCCCCGGGCAGGTACTGAACTAGCTCCTTCTGGTTAATTTGTTGATT GGATTGGAAATTAGAACATGGAGCTGGTCAATGCACGGTATCTGGTAATTGTGGATGGGG GAGATGACTGGGGCAGAACTGAGCTCATTTTTGCCAACATAGTACCT

Sequence 1066

Sequence 1067

CCGCGGTGGCGGCCGGTGCCACACTGGGCCAGGGTAGTCATCCTGAAATACATGTCCAGG GTCTTGTTTGTCTATGATGTGGGTGAAAGCTGCCTCAGCCCGCACCACAGTAGAGAGCGG

GACCACCTCACGAAAGTTTTAGCAAACTCCCAGGGTCTAACCTGAAAGCAGCCAGGAACA AAGACCTTTCCAGAAAGAAGGACATGAACAAACGCTTAAAGAACGACCTGGGCTGCCAGG GTAAGAACCCTCAGGAGGCCGAGAGTTACTGTGCACAGTACCT Sequence 1068

Sequence 1069

Sequence 1070

Sequence 1071

Sequence 1072

Sequence 1073

AGGTCACGCGTCCGCTGCGGCTGAACCAACCAAAGATGGAGTGGCAGAACCCTGGGAG CTGATCGGGGTTCTTCTAGTAAGTAGTTGCCAGGCCTTAGAACTGATTGGTGTCACCTA CTTCAGTGTTCATTCATTTCAATGACAAGATCAAAATCAGATTTTACAGGATGACCAAGA TTCTGAGTTTCTCCCATGGCAACAAGTTCTCAGGTTAAAGTCTAGGAATGGTCATACTTG CAGCTTGTTCTTCCAGAAGACCTGACTTTGGTTCCCAGAACCCATGTTGGGTGGCTCACA ACCATCTATAACTCCAGCTCCCGAGAGCCAATGCCTCTGACCCCCAAGAGTGCCTGCACT CATGTGTATATATCCCATAATTAAAAATAAAAATAAA

Sequence 1074

CGGACAGGTTGCAGAAAGGGAAGAAATGCCAGAAGGAACCAATGAAGGATGAGCCCAGCT TCCAAATTTTGATGAAAGCTTTCGTCTCTACATCAGAGAAATTCTGCAAGATCTTAGAAG GATGCGCTCAGAGAGATTCACACCTAGAAACACCATACTCAAAGGGTAAGGAGAAGAGAG

Table 1

CCCCAGGGAAGAATACAGAAGGGGACACATGACTGGCCACACAGAAGCTCATCAGGAAGAAACATGACTCCCTGTCAGAAACCCAGGGTCCAGAAGGAGTGGGATGACGTTTGCTAAGTTATAAAAGCGAGCTGTGCACCCAGATTCTATAC

Sequence 1075

Sequence 1076

Sequence 1077

CGGNCAGGTGCTTGAGTCGACCCACGCGTCCGCACTAAGATTNTAAGTGAATACCACCAA ACCCAGGAATAAACTGATTTTTTTTCCCTCTTAACTGGAAAATAACCTGAATGTNTACN CAGNTAAAAAATGAGATTGGNGGGAACCNTAAACGACCCGGGCTGNTGTTTGCTCTCCAC AACCTGATGGCAAGGCCCTGTTGNTGGAAATAACACCCACACGGTTNACTGAACATGGGA AGTGGAGCTGGTGCNTTTNTAGAGTCTTNAACCCCATTGGNTGGCGTTCTTGGAACCAGA GGTAGCCTGCATGC

Sequence 1078

AGGTACCCAGAAGAAGGTGCAGATATCTGATTGAAACTGTTCATCTTACCAACTCTTCCT
ATTGCAGAGAAGACTAAGGTCCAGAGAGGGATAGTGACTTTCCCAGGTCACACAGGAAGC
CACAAGAGCACATTGAAGCCAGATACACATTGTCAAAGCACGCATGTCCAGCCGAAGCAA
GGACCCGAAATGCTGATTGTTTCCCCTGCAAGGAGGATCCTGAGTTTGTCCCCGGGAAAG
GTTTAAGAGAACTGGCAGGAACCAGCCTTCATTCTTCTAGGTCCGGTTACCCTTG
Sequence 1079

AGGTACAGCTAGGACAAACCTTGACTCCGGGTCGAGCGCTCATTGTATAACATGCAGTGGCATGGCCCGTGGTTAGGAGGAGTCTGAAATCAGATTGCTGAGGGTTCCGGATCTGGTTCTACACTCACAAGTGACTTCGTAGGCCTTTCTTATATTCTGATTTCTTATATCTGAACTGGAGCTTACACACAGCAGCACACAGGCTAAAAGTGGTTACCAAGAGGCCAGGCAGTTGGGGGGATCACCCATATCACAATAATTTGTCATTGAGCTAGAGCATGAGTTAGTAGTTTCTCTTCATGGGATGACA

Sequence 1081

ACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACAGAGCTAACACTTATCC TCCAGTGCTCTACTAATTGCTTGGTGCTATGTTGACTACTGGGAATGAACCACAAGATAC ATCACTGTAAACTGCAGGAGNGCTTCACTGATCATGAGGTNAAAATCTCCCCATCATCA NAAAGAGAATTCTTTACTTAACTTAGTGGTACCTGCCCG

Sequence 1082

AGAATACATATAAATCTGAGTTCCCTATGGCGCTAGTNTACTGGGCAGACTTCTGGTCTG GGGTTCTTTCTTTNTTTTAATAGCCTTCTGAAAACCTCANTGCCACCAAATGCATGGATC GTAGCACCTAGTTCTAAGTGTGTGCTATGCTTTGGTCTAATATCCAAAGAGATGTCTAAA GCAANTGTGCTTTCATGA

Sequence 1083

TTAGGGCAATTGNAGCTCCCGCGGTGGCGGCCGAGGTACAAGTTGGTCTCAAACTCCTG AGCTCAAGTGATCCTCCCACCTTGGTCTCCCAGGCGTAAGCACTGCACCTGGCCTTAGAA ACCTCTTTAAAAGTGGTTGTGGTATCCTCATAGAATCTAGGAATCCATTACTCAAAAAAG CAAGACTGCAATGATACACAGTACCTGCCCG

Sequence 1084

AGGTCGACCCACGCGTCCGTGTATCTCCTACAGTTCATTATGCAGCAGACACGGATGTAA ATGGGGACAAANATGAAAATACCNACTCAGACTCTTTGTGAGACGTTCANCATTTTTCT GAAATGGCGCAATGTATTCATTTTCCA

Sequence 1085

ACTCCTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACTCTACA GTGAAACTGTTTCTACTGTGGCTTAATTTGCAAAATCCAAGCAGATATTACTTTTAAAAA TCCAACTATCTCTTTCAAAGGATTTGTAAAGTTGCTTACAGACATAAGGTGACATCAGAA AAGCATGTTGGTATAATGCAATTAGCTAAGGTTTCTAGGAAGCTTTGGAATGTTTTGTTT TTAAAGAAGGCATANATAAGTGCAAGTCCTACAAGTAATGAACTGTCCTAGAAGCAAAGA AATTCATTAAATAGATCTCCTTGATTTCTCCTTCATGGCCCCCATGTCCATAGAGATTGGG GAATGTACCT

Sequence 1086

CGGGCAGGTACTGACTTAAAATAACAGAGTAACCTGTCTGGCTTACTTGTCTCTGAAAGT
GAATGTTCAAAGTGGGTGGAATNGAAATCACATATTAACGATAGTCCATACTTATATGCA
AAGCCATATGATTCCCTAAGCTACTTAAACTGGAATAAAGACACTAATAAAAATTTCATA
AAACATTGAACCTGGTGCCAGCCTCACATTAAACCCATAGGTTCTTCACGATTAAGGCTG
ACAATTTTAGCTACTGCTTAGAAAGTTGCAAACACAAATAGGGGGGAGTTTAATGTTCCA
TCAGAAATTAACCCAANCTGGTTTTGAAACTCTACTTGGCACTTA
Sequence 1087

Sequence 1088

Sequence 1089

AGCCCCCTTCAGCTATAGGATTCTATGATTCTTTTCCTGTGAAAATTTGGAACACCGTGA TAGTGTANTTACCCTCTCCAGATCATAGGGGCACCATTTAATAACTTACTACATTAATGT ATTAAATTGTACCTGCCCG

Sequence 1090

AGGTACGCGGGGAAGCAATGACGTGGGGAGAGAGCGCGGAGGAAGGGAGAGATCCAGAAA GGTAGATTCTTCTGTGTAGGTGAGTGGATGAGATAATGAAGCAAGTTAATTTGGGCTCTG CTGACTTATTTATCTGTCCCGGGCACTTTTCTCCGTACCTTGCCCGGNCCGGC

Sequence 1091

Sequence 1092

NGATTACCCTNGTNCGCCCTTTTCCTCCTTTTCGNGGTAAAGCCGGTGGGNCGCCTTT
TTCTTTCANTAAGNCTTCAACAGCCTNGATATGGGTNATTNCTTNCAANTTCTCNGTGTN
GATAAGTGGTTCTGTTTTTCNGNCTTCCCCAAATGACCTTGGGAGGCCTTGGTTGGTAGT
CCAACCGAANACCCCCCCACANGGTTTACAANNCCCCCGNACNCCGGCTTTGTCGCCTC
TTTAATTTNCNGNNTTAAANCTTATTCCGGTTACTTTGTAGGTTTCCCAAACCCCCGNGN
TTATAAGTAACCAACCNGAANCCTTTTAATTTCCGGCC

Sequence 1093

Sequence 1094

GGCCGCCCGGGCAGGTGCAGAACGCTGGAGAGGGTGCAGTCTCTGTGAGGGTGAGCGGTG TGGTGCCCTGGAAGGACTCCTTCCCACCAGTCACTAAGCAGCAGAGGCCAGGCAATCACA GGCTAGGAGCCTTCTGACCCAGGAATAGGCATTCCCGCATCCTTAGACCACCACAATGCAT GCCCACTGTGTCACTGCAGAAGAAAGGATAAAGGTGGCCATGGCTAGCTGGCCATGCAAG GCACTCACCAGCGTTAATGAGACCTGGCCGGNCAAGGCAGTTACTCTGATGGTAACTAGG GCTTGTCTCCTTGCCATGAGAAGAGTTAGGGACACAC

Sequence 1095

Sequence 1096

GGCGAATTGGAGCTCCCCGCGGTGGCGGCGCCCCCGGGCAGGTACTAGCCCTGCTTGTCTG CAGATCCAGAGAGCCTTAATTGACAGATTCAACTGTGCCTATTCCTGAACCAATTCTGAT CAAGAAAGTGGTCCCACCAGTCAGTGCTGACAGGAATTAGTCTTTTGCTGTCAACTAATG GTTTCCAATTAAGGGCAACTTTTTCCACCCAGAGATATTTGTCAATGTCTGGAGACATCT ATGGTTGTCACAGCTGAGGGAATATTAATTAATAACCACCTAGTGGGTAAAGGTGAGGAAT

Table 1

GTCATTAAATACCCTACAATGCAGAGGGTAACCCCCCACCAACAGAGTACCTCGGCCGCTCTAGAACTAGTG

Sequence 1097

Sequence 1098

TCTAGAGCGGCCGAGGTACTCAAAATCCTAACCAGAGCATTCAAACAACAACAAAAAGTAGGT
TAAAGGGGATACAAAACTNGGAAAATGAAAGNAAGGTCAATTAATTATTCACCTANTTTT
GCCAGTATGGAATNATGNATTAGGTTTTTACCTTTTAAAGNTGACCNCCCCAAAAAAGGT
TTCNCAACTCGGGAAGNAAAACCTAACCTATATAGNCNTTGAATTAAAAAAACCAAANCTT
TTCCGAACCAAAAGGGGTNANGCCTTGGGGGGTTAATTAAAAAACCNTAAAACNTTTCCA
AANTTTCCAATATTAAAGGNCCCCTTTTCNCCTTTTTTNAACCTTCCAAAAAAGGGGGAA
TTNAAAATACCAAGGGGGNTNTTGGGAAGGNAAAAAANAAAAATATAATTTTAAGNGGGG

Sequence 1099

AGGTACACACACACACACACACTCTGCAGAAATTACTCACAGTTTTGGCCTGTAAGCA
GTATTCATTCTTCCATTAAATCTGCTAGTATTAATATAGGTTTTCTCCCATTTTATATTC
CTTTGACTATTAAAGTAAGAATTCAGGACTTGGAGAGAAAGTGGAAAATTTCCATTTAAT
TCATTAAGTTTTAAATTATTAGCTATACCAGAACCCTTTATTATTATTTTATGGTGTATG
GATATTTTGCCTATATGTTTTGTGCACCATATCCATGACTGGTTGCTTGAGGTCAGA
AGTAGGCATT

Sequence 1100

CGGGCTGAGCCGGAGCCTGAAGCCCAGCTCNGAGTTATATTGGGGACAGGGCTCCTTTG
GCTCNTGGTAATGGAGNAAAGGGCCTTGANGAATTTAAANGGGAACNCTTGAAGGGGAAC
CAAANNAAAAGNAAAGGCCACCCCTTCCAATTTTAATNTTGGGGTTGGTTGGTTCCCCTT
CGGAGAAATACCGAAAGNGGCNCCATNTNTTGGTTGGGGTTGNCCTTTANTTTCNAATTT
TNCCCCTTNCCCCGCGGGGGGGGCTTTAAAAAAACCAA

Sequence 1102

GACGAGGCAACCCAACACCCTAGCCTAAAGNCCCGTTGACAACTGCAGNCATGGGTTGG
CTTGGCCCACCGCCTTGGCANCCGNTCACGNAAGGAAAAAAAGNCCGCGGGCCCTTAAAA
GGCGGCGGAGGTTCTTGGGTTGAACCTTGGGGCANCCCCACCCGGTTGCCANGGCCTGGA
TTGGGGTNACCCNCAAAAGGCCTGTCCCCAAGGCCCGNAACCTTGGGGAAAANGAAATGG
TTCCTTTTNGNGNNAAAAAAAAAAAAAATGGAACCCCGGTTGGGGGNANGGCCCCTTGGGGG
GGCCTTTGGGGAAGTCCNCCCCGNAAGGGGTTCCCCGGGCCTGNTTGGCCGGGGNCCCCA
AAAANTCCAAAATGGNCCANGGGGNTGGGGNCCAACCCCCG

Sequence 1103

AGGTACCTAGAATATTTATTTCAGATAATATCAAGATTTACCTATATTTCTACCAAAGAC

Sequence 1104

Sequence 1105

TCGACTNCTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACACTTATAGTT
GAGAGCCAAGTCTCCCTTATCATTGGTGAATGAGGATGAGCTACTGAAAACAAAAAGAGG
GTCTTCTACTCAGCCTCTACCCCTAATATTTATATCAGAAGCAGAGATTAACTGTCCTTA
CTCATTCACACGTTAATGGAAGAAGAGGAAGTTTCCTAGAAAAATCCTCCCGCTCCACCC
TGCAAACTTTATGCTTTTCTGTTACATAATCAGGCAGGGGCAAGACCTAAACTATTTTGA
ATTGGTGGTGTTGAGGCTAAATTCTCTGCTATTGACAGAATTGAGAATGTGATCAATTTC
AGAGTAGCCATGTTACAAATTTTTGTCCCCAATTTCAATGGGGGAAGAATTATAACCAAATC
AAGTAGTGGTTGGGAAGA

Sequence 1106

CCGGGCAGGTACGCGGGGAGTTCTCTCAGGCTCTCCAGAGCTCAGGACCTCTGAGAAGAA TGGAGCCCTCCTGGCTTCAGGAACTCATGGCTCACCCCTTCTTGCTGCTGATCCTCCTCT GCATGTCTCTGCTGCTTTCAGGTAATCAGGTTGTACCT

Sequence 1107

Sequence 1108

Sequence 1109

AGGTCACGCGTCCGACCTAGCTTGAGTCGACCCACGCGTCCGATTTCTGGTTTCTTTGGA GACTCGGTTGTGCCATGTGATGCTTTTCTGGAAACTGTCTTATGAGAGGAAGCTTTTGCT GAAGCAGACACATGGGAGAATGTTTTGTTAAGAACAGACATGTAGTATTTTTCTAGAGGC AGCTTGAATAAAGAGCATGTGGTATTTTGCTAGAGGGGACACTTGAGAGAACATGTGACA TTTGGAAAGGATATATGTATAACCTAAAAGGACAGTGGCCAATGCTGTGTGGTATTTGGG TGTGCCTTACCATTCTTTGCTGGC

Sequence 1110

TCGTGATCTAGATCCCTATAGTGAGCGGACGCGTGGGTCGACTCAAGCTAGGTCGGACGCGTGGGTCGACTCAAGCTAGGTCGGACGCGTGACCTTCCCCAAAATTCTTCTTTTTTCAGA

Table 1

TGAAAGTCATACACTCAGCTTTCATATTTTAATATACATAAAACAGCTCAGTGACTGGGA CACTTCCTAACCTCCATTTGGGTAATTCACTTCCCTCCAATAATCCTGAGTTATCATTTA TTATATTTTGTATTTTACCTTGGCTGCACTGGAGCCAGTTGGGCAGCCCCTCTTGGGCCT CACTCTCATGTTCCTACATGGGCAG

Sequence 1111

Sequence 1112

CTACTGAGACCATTACAAAATTAAATGGTGACTTTTTAATCTGGAATTGCAAACCGACAG CANCCTGTCTGGGGAGCTCCATGTNATGAGTGTATGTCTCCAACAGNCTTCAATGACTGA CAGGTGAAAAGCTGTGCCACAGCCTGGAATTATTATGCTGACACACAAAAGAGGGCGGGA GTGACAGCGTGGTGATCTACCANTGCTGTCTGTGGGGNTAATGGTAAGCTTTCCCACTGC TAATGGTTTATNNANAGAACAAAGAAAAGGAAAACGGTGCANGGGAAAATCAATANNTAT TAACATAGTCATGGTAATGAATGCAATCCNTTATTTCTGGGAT

Sequence 1113

AGGTACATAAAACTTGTAGAGATTTACACACGCCAGCCGCACATCGCCCCTTCCCAATGG CTTTACATCTTGGTGACCTTTCAGAAGCCAACGGCACCCTTCCTGTTGTTACCCGTAATT GGAAAAGCATCAGAGATAAAAAAAAGTGC

Sequence 1114

CGGGCAGGTGAAACATTTTATTATTATTTTTCTTTGTTACAAAAGGACTAAGTGGTTC
TGAAAGCCAAGGCAGAGTTCATGTGTCTGGGCTGACATTCCCATGGCCTATGAGCACTGA
GCAGCCACAGGCTTTTCCAAGGAAGGCCCAAGGCCATCACATCCCCATCTACATCACAA
TACTTGAATGTATTTACATGTGTTGTTCTTTAAAAAAGGATTACACATTTTATTCTTTAAA
AATCTAAAAAATGATGGAGAAAAGGAACACAGTTTATCTTACACATTTTGCAGGATATACA
AGGGTAACT

Sequence 1115

TTGTGTGGATTTACTTGTTGCCCACTGTCCCCATACCCTCCACCCCCACATGGTGTGCTT CCTCCAGAAAGGGACTACTTCTGCTGACCACACAGAAGACGTGTGTAAAGTCTGTGTATC AATGAATGGATTCTCATCTTTCATAGTTTTTTTTTAAATAGTTTTATGTAGTGTTTAACT AAATTTCACTTAAAAAGATATTTACCAGAAGCTGANAGTANGGTGTGATGAGGTTGGGTT CANGAAGGACTGNTATCACATGGCTTCCCTAAGGTTGTATATTACATTGCTAGGACACCT GACA

Sequence 1116

Sequence 1117

ACTITITITITCTCTGTAGGAAGTCAACGATAGAGTGACATGTTGGCTCTTTCATTTCAA CTGANACACCTGGTAGCTATTGGATGGCATTTCTGTAATTATGAATAGTAGTTGTGATAG GCTTATTTGCACCTTGTACATTCTCTTACTTGGGAACGCCATCTCATGCCATTTCTACGT TTCTTATGCAGTTAGTTTGGGGCATGNGGTANTCCACTGGAAAATGACTCAAGCGTGGAA TGTATTTATGATCACAGATAAGGAAGTGGCCGTCCACAAAGCTTTGGATGGTTGTATTTG

Table 1

TCATTTGAACA

Sequence 1118

GCGGCAGGTGTCCGCTCACTATAGGGATCTAGATCGGACGCGTGGGTCGACTCAAGCTA GCTTGTACAAAAACTTTCAATAAAATGCTTCAAATAATGATTGTCCGAAGCTTGCTAGAC ACTTTGTAAATGTCAGGAACACATTAAATATGTTAAATGAGCATGTCCAATATCCAGAAA ACAACACGAATGATTTACTATCAATTTCACACATGCCTGGGAATGTCTCCCTGATGCAAG ACAAAAAGGTCCTCTTTGACCAGAGCATACTGACCCCAAGTTTTGGTCCTGGCACAGTAT TCATGGGTGCCATTCAT

Sequence 1120

GGGTACAATGGAAAAGGGGCTGTGTTACTAAGACTGACCAAAGAAGAGAGTTCCAATATCT
TATGATTTGTATGGTCACTGTTAACTGCAATTGTAACATGAACATATTGCCTATAAGCCT
GTGCTCTCCCCTTTAAACACAAAATAAAAAACAAGAAAAACAAAACAAAACAAAACAAATGAACC
AAAATAGAAAACCTTTTACAGCGTGAGTTGTTTCTACTTAGGATTGGACATCAATGGGGTA
GATCTGAGTCTGGAGATCTTAGGCCAACTTAACAACCTGTGAAAACTTCTCAATGGGGTA

Α

Sequence 1121

Sequence 1122

Sequence 1123

Sequence 1124

Sequence 1125

TCACTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGGGCTCTC
TCAGATTAAGGATATGTGTCTGCTAGGTAAAGCGACATCTGGATTCATTGTGTAGGATGA
AAGAAACCAAATTCTGACTGCTTATTTGTGGATCCGCCAAATCTGGCACGATGCCTATCT
CACGTGGGACCGAGATCAAGTCCTGGCCCG

Sequence 1126

TCACTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCCCGGGCAGGTACTGATC
TCGGTCCCACGTGAGATAGGCATCGTGCCAGATTTGGCGGATCCACAAATAAGCAGTCAG
AATTTGGTTTCTTTCATCCTACACAATGAATCCAGATGTCGCTTTACCTAGCAGACACAT
ATCCTTAATCTGAGAAGAGCCCCCGCGTACCT

Sequence 1127

CCGCGGTGGCGGCCGAGGTACTGTAGTTAAATGTGGGTTCTACATGGTTCTGCAGTTTCT AGCCCTATAAACCTCACATGCCATGTTCTCTCCCATATATCTTAATCACCTTTAATTTG GAAATAACAGATCTACCCTGCTTATCTTACATTGTTGCAGTGAGAAGAATGACTACGTTT TTTGAAACCACCAGCGATGCTGTACCTGCCCGGGCGGC

Sequence 1128

Sequence 1129

Sequence 1130

Sequence 1131

CTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACACTTTCGTGG CTTATGGGTATCTTAGTATAACCTTTTCTGGTTGAGTGAACTGTGTCATTTCAAAAGCCT GAAGACATTGTGATGAGTGCTGCCTCCATAATGGCTACATTCTAGGGGCTTTGCCCTGAA TCGCATATATTAACTCAAAAAACAAACAGTACCTCGGC

Sequence 1132

CGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACATGAAAACCCTAAAGCAAATGAACA GCTTAACCGGATATCACAAAGGCTACAACAATTAACAGAGGTTTCAAGAAGGTCGTTACG CAGTAGAGAAATTCAGGGTCAAGTTCAAGCAGTTAAACAGAGTTTGCCACCAACTAAAAA AGAAGCAGTGTAGCANGTACCCTTGCCCGGGCGGCCCGCTCTAGAACTA

Sequence 1133

Sequence 1134

CCGCGGTGCCGCCGAGGTACCTACATTCTAAAAGTATAATAAAAATATACAACAATAAA
AATGTAAACTGTAGGCTATAAAGAAAAATAAGAATGTTAAAATAATAACAAATTGTGCCA
AGAAGTTATAAATCATCTGGTAGGCAGTCCACTGGTAAAATTAAGAGTTATACATAGAAA
TGACACACTGAAATAAAACTTTTATTTCTGCCTCATTTCTCAACTAAAACACCAGTGACA
CTTAGCACAAAGTTCACATGCACAACTGTTCAATCACAGTTTATAAAAGCACCTGAACAT
AACACAAAGCCAAAGCAATCCTGGACAAATGGACTAAAGCTGGAGACATCACACTACCTG
ACTTCAAAATATAATACAAATCTATAGTAGCCAAATCAGTATGGCACTGGCATAAAAACA
GACACATAGACCAATGGGAACAGATAGAAACTCA

Sequence 1135

AACACACATACCATAGGGATGAAGATAAGAAAGGAATGATTGTGACTCTGGATCAAAATG CTCCCAGTTCCTGAAGGTGCATGATTTAACTGTGAATGCCAACTGAGATCCTAACATCCT ATACAACCAAAGATGAACTAGTCTCTGAACTGGTAACTCATAAAAGACAAATCCCACAGT ACCTGCCCG

Sequence 1136

Sequence 1137

Sequence 1138

Sequence 1139

CTGGTGAGTGGAACTCTTTATCCCGTGTGACAAATGCGTATTGAGGCCCTAACATGCCCC CAGACCTCAAGATGTGCTGCTCATACATTTGAAGGTAGCCCTGACTTGTTTNGGGGGGNG TGGGGNGGCCTTTTCCATCAGTTGTNTTGGANGNTGTGGCCAGCAATCCATTCCAAAT TGNCTGAGTTTTCTTNATTTTACTTTNGGA

Sequence 1140

Sequence 1141

Sequence 1142

ATAGGCCGAATTGGAGCTCCCCGCGGTGGCGGCCCGAGGTACAGAATGAGCTATAGCCTG
CAGTGACCAGAAATCTCCAAGTAAGGGAGTATACACTGAATGTCATGCCCTTCATTAAGT
TAAGGCCTGTAGTTNAAGTTCTTTCAGTATGTGCCATGAACAACAATAAACAATGTCCTT
GGTGTACTCCTTTGAAAGATGGACATTGAAAGTTAAAAATCAGTCACTATATAGGGCCTG
TTGATNGGAAAACCCATTTGNGGTTCTTACAAATTGTAAGCNGGAATGCCTT
Sequence 1143

CCGCGGTGGCGGCCGAGGTACACCGTAGCTTATTTCAAGTGACACAGACCAGGCAACTGA CAAATACCGACAAGTAAATATTGTTCATTTTCCTAGGTAATCTCTATAATCAAGGGGACT GATTTTATTCTGGAATTTTCCCCAAATGTTTTCTTTGTAGAAATTATGTTGCTCTCAAT TGTGTGCATGGTAGTACCTGCCCG

Sequence 1144

NTCCAATTNTTAAAATTAAAAT

Sequence 1146

Sequence 1147

Sequence 1148

Sequence 1149

AGCGGCCGCCCGGGCAGGTACCTTGCAAGTATTAGACTTAGAATAAAACTGTGTTGACTG
ATATAACTGATGCATGGTTGGAATAGTAGGTTCTTGGGTAAATTAATCCTAACATCAATA
GCTCAATTCCATCATAGTCCTTGAACAGGCAAAATGTATGCTAATCACAACAGCCGTACC
T

Sequence 1150

AGCGGCCGCCCGGGCAGGTACCTTGCAAGTATTAGACTTAGAATAAAACTGTGTTGACTG
ATATAACTGATGCATGGTTGGAATAGTAGGTTCTTGGGTAAATTAATCCTAACATCAATA
GCTCAATTCCATCATAGTCCTTGAACAGGCAAAATGTATGCTAATCACAACAGCCGTACC
T

Sequence 1151

AGGTACTATTTTCAGATGGTAGGGATACAAATATATTTTCCCTATATTCAAGGGATTTAC
AATTCAGTAGCAGAAACAGACATGTAAGCAAATAACCGCAAAACAACGTATTAACTACAA
TAGCGTTGTATTCAAAACATTATGGAAAGATAGTAATTAGCAAAACTAAGTGATTAATAA
AGTTTCATTAAATCTGGCCAGGCAGGGTGGCTCATACCTGTAACCCTAGCAGGTTGGGAG
GTTGAGGCAGGCAGATCACTTGAGCTCAGGAGTTCGGACCAGCCTGGGCAACAAGGCGAA
AACTTCTCTCTACCAAAAAAAATACAAAAAGATTAGCTAGGTATGGCGCATACCTGTAGTC
C

Sequence 1152

CCGGGCAGGTACCCTTGGTTTCTCAGACAACTCACTGATTTATGGTCTTGAGACCATAAA CTCATTTTCCTTATATGAATGACATTTCCACATCCACAACAATACCACCAAATATATGTA TCTAGTTCTTACTAACTGCAAATCCTCAAAGTGAACTGCGTGCATTTTAATGTTGCGTAG TTTGCTGATTTATGATTTCCCTTAATGTACCT

Sequence 1153

CCGCGGTGGCGGCCGAGGTACCAACCAGGGCTTTGATTTTCATGCTGTCCCAAAGTTGCA

Table 1

GACATGTTCACGACACAGCTGCGTTTGTTCCTTCATCTTGTTCAGCAACCTTTGGTAAGA
AACTACCATATTTAAGATTGGTATTCTAGATCCAAAAGAAAAATGCATGTGTTTGCTGTG
TGTGCATGGGCACATGTATGTGTATGTCTGTCTGTAAGGATAGAGAATGGCTGAAAATTC
ACAGGTTTTTAAATTCTTAAAAACAGGAACGAAGGAATTCTAACAGCTATGACTCAAAAC
AAGATTCTTAATAAAGTTNCATGACAANGTAAAACAACTATTTNAATTGAGAATGTTAAA
TAGCCTTGGTACCTGCCCCCGGCCGGGCGNTCTTAGAACTAGTGGGATCCCCCCGGGCCT
TGGAAGGGAATTTNGATTNTTNAAGCCTTTATCCGAATANCCCGTCCCACCCTTNGAAGG
GGGG

Sequence 1154

CCGCGGTGGCGCCCCGGGCAGGTACAGGAGGCAAAAAAGCAATCAGTATGACTTGAA CTGCTGGGTTTAATTACTCAATATAACACTTGCCATTTAAAGATCCATATGCCCATCAGC ATGGCAACAGTCTCTCATAAAGATTCCGGTATCATATGGCACAATTTGTACCT Sequence 1155

Sequence 1156

Sequence 1157

Sequence 1158

Sequence 1159

CCGGGCAGGTACTGTGTATCATCGCAGTCTTGCTTTTTTGAGTAATGGATTCCTAGATTC
TATGAGGATACCACAACCACTTTTAAAGAGGTTTCTAAGGCCAGGTGCAGTGCTTACGCC

TGGGAGACCAAGGTGGGAGGATCACTTGAGCTCAGGAGTTTGAGACCAACTTGTACCTCG GCCGCTCTAGAACTAT

Sequence 1160

TCCTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACATTTTCAAATGGTTA
AAATGGTAAATTTTATGTTACATGTATTTTACCACAATTTTTTATAAGACCAGATTTTA
AAGAGAATCAAACAGAACCTGCAGAAATAAAAGACATAATTGAAATTAGTTCGATGG
ATGAATCAAATAGCAGATTAGCTCAGCTAAAGATGACTGTGAATACACAAAATGTAGCAT
GGTGATACAAAAATTGAATATATCAAACAGAAGTTATGCAACATGAGGACAGAATAGAAT
GTCCAACATATCTAAATACCATTCAAGAGGGAAAGAAAAATGGAGGAACCGAGGCA
ATATTTTGGAGGATNTTATTGCTNGNACTTTTCCAAAAACTGCTGTAGTTTCTGGAAGC
Sequence 1161

Sequence 1162

AGGTACTCCATAATGGATGTGGGCCAGGGTAAAAGCAGTTGTTAATGTATACAGGAGAAT GCTCTCAACGTAAGAGGCTACTCCTAGGTTTACCACTAAGACAACCAAGAAGAGAGGAAC CAGCAACCAATTCAAAAGTTGGGACACCGGGTACCTTGCCCGGGCNGGCCGNTCTAGAAC TANGTTGGATCCCCCGGGGCTGCAGGNANTTCGATATNAAGCTTATCNNTANCCGTCGAC CTCNAAGGGGGGGCCCGNTACCCAGCTTTTT

Sequence 1163

Sequence 1164

ATTGGGAGCTCCCGCGGTGGCGGCCCGAGGTACACTGATCGTTTCTGCAGCTGCAGATT CTGCTGTTCGACTCTGGTCTAAAAAGGGTCCAGAAGTAATGTGCCTTCAGACTTTAAACT TTGGAAATGGATTTGCTTTGGCTCTCTGCTTATCTTTTTTGCCAAATACTGATGTACCTG CCCG

Sequence 1165

CGAGGTACGTTGTCAGGACATTTTGTAATTCGGTATTCTTGGTCTCCTGGCCCCAATTCT
AAAAAAAGTTCACGTTTTGATGAAAAAAAGATATGGGCATTATGGATGTTGAGGAGATCA
CAGCTCAAAAGATTGACAGGGGCCCCAGGGCATATAAGAAACATATGGTACCTGCCCG
Sequence 1166

CGGCCGCCGGGCAGGTACTGGTCTGNCTGCAGAGGCACCAAGATGATATCTTCCTCCAC TGTCAGAGTTATTTANGAAAAATAATCTCTGGCATANGCCGAGTGCTCATAAATACTTCA NGATGAGACAATAAAGCCGCTCCCAGGTCCTGGCATGGCCCAACCTCAGGACACTGGCCT

Table 1

CTCTGCTCTCATTTCCTGCAGATTCTCTGAAGCCTATCTGTGCTTCTCAGTATTCTCTAG CGGAGTTGAAAAACGCCCCTTAGAGGTGCACAGTTAATTATAGAAGCTGTTAGCTTTCCC ATCTGTAGTCATGCCCTGGAGCTAAGAGAAGGACTTGAATACAGAAGAGGAGATGCCCCC TGTACCT

Sequence 1168

Sequence 1169

Sequence 1170

Sequence 1171

Sequence 1172

CCGGGCAGGTACCCTCCAGGCCCTGTGTATTATTAAGATCTTTTAGTAGCGAGTTGCTCT TTCTCTGGGAAATCGGCTGTTAAAGTCAGAGGGAGCTCTTAATAGTTTGCATGGTATTTG ATTAAATGGAACAGTTGGATCAGTACCT

Sequence 1173

CCCTTGTTGAACAGGCGATNTNTNNACCATGCNCACAATGAAATCAATACTCAGAGAAGG

CAGATAATTCTCCACGAAGCCAGAAAACTAATAAATGAACAACTTGGGTGAAATGTNCCA CCAGACGGNGTGATATTTAGTAGCCCNTAAAGCTGCCANGGGGTTGAATGACACTATCTG AAGATATGAACCANTTTGNTCTCCATAGGGAGGATTTTATCAACAGGAAACANATGCCTG GAAGGCATTGGATTT

Sequence 1174

Sequence 1175

Sequence 1176

Sequence 1177

CCGGGCAGGTACAAATATTGAAGGGGAAGAAAATATAATTGTCCTTTCTATCTTTTTTCT CATAATTTAGCTCTTTCTCCACCACGTCATGCAGCTGAATTGAGCCAAGCATTAGTGGTA GGGATAAAAATAATGCCGGAATCACTCTCCCCCATTTCCAACTTCCACTCTTCATGTG CGCAGCTGCACTTCGTACCT

Sequence 1178

Table 1

GGTACATGGAGGCAAAAAAGCAATCAGTATGACTTGAACTGCTGGGTTTAATTACTCAAT ATAACACTTGCCATTTAAAAATCCATATGCCCATCAGCATGGCAACAGTCTCTCATAAAG ATTCCGGTATCATATGGCACAATTTGTACCT

Sequence 1181

Sequence 1182

TACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACACTGATCGTTTCTGCA GCTGCAGATTCTGCTGTTCGACTCTGGTCTAAAAAGGGTCCAGAAGTAATGTGCCTTCAG ACTTTAGACTTTGGAAATGGATTTGCTTTGGCTCTCTGCTTATCTTTTTTGCCAAATACT GATGTACCTGCCCG

Sequence 1183

TGAATNAGGGGATAACGCAGGGAAAGAACATGTTGAGCAAAAAGGCNCAGCAAAAAGGCC
AAGGGAAACCCGTTAAAAAAAAGGCCCGCGTTTGCTNGGCCGTTTTTTTCNCATTAGNGC
NTCCCGCTCCTACCTTGTACCGTAGCCATTACACCAAAAAAATTCCGACCGTCTCAAAGT
TCNAGNAAGNGTTGGGCCGANANACNCCCGAACCAGGGACCTTATTAAAAGGAATACCCC
AAGGGCCGT

Sequence 1184

NGGTGGCCGACGTACCTNTCCACAAGCCTGAACATGGAGTAGATGCATGGCACGGC CAGATTAATGCAGGACGCAACGAAAGGCAGTAACAGCACCGCCCCAGGGTTACTGTGTGT CTTCAGGAACTCTAAGTTGTACCTGCCG

Sequence 1185

ATGCATGGCACGGCCAGATTAATGCAGGACGCAACGAAAGGCAGTAACAGCACCGCCCCAGGGTTACTGTGTGTCTTCAGGAACTCTAAGTTGTACCTGCCCG

Sequence 1186

AGGTACAAAGGGAATAGATAACAGGGACATTGATCTAAAGGGAGGTTAGGGAGGACTTCT
TGGAGGAAGTGGTATTTGTGTCTGAGTTATATGGGATGTGTGGGATTTCTTAGGTGAAAG
AGGCAGAGCAATACGGTGGTAGGCTAGATCTGTGCAGCCGGCTTATTAGACAAGACTTG
TTACCCTGCCCGGGCCGGCTCGTCTTAGTAACNTAGGTGGNATTCACCCCGGGGCCTGC
CAGGGAATTTCCCATTATCAAAGNCTTATTCGCATTACCCGTGCGAACCTCNTAGGGGGG
GGGCCCCCGGGTACCCCAGNCCTTNTTTGTCTCCCNTTTTAAGATGAAGGGGGTTTAAA
TTTGNCGNCCGCCTTTGGGCNGTAAATCATTGNGTGCAATAAGACTTGTTTTNCCTGGTT
GNTGGAAAANTTNGTTTAATTNCCGCCTTCAACCAATNTTCCCACCANCAAACNANTAAC
NGNAGGNCCCGGGGNAAGGCCATTAAAAAAAGNTNGGTAAAAAAGNCCCTGGG
Sequence 1187

Sequence 1188

CGAGCGGCCGGGCAGGTACCTTGGCAATAAGTTGCTAGTTATCTCAGCCTATAAAA

Table 1

TGTAGGGCATATGGACATTAAGATTATAAATTAGCTTTGGTGTAATCAAATTTTATAATT TGTAAACTGGACTATGTTGTGCATCCTTTCATAGTTTAGGATGATTAAGAGTTTGGACCT TATAAGTAAACTGCCACATTTTGAATCATAGGCCCCAACTGGGTACCT Sequence 1189

Sequence 1190

NCACACAACAATACAGAGCCCGNNGTANCCATTATANTNTGTTAAAANGTNCTNGGGGGT GCCCCTAAATGGAGTTGTAGCCTAACTCCACAATTTAATTTTGCCGTTTGCGNCTTNACN TGCCCCTCTTNTCCNTGTCNTGGTAAACCCTGTNNTTTGCCAAGCCTNACAATTANATGN AAANTNTGGCCAAACNGTNTCGTGGAGTAGGAGNGGCGGGTNTTGGCCGGTAATTTGNNG CCGCCTTCTTTTCCCG

Sequence 1191

AGGCCAGCAAAAGGCCCANGAAACCCGTTAAAAAAGGCCCGCNGTATGCCTGGCCGTTTT
TTCCATAAGGCCTCCCGCCCCCCCTTGACTGAAGNCATTCACCAAAAAAATCCGGANNG
CCTCAAANTTCAANTANGGGTGGGGCGTAAAAACCCCCGGACCAAGGGAACCTTNTTAAA
AAGGAATANCCCAAGGGCCGGTTTTTTCCCCCCCCTTTGGGAAAAGACCTTCTCCCTTCN
GTTGGCCGGCCTTCNTTCACCTTGNTTNTACCCCGAACCCCCCTTGGCTCCNGCNTTTTT
ACCCCCGGGAATTAACCCCTNGTTCCCCCNNCCCTTTNTTCTTCCCCCCTTTT
Sequence 1192

GGGCGGCCGAGGTACCCATCCAGGGCTCCAACATGAACCACAATGGACCTTAGGCCCA TTCCAGCACAACAACAACAAGGATGCTTAAAACATTAAAAGGATCTTTACTATCC TCTTGGCAAAGTACCTGCCCG

Sequence 1193

Sequence 1194

GGCGGCCGCCGGGCAGGTACANGCATCGCTGGTGGTTTCAAAAAACGTAGTCATTCTTC
TCACTGCAACAATGTAAGATAAGCAGGGTAGATCTGTTATTTCCAAATTAAAGGTGATTA
AGATATATGGAGAGAACATGGCATGTGAGGTTTATAGGGCTAGAAACTGCAGAACCAT
GTAGAACCCACATTTAACTACAGTACCT

Sequence 1195

Table 1

GATTTATGTATTAATATTGACAGAAGCCAAGGAACACCATCTGAAGTTCTGACGGCAACA
TCAGAAGCTAAGAGAAAAGGCATGGAAAAGATTTCTCACCTTAGTAGCATNCAGAGGGAT
GAGGTTGGNTCNCTGCANNACAANCNCTNTGNTNTTATCTTGACCCTTCTNGACCCTTCN
CNNAAAACCTTGTAGNAGNGAAAAGAAAAATTTTTCCTTGNTTTGGCTTTTAAAANAA
CCANCAACCAGGCCTTTGGTNGNGGTTACCCCTTGCCCCCCGGGNGNCNGGGCTNCGTCN
TTCTTTAGTAAAACNCTAAGGTTGGNGNNATCCCCNCCCCCCNNGGNCNTTGGCAANNGG
AAANTNTTCNNAATTAATTTNNAAAAGTCCTTTTATTTCNGAATTACCNCCGNTNCAGAN
CNCNTTCTGATAGGGNGGGGGGGGCC

Sequence 1197

Sequence 1198

ACTNCTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGGGAACTTG
TGTGCTTAGACCTGACGCTGGGAGGAGATGCTGCCACCTAGGTTACTTGTAGGACCCTAT
ACGGCAACCTCCTTTGCCAGGAACTATTTATAAACATCCTGCAGGAAAATGGTAAGCCCT
TGGTTAAATTTATTGGCTTCATTTATGTATCTCACAACACTTCTTTTCTGTTTTAGTTCT
AGGAATAGAAACTTACTTTTGGAAATACAGTACCTGCCCG

Sequence 1199

Sequence 1200

Sequence 1201

CCGCGGTGGCGGCCGGTGCCACACTGGGCCAGGGTAGTCATCCTGAAATACATGTCCAGG GTCTTGTTTGTCTATGATGTGGGTGAAAGCTGCCTCAGCCCGCACCACAGTAGAGAGCGG GACCACCTCACGAAAGTTTATAGCAAACTCCCAGAGTCTAACCTGAAAGCAGCCAGGAAC AAAGACCTTTCCAGAAAGAAGGACATGAACAAACGCTTAAAGAACGACCTGGGCTGCCAG GGTAAGAACCCTCAGGAGGCCGAGAGTTACTGTGCACAGTACCT Sequence 1202

Table 1

Sequence 1204

CCGCGGTGGCGCCCGCCCGGGCAGGTACAGACTTTATTCTCTATTTCAGGGGCCTTGTT
TATTAAGCAGACACACCTTGCTTGATTATTCCATGAAGTCGCCAACCATTAATCATGCA
CATTTGTTTAACAGGTCAAATGAAGAGAGAGAAATTTGTGTGCAGTCACGGCAAATACTGC
CTCATTTTACCCACTGTGATACTAAAGGTACCT

Sequence 1205

Sequence 1206

ATTGGACTCCACCGCGGTGGCTGCCNACGTACCATGTCTGCACCAANAGTGGCAATAAGG AGGAGGTGGCATGTGGACNGANGGANAGCCANATTCTGTTTCAGGTTACANCATGCA AANAAGGCCGATGAGAATNTTTGCATTATACATA

Sequence 1207

Sequence 1208

CCGCGGTGGCGCCCCCGGGCAGGTACAACGATCTCTTTTGTGGTCTTCTATGTCAACT CTCAAACTAATCTCCTACAACTTTTCCACCCCCCACGCACCGTGCCACAAATCATCTGTT ACCTAACACATAAGTGACAACACAATTCTGTTCCTGCCATTTTCTGCTGAAGATTGTTCC AATTTACTTCTCTGTTGACATATAAAGTAGCCTTTTAAAGCTTTTAAAGTTTTAAAGTTTTC TAAAGTAGCTTCAACATGATTTTGATTCTGCTTTTTATTCTCATTAAAATGAAATATTTC TGGGATTGAACAATGAGAGNAAAATAATAGAAGAGTAGGTGGTGAAAAATTAAAAAAGTA

GGGCATAAGCAAAGTNGTCCCTATTGGTCACAAGACCGTCAATTAAANGGCAATGAAAAA TACAGAAGCNTGAAATGGTGGAATTTA

Sequence 1209

Sequence 1210

TCACTACTTAGGGCAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTGACCATAGATAT CCCTGGGGGATGTAGTGGATTCAAAACATGAGTTGGATTCTCCAACGTGCCATCGGAATT CTTCTAATATTCANCAGCTTTGATTGTTTTTACATCTGACCTGTATTTAGATTTCTCT GATTCCTGGAATATTTGTGGAAAATAAGTACCTGCCCG

Sequence 1211.

Sequence 1212

CTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTAGGAAGGTTATTGC
ACAGCTCCTTAACTGATCGGGGTCAGGGCAGAGTGGTCACTTTCCCCACAGCCAGGCTCT
GGATTTGCCTCCTGTGAAGACACCATGCCTAGCACAGGCTGACGGGGCGGCTGCAGTCNA
ACCTTGCCTCCAGATTNATGAAACCAGTTAAGTAGCACAATTTCTCGTTGGCTACTTTCA
CTTCAAGAGTGTCATGTTTATTGATGTGGAGCT

Sequence 1214

GGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTTATTGTCTCTCATCTTGTCCAT
CATGTTGTTTCTCCTTTTTAGGCGTATATATATCTATGGAAGAAAAAGTTTAAATAGAA
ACACTCATTTGATGAGGAATTTTGGTGTAAAGAAAGGGTAAAAATGGGAAATNNATAGGA
AAAAAAAGTTTNCT

Sequence 1215

CTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGACAGCAACTTC
CTTGATCCCTGCCACGCACGACTGAACACAGACAGCAGCCGCCTCGCCATGAAGCTGCTG
ATGGTCCTCATGCTGGCGGCCCTCCTCCTGCACTGCTATGCAGATTCTGGCTGCAAACTC
CTGGAGGACATGGCTGAAAAGACCATCAATTCCGACATATCTATACCTGAATACAAAGAG
CTTCTTCAAGAGTTCATAGACAGTGATGCCGCTGCAGAGGCTATGGGGAGATTCAAGCAG
TGTTTCCTCAACCAGTCACATAGAACTCTGAAAAACTTTGGACTGATGATGCATACAGTG
TACCTGCCCG

Sequence 1216

GCTTCTATTTCGACCGCGATGATGTGGCTCTGGAAGGCGTGAGCCACTTCTTCCGCGAAT TGGCCGAGGAGAAGCGCGAGGGCTACTGAGCGTCTCCTGAAGATGCAAAACCAG Sequence 1217

AGGTACCCAAGTGATGTCATCTCCCCATCCTCTTGAGAGTGTCTGAGGAGGCCTCTTTTC
CTTTTTTATTGCAATGGCAAGGTTGGAAGAAACTGTGACNAGTAAGAGGCAGAGACCCAN
AGCTGAGTGTAGCATCATGTCTTCTAGAGACTCTCNCNNAANAAANCTGACTTNGGCCAG
TGCTNTGGTTGGAAATGTATTCTGGATCCCCGCAGTACCTGCCCGGGCGGNCGNTCTAGA
ACTAGTGGA

Sequence 1218 -

GCAATTCTNCAGTGGGAGTAAACCACAGACTACGAGGGAGTTTGACAGCTATTAAAACCA GGGCTCCACAGTTAGGAGGTAGCTTTGCAGTTTGGGGAGGGCTGTTTTCCATGATTGACT GTATTATGGTTCAAGTCANANGAAAGGAAGATCCCTGGAACTCCATCACAAGTGGTGCCT TAACGGGAGCCATACTGGCAGCAAGAAATGGACCAGTGGCCATGGTTGGGTNAGCCGCAA TGGGTGGGCATTCTCCTAGCTTTAATTGAAGGAGCTGGTATNTTGTTGACAAGATTTGCC TCTGCACAGTTTCCCAATGGTCCTCAGTTTGCAGAAGACCCCTCCCAGTTTGCCTTCAAC TCAGTTACCTTCCTNACCTT

Sequence 1219

Sequence 1221

ACTACTTAGGGCAATTGGAGCTCCCCGCGGTGGCGCCGTCGCACTCATTTACCCGGAGA CAGGGAGAGGCTCTTCTGCGTGTGGTGGTTGTCAGACCCTCATGCATCACGGAGCATGA GAAGACGTTCCCCTGCTGCCACCTGCTCTTGTCCACGGTGAGCTTGCTGTANAGGAAGAA GGAGCCGTCGAGTCCANCACGGGGAGGCGTGGTCTTGTAGTTGTTCTCCGGCTTGCCCA CTGCTCTCCCACTCCACGGCGATGTCGCTGGGATAGAAGCCTTTGACCCCCGCGTACCTN GGCCG

Sequence 1222

CTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGATACCTCACCGTGGCTGCTGT CTTCCGTGGTCGGATGTCCATGAAGGAGGTCGATGAGCAGATGCTTAACGTGCAGAACAA GAACAGCAGCTACTTTGTGGGATGGATCCCCAACAATGTCAAGACAGCCGTCTGTGACAT CCCACCTCGTGGCCTNAAGATGGCAGTCACCTTNATTGGCAACAGNACAGCCATCCAGGA GCTCTTCAAGCGNAT

Sequence 1223

Sequence 1224

CCGCGGTGGCGGCCGGAAGGAGGATGGTATCACTCAGGCTCTCAGGGTGACACTGAAGCA

AGACACTCATGGGGTAGGACATGACCCTGCCAAGGAGTTCACAAACCACTGGTGGAATGA GCTCTTCAACAAGACTGCGGCCAACTTGGTAGTGGAAACTGGGCAGGATGGAGTACCTGC CCG

Sequence 1225

AGGTACACTTTTGGCCAGGGGACCAAGCTGGAGATCAAACGAACTGTGGCTGCACCATCT GTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGC CTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACCTGCCCG

Sequence 1226

CCGCGGTGGCGCCGTGGTACTCCATCCTGCCCAGTTTCCACTACCAAGTTGGCCGCAGT CTTGTTGAAGAGCTCATTCCACCAGTGGTTTGTGAACTCCTTGGCAGGGTCATGTCCTAC CCCATGAGTGTCTTCAGTGTCACCCTGAGAGCCTGAGTGATACCATTCTCCTTC Sequence 1227

Sequence 1229

GGAGCTCCCCGCGGTGGCGGCCGAGGTACTCCCTTGTGGATAAACGCTTCTAGTTCTTGG
CGTGTTTGGGTTGCTTTTCCTCCTAAAAACTGAATGGAACTAGAACTTTCTAGGAACCCT
TTCAAGCTGCAGTAATGATTTACTGAAGCAGAAAGAACATGGTTATTTTGAGTCTCACNA
NAATAAAANANANATAAAAGTNCANATTTNCANCTNTTTGAATCAGGTTCAGGAAAAAAG
CAAACATGCACACCTAAAACTTAAAAGACCGTTTCATCACTATGCATACGTTTATCATTT
GACATCCATCAACTGTATACCTGGTTTCAAAAGTAAATTTAACTTGTGATCTCAGCATAG
CTCATGTNCACATTTCATGCANAGGGTCCAGGAAACTCAAATCACACTTTGGTAAGTCAC
CATGTTCACTCATTTTT

Sequence 1230

Sequence 1231

Sequence 1232

CCGGGCAGGTACCANGCTGTAACCAATACGATTCTGGGGCAGGTTGTGGGCGAGTAGAAG
AACCTCCTTCCCCTCTGCGACATTGAACGGCGTGGATTCAATAGTGAGCTTGGCAGTAGT
GGGTGGGTTCCAGAAGGTTAGAAGTGAGGCTGTGAGCAGGACCTCCTTCCAGGGGACATG
CAATCTGCAGGGAGGGGCTGAGGGGGGTCCCATGGTCTCTGCTGTCTTCTCTGTCCACCT
CTTTGTAGAGGAGCTTGAGCTCCAAGGAATGCTCTGGTCAGGGCTGCTGTAACACTTTGGC
CCTGCTGTCCTTCCTTCTTCTTGTCCCCGCGTACCTTCGGCCCGNTTCTTAAAAACTNGT

Table 1

GGANTCCCCCGGGCCTTGCAGGGAATTTTCGAATATTCAAAGCCTTATNCNATTNCCCN GCCGAANCCTTTCNAANGGGGGG

Sequence 1233

TGGCCGAGGTACTTTGGCCTCTCTGGGATAGAAGTTATTCAGCAGGCACACAACAGAGGC AGTTCCAGATTTCAACTGCTCATCAGATGGCGGGAAGATGAAGACAGATGGTGCACGCCA CAGTTTCGTTTTGATTTCC

Sequence 1234

Sequence 1235

Sequence 1236

Sequence 1237

CCGCGGTGGCGCCCGCCCGGGCAGGTACTGAACTAGCTCCTTCTGGTTAATTTGTTGAT TGGATTGGAAATTAGAACATGGAGCTGGTCAATGCACGGTATCTGGTAATTGTGGATGGG GGAGATGACTGGGGCAGAACTGAGCTCTATTTTTTGCCAACATAGTACCT Sequence 1238

GGCGGCCGCCGGGCAGGGACTTTCTTCTGTGTGACAATTACTGCACAGTCTTTCCCTCT GACAGCTACTGATGTAAGGCCACCCTGGTTAATAGCCTTAAAAGCATATTCTACTTGGTA GAGCCGACCCTCGGGTGAAAAAATGGTAATGTGGCGGTCAAAACCGGCGCTGGAACCACG GGACATGTTGGTACCT

Sequence 1239

AGGTACACTTTTGGCCAGGGGACCAAACTGGAGATCAAACGAACTGTGGCTGCACCATCT GTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGC CTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACCTGCCCG

Sequence 1240

CTNCTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTTTGGCCTCTCTGGGATAGAAGTTATTCAACAGGCACACAACAGAGGCAGTTCCAGATTTCAACTGCTCATCAGATGGCGGGAAGATGAAGACAGATGGTGCAGCCACAGTTCGTTTGATCTCCAGCTTGGTCCCCTGGCCAAAAGTGTACCTGCCCG

Sequence 1241

CCGCGGTGCCGCCGAGGTACAACTAAATATTAGCTAATGGTAGCACAAGTAGAACCTGT
TTAAAATTTTTAAAAAAACAACCTGTTCACTGTAAGAATGAGATACCCAAGGAAAGAACAG
GAAAGAGGTGTATTTTTAATCCTGCCTTTTGTATTTAGTGTGCCCCATGACTAGCTTGTT
CATCTAACATGCTTCTTGGTTCTCGGCAGGTGAATGGCTATGTCGTGAACCTTTTCTGGG
CATTTGACACCCACAAGCAAGAGAGAGAGAGAGCTTTGAACTTNCGAGGAAAGCATATTGTCA
CACAAAGGTAACACTTTTTGGTGCTGGTCAGTGTTGTGTGCCCAGGAAGGGGGTAAANGGC
TNGGACCCAATNCCTTTTCCCCGCCCGTAANAAGCCTTTGAACTNGGGGGGTTCCCCAGG

GGAAAAGG

Sequence 1242

Sequence 1243

CCGGGCAGGTACGCGGGGGAGGAACTGCTCAGTTAGGACCCAGACGGAACCATGGAAGCC CCAGCGCAGCTTCTCTTCCTCCTGCTACTCTGGCTCCCAGATACCACTGGAGAAATAGTG ATGACG

Sequence 1244

AGGTACCTGCAGGCCTCCTACACCTCTCTCTCTGGGCTTCTATTTCGACCGCGATGAT GTGGCTCTGGAAGGCGTGAGCCACTTCTTCCGCGAACTGGCCGAGGAGAAGCGCGAGGGC TACGAGCGTCTCCTGAAGATGCAAAACCAG

Sequence 1245

CCGCGGTGGCCGGCCGCCCGGGCAGGTACAGCTATTCAACATGTTTAAACAGATGTTTGC
TGACAGCACTGACTTCTCCAAGAGCCTAAGAGAGGAGGAGCAGCCAATTAAACTCCACTGT
CTTCTAAAATTTTAATCCTAGATTGGTTTCAGATGGGTTAAGACAGTCATTCAACCCACA
AGTATTTAAGGAAGGCACCTGGGACTGACTCAGTTCCTAGATTTAAACCTATTCTGTGAA
CTGCCCACCCTACCTTCAAAGTACCT

Sequence 1246

CCGCGGTGGCGCCCCCGGGCAGGTACAAGAGTTACAGCCCTTATGACATGTTGGAAAG CATCAGGAAAGAGGTTAAAGGAGACCTGGAAAATGCTTTCCTGAACCTGGTTCAGTGCAT TCAGAACAAGCCCCTGTATTTTGCTGATCGGCTGTATGACTCCATGAAGGGCAAGGGGAC NCGAGATAAGGTCCTGATCAGAATCATGGTCTCCCGCAGTGAAGTGGACATGTTGAAAAT TAGGTCTGAATTCAAGAGAAAGTACCT

Sequence 1247

TCGCACTCATTTACCCGGAGACAGGGAGAGGCTCTTCTGCGTGTAGTGGTTGTGCAGACC CTCATGCATCACGGAGCATGAGAAGACGTTCCCCTGCTGCCACCTGCTCTTGTCCACGGT GAGCTTGCTATAGAGGAAGAAGGAGCCGTCGGAGTCCAGCACGGGAGGCGTGGTCTTGTA GTTGTCCTCCGGCTGCCCATTGCTCTCCCACTCCACGGCGATCCCGCGTACCT Sequence 1248

TCACTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACAAAGGGAATAGA TAACAGGGACATTGATCTAAAGGGAGGTTAGGGAGGACTTCTTGGAGGAAGTGGTATTTG TGTCTGAGTTATATGGGATGTGTGGGATTTCTTAGGTGAAAGAGGGCAGAGCAATACGGT GGTAGGCTAGATCTGTGCAGCCGGCTTATAGACAAGACTGTACCTGCCCG

Sequence 1249

CCGGGCAGGTACGCGGGCCGCAGTAGTTGGAGTCTAAGGACTCGTGACAATCTTCGGGT GCCCTTCGAGAGAAAAGGGGAGGATGCCACTGGAGTCATCCTCTTCAATGCCACTATCCT TCCCATCTCTTTACCCTCAGTACCT

Sequence 1250

CATACTTAGGGCGAATTGGAGCTCACCGCGGTGGCGGCCGCCACCATGTCCGCCTCGGCT GTCTTCATTCTGGACGTTAAGGGCAAGCCATTGATCAGCCGCAACTACAAGGGCGATGTG GCCATGAGCAAGATTGAGCACTTCATGCCTTTGCTGGTACCT

Sequence 1251

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Table 1

ATGGAGAGAGAAATTACTGGAGTAATGACTCTGAGCAGATGTGGATGGCATTAATAA Sequence 1252

GCGAATTGGAGCTCCCCGCGGTGGCGGCCCGAGGTACTACTGGCACTGAGCCAATGTATG CTATCAAGGAAAGCTTTATCTGTCACTGAGCAAAAGGTGAAGTTCAATTAGGTCAGTTTT ATCACTTCTTTTCCTACACACAAACTATGAGGAGAGATCATTTCTTTTCTTTTATT TATTTATTTTTTTTGAGACAGGGTCCCACTCTGTCGCCCAGGTTAGAGTACCTGCCCG Sequence 1253

CCGGGCAGGTACAGTAGTCAGCTACTTGGATATCAAGACTAAGTGCTGATATGAAGACTT GCCTTTGTGTTTTGTTATGAAACACGCAAGCATAAAGCAGGACTCAAGCACAAGGCTGAC TGTTCTACTTTGAATAACAGCTTCCTTGCAGTCTCCTCCACATGGGTGGTACCTCGGCCG CTCTAGAACTAGT

Sequence 1254

CCGCGGTGGCGGCCGCCCGGGCAGGTACAGAACTTTTGGAAACACCGTCCCTTCAAATGC
TACCTTACTTAAAATATGTAGACATTAGTCCATCCAACCTCTGCTACCAGGCAGTAACCT
TTCATAGATCTTCCAAAGAAAATGTTCTTGATAAAACCAGAAGAATCTTCTCAGAGAGAC
CCAGGGGAGTGATCTGACCTCACTGCTATCTTGACTTAAGTTTTAGCTGCAGCCATGGC
GACTCAAGTACCTCGGC

Sequence 1255

Sequence 1256

CCGGGCAGGTACTCTTGTTTAACCATCAGAGGTGATTCCATCACCTTCACAGCCCCAGCC
TCTGCTCCAGTCCCTCCCCAGCGAAAAGGGCCGCCCATGCCATCCTGCTGCTGGTGATTT
GCTTTGTGGTCATGGACTCAGTGGACATCATTATTTTATTAACCGTGTGGTAGGTTTTTA
ACTCAGTTATCCTGGATATCCAAAGGTTTGTGGTCCATCTTTAGGCTTCCGTTTGTTCTT
TGGTACCT

Sequence 1258

CGNGGTGGCGGCCGAGGTACAAGATGCACTTGGTCACCCGGTTGTAGGCTCCAGGCTCCA TGAACCAACAGAAGCTTCTCTAAGTAGGAAAACTGTGCGATGGCGTAATCCGAGTTGTTG GTGGCCTGCATGCCTTCATTCCCACTGATTCCCACCCACGTGGGCTGTCTGGATCATC CCGACATCGTTGGCGCCGTCTCCGATGGCGAGGGTGATGGCCTTCACCCGCTTCTTCACC ACATCCACTATCTCAGACTTCTGCAGAGGAGACACTCTGCAGCATATGACCGCTTTGCAC GAGAGTGCCAAATCCAGGAAACTCCTCCGGACTTCGAAGGAGAGCGCGACCTGCCCGGGC GG

Sequence 1259

AGGGCGAATTGGAGCTCCCGCGGTGGCGGCCGAGGTACCCTCGGTTGCAAGCACAAGCA
AATGTGCCAGGGTGGTTGATGCAGCTGTGGTCACAGGTCCTATCCAAAGAGCACTCATCC
ACATCTTGGCAAGACTTCTCATCTGTTAATAATTTAAATCCTTTCTT
Sequence 1260

AGGTACTTTTTTTTTTTTTTTTTCACCTTAAGGGAGGATTTAATTTGCTCCCAA CTGATTGTTCACTTAAATGAAAATTTAAAAATGAATAAAAAGACAT Sequence 1261

Sequence 1262

AGGTACTTTGATCTTGGACTTCCAGCCTCCAGAACTGCAGTGTTGGTCTGCAAGCTTCAA GAGCCAGTGCCCTGACTGCCAAGTGATTTGCCGAAGGGAATTATGGGGAATTCGCAGGTA TTCCTGATCTGCTATGTATTCCAGAAAGGCCATGGGCAAAAGGAAGTACCTGCCCG Sequence 1263

AGGTACCGATTTAGCGTGGTCCCAGGCATGTCGGATGTGGGAGCATTCGATCCGCGGCGC
TGCCTTCCGTCGAGCATTCCGGTTCAGACGCTTTCGGTTGACACTGTAACCAAACTTCTG
CCTCCGGGTTTTGCCCTTGGGCCTTGGGGCAATTNGCGCTGNACACACCCGGCACNCAGNC
AAGACTCAAACAACGCTGCNCTCTGTACTNTTCAAAACNCTNNGTGTTCCCANGCCGATA
ACCTTGCACCGGGGCCGGNCCCGTTTCTTAGGAACCTTAGTTGGGGAATNCCCCCCCGNG
GNCTTGGCAAGGGNAAATATCCGAAATATTCAAANGCCTTTTATTCNGNNATAACCCGNT
NCAGAACNCTTNTGAAAGNGGGGGGGGGGNCCACTCGGGNTTAACCCCCAAGANCTTTTT
TATTGGTTATNCCCCTTTTTAAGNTTGGGAAGGGGGGGTTTTAAAATTTTTGATCNNCCC
GNCCCTTTTGGGGGCCCGG

Sequence 1264

AGGTACCTATGATTCGATAATTGACAATGGTTATCCGGGGTTGTCATACACTTGTGCTAGG AGAATTGGTTCTTGTTACTCATATTAACAGTATTTCATCTATGGATCTATAGATTAGCCC AATTTGTAATATAGGAATTTATTGAGGTTTGTGGAATTAGTGTGTAAGTATGTATG TTGAGCTTGAACGCTTTCTTTATTGATGGCTGCTTTTAAGCCTACAATGGTTAAGTGGAT TGTAGTTGTTTTATTCACTATTTAAGGNTTTTTCCCG

Sequence 1265

Sequence 1267

GAAACCTATTGGGGACCAACTGAATTCACCGTAATACTTAGATTCCGTTCTTTAAATGTT GCTATATATTTAAATGCACACTCATATAAGCATGTCCCATTGGNAACTCTCTGAAATCGT CTAGAAATTTTGACTCCATTCGTGAAAATTTTTTNTACATCCGGGAACAGTCCACTTATT ACTTTCTGTGGCCTA

Sequence 1269

GGGGCAGGTACATGCGAATCCTATTGGGAACCTACTGAATTCACCATGATACTTAGATTC
CGTTCCACAAAATGTTGCTCTATAATTGAAAAGCAAACTCATACAAGCATGTCCCATTGG
GAACTCACTGAATTCGCCTAGAAATTTTGATTCCATTCGTGAAAATTTTTGTATATCCCG
AACAGTCCACTTATTACTACTGCGGCCTACTGGGAACTAACCGAATTCACCATGTTACTN
AGATTTCGGCTCACCCAAGTTTGGATAAATCTTTGA

Sequence 1270

Sequence 1271

Sequence 1272

Sequence 1274

nnnnncGACCTTCGAGGGGGGGGCCCCGGTACCCAGCCTTTTTGTTCCCTTTAGTGAAGGGGTTAAATTGACGCGCGCTTTTGGCCGTAAATTCATGGGTCATTAAGCCTGTTTTCCCTGTGGTGGAAAAATTTGGTTATCCCGCGTTCAACAAAATTTCCCACACCAAAACATTAACCGAAGCCCGGGGGGAGGCATTAAAGGTGGTTAAAANCCTGGGGG

Sequence 1275

Sequence 1276

Sequence 1277

Sequence 1279

Sequence 1280

TACTTAGGGCGAATTGGAGCTCCCGCGGTGGCGGCCGAGGTACCACCTATGTGGAGGAG

Table 1

ACTGCAAGGAAGCTGTTATTCAAAGTAGAACAGTCAGCCTTGTGCTTGAGTCCTGCTTTA TGCTTGCGTGTTTCATAACAAAACACAAAGGCAAGTCTTCATATCAGCACTTAGTCTTGA TATCCAAGTAGCTGACTACTGTACCTGCCCGGGGCGGCCGCTCTAGAAACTAGTGGATCC CCCCGGGCTGCAN

Sequence 1281

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Sequence 1282

Sequence 1283

Sequence 1284

Sequence 1285

CGAGGTACAAGGACCACCAGCATCAGCATCACCTGAGAACTTTTTAAAAATGCAGAATCC CAAGTCAGCTGAATCACCAGCTGTGAATTGTTAACTAGGTTTCCCGCTGATTTTCTATGAAA ATTTCTGGTCTATACGGAGTGTATATGACAAATATATACATGTGGGCCATGCAGACATG CTTATTCTCACCTATGGCAAATAGAACACAGCTCTCCATGGTCAGGTGCTTCCATCCCTA ATGGCTTCCACCAGTGAGAAAGACATTAAGAGTCAGAATACTTTTGCTGTAATTCTCTG GTAAATTTTGGTACCTGCCCG

Sequence 1286

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ACCTCTCCCAGAACCACCAGCACCACTACCTGAATTAGTAGACAAAACCCGAGACACACT TCCTCCCCAGAAGCCTGAGTCGAGCGGCCGCCCGGGCAGGTACTTTGGCCTCTCTGGGAT AGAAGTTATTCAGCAGGCACCACAACAGAGGCAGTTCCAGATTTCAACTGCTCATCAGATG GCGGGAAGATGAAGACAGATGGTGCAGCCACAGTTCGTTTGATCTCCAACTTGGGCCCCT GGCCCAAAGTNTACCTTCGGNCCGNTCTAGAACTAGTG

AGCTCCACCGCGGTGGCGGCCCGAGGTACTGGAGGACACTGTGCTTGGTCTCATTGATCC
TGTTAACTTGACTGACTGCTCGATGGTCCAGCCACATGGTGACGTTTCGATGGGAATCCC
CTTCCTGGTTGACTGGTAATGGGTGAAACTGCTTATCAAAACAACCAGAGAACACGTGGC
ATCAAACCCAAGTCCTCGAATTTGGTTTAAATCAATCCCTTGTACCTGCCCGTGTNTNTT
AAATCTANAATGATGNAAAGTTTTGAATAAGNNGACTATCTTACTTCATGCAAAGAAGGG
ACACATATGANATTCATCACCATGANACAGCNAATACTAAANGTGTNNTTNGATTATN
AGAGTTTAGATAAATNTNTGAAATGCANGACCACNNNANGGNATGTTTATGGGG
Sequence 1288

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TTTTGTTCCATGCTAAGGTAGGAAGGTTTGTTCTTGAGACCTATCACTCTTCTGTGGAGG
AGGAGTTCACAGAATGGTGAGCCGCTTTATCACCATCTCGGAGGCTTTTGAAATATGTTG
ATAATGACCTGGGAAAGAGGGCCGAGTGGGATGAGGAGGAGAAGAAACATTCG
GCCCACACAGTGTTCATATCTTCTCTTGTTTTTGTATCTGTGGCAACTGCAGATTAAATG
AATTAGGTTATTCTTTTCCATTGCCTTCTACCAAATAAGAAGTACCTGCCCG
Sequence 1289

Sequence 1290

Sequence 1287

Sequence 1291

CCGGGCAGGTACTCATCAGATGGAATGTTTTACCCTGCCGAGGTTTTAGTCATGATGTGC
TGAGCTCTCTGCGTCTGACGTGACTGACTGGTAGCTGGCGTCGCCGTGACCCTTCTTTC
CCTCTAGGATCACATCATGGAGATATTTTCCACCTATGGGAAAATTAAAATGATTGACAT
GCCCGTGGAAAGGATGCATCCCCATCTGTCCAAAGGCTATGCGTACCT
Sequence 1294

Sequence 1295

Sequence 1296

GCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACGAAGTTTGCGTTCATCGTCCACTT CAATGAGTTTCTGGCAGCCAGTGGCTGGGAAGGAGATGTTCAGCTTCATCTTGAAGCAGC TGAACGCCTCCGAGGCGCCACGGAAAAGAGGCCCCGCGTACGCGGGATTGGGGTTGGGGG GAAAGAGGGGAGCAACGGCCCATAGCCTTGGGGTTGGACATCTCTAGTGTAGCTGCCACAT TGATTTTTCTATAATCACTTGGGGTTTGTACCTGCCCG

Sequence 1297

Sequence 1300

CCGGGCAGGTACAGATCTCTGCAGTTACAGGAACATCGTCTGCTTCATGGTAAATGCAAT TTCCTGTTCAGAAACCACACACACATTACTTCTTTCAGTATTTCTGCCTCAAAGTTGGTT TAAGATTATCATCATTATAAAGAAAAATTTTGTNCTANTTGCTGGNCCAAAGGGAAAA Sequence 1302

Sequence 1303

Sequence 1304

TAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACAGGCCAAGGTCCT CTGTGACTCGCCGCCCACTACCCAAGTGAATGAGTCTCCCCTAGAGCTTTGCTACTCAGA GGGGTCTGAGGACAACAGCATGGGCCAACACGTGCACTCGAGCTGCCTGGAGATCTTGTT CAAAGGCAGATTCTGAATGAGTAGGTCTGGGTTGGAGCCTGAGAGTCTGTACCT Sequence 1305

GAGGAGACTCTTCTGTTACCACCAAGCCAGGAAGTTTCATGGCTTGGGAAGCCCCGCGTACCTN

Sequence 1307

AGGTACGCGGGAACACATTTCTTTGGGATTTTGCCCTTCCTGGGGTATAGGGGATCAGAA
ATATTGATCCATGTGCACGCAGATAAAATGGCTTCTGCTAAACAGACTAAAATCTTTCTC
TCTAGTCTTTCTCACTTGTACCTGCCCGGGCGGCCGCTCGACCGTCTTTCCCTTTCGCCC
TCCACCTCCTTCCTGAGACCAGCTGTTTTCAGCTCCCCTTCCCTGGGCCCACACTGAA
TCTCTGTTACCCTTACAAACCCCTGCTGCCTCTAAGAGTAAGGACCCCTATCCCATCCCA
AACTCAAACCTAAGCACATGCAGCCTCATCCCATTTCTCCAAAACATGTGAAAGCAAAAG
AAAATAAAAAACTAACTCAGCAATCTTGTTCTTTCCTACAGTGGNCTTTTGGCTAC
Sequence 1308

Sequence 1311

AGGTACGCGGGGACACTTCCGGGCGCGGCGCGGCTTGCTGCCACTGCAGAGCCCCGCCA

Sequence 1313

Sequence 1315

Sequence 1316

Sequence 1317

Sequence 1318

CCGCGGTGGCGGCCGAGGTACGCGGGATTGATGATGGGAGGCAGTGAGTCTTGATGATAA GGGTGAGAAACTGAAATCCCAAACACTGTTTTGTTGCTTGTTTTATTATGACCTCAGATT

Sequence 1319

Sequence 1321

Sequence 1323

Sequence 1324

Sequence 1325

Sequence 1327

CGCGGTGGCGGCCGAGGTACTGNAAATCGTCAAGGGTGAAAGGTCGATCGCNTGCCAGCT TGCTTCCACTNGATTCTCGGATTTTTTTACCGGTANTGATGTTGTAACATTCGTATCCAA GGCTCCGCAAAGTTNGNCACNTCGGTATGTGANAAGGCTNTCCTCATTCCCACNTATATT GGNGTTACCCTTGGCCCNCGGGTCCNAGGCCCNCCTTAATTAANAAACNTTANNTTTGNT ATTCNCCANCCGGGNCNTGNCAANNGTAAATTTTTCGTAATTAATACNANANGNCTTTTA ATTCCGNNATTANCCCGGTTCTNTAACCCCCTANGATAGGGGTGGNGNGTGNGNCCACAC CGGNGNTTANCACCCNAANNATCCTTTTTTNTGNATATTTNACCCNTNTTTNNATGNTTG GNAAGGGGNGGTAATTAAAAAANTATNGACNCNTCCNTCCNTATTGGGAACNGAATAAAAA NTTCAAATTGNGGGATTCCAANTTNAGTCCATTTGNCTATTNTTCCCCCTTGGTTGGANT TGNTAAAAAAAA

Sequence 1328

GGTGAAGATGCTGAGCCGGAATCCGGACAATTATGTCCGCGAAACCAAGTTGGACTTACA GAGAGTTCCAAGAAACTATGATCCTGCTTTACATCCTTTTTGAGGTCCCACGAGAATATAT AAGAGCTTTAAATGCTTNCCAAAACTGGAACGAGTATNTTGCAAAACCATTCCTTGCTTC GNTGGATGGTCACCGTGATGGAGTCAATTGCTNGGCAAAGCATCCAGAGAAGCTGGCTAC TGTCCTTTNTGGGGCGTGTGATGGAGAGGTTAGAATTTGGAATCTAACTCAGCGGAATTG TATCCGTACCT

Sequence 1329

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AGGTACAGATACATGGACACAATCATGGCAGCCAGCTCGAGGCCCCCAATTCCAGCTGCC
ACACCACCCACGGTGACTNGCATTAGTTCGGATGTCATACAAAAGCNTGATNTGAAGCAA
CACCTCTACGTTTTTGGTCGTAGAGCTCTTTTTGCTTTGNGNTGCAAGGATTTTCATTTT
GGGGCTTGTTGNTTTGGGATTGNACNGNTTTGTTCATTTTGNNAANACCATNAAATTGGG
TGTGTGTAAANAANGGNCCAACCTTGATTTTCATTCTTNTTTGGNATAGTATATGGGNGN
TTGTAAGGTTTCNCCTTTCAAAAAAAANTTCCCCGNTTTANTTAGNATTTGGNGTTTGTA
AAANGACTCCAACCATGTNCAAACCTTTTGGAAGGCCCCCCTTTT

Sequence 1331

AGGTACGTGGGCCTGTCTGCAAACCAGTGTGCCGTGCCAAGGACAGGGTGGACTGCGGCTACCCCCATGTCACCCCCAAGGAGTGCAACAACCGGGGCTGCTGCTTTGACTCCAGG

ATCCCTGGAGTGCCTTGGTGTTTCAAGCCCCTGCAANGAAAGCANGAATGCACCTTTCTT GANGGCCACNCTCCAGCTGACCCCCGGCACTGNTTNTAGTAACCTAGCTGGGTAATCTCC CCGGGTGCCTGGCNAAGGGAAATTTCCGNATANTTCAAAAGGCNTTTATNCCNNNTTAA CNCGGNTNNGTACNCCTTCNGTAAGNGNGGGGNGGGGCCNCTCNGGGTTTACCCCCAAAT CTTTNTATGGNTTTTCCNCNTTTTNAAGCTTGGAAGGGGGGTTATAAAATTCTGGACCG TCCGGCCTTNTNGGGCCNGGTTAACATTTCTAATTGNGTNTCCAATTAAGGGTCCNTGGN TTTTATTCTCCTTGGATTGGA

Sequence 1332

Sequence 1333

AGGTACTAAAGCATTCATGGAGGCTCTTCAGGCTGGTGCAGACATCTCCATGATTGGGCA
GTTTGGTGTTGGCTTTTATTCTGCCTACTTGGTGGCAGANAAAGTGGTTGTGATCACAAA
GCACAACGATGATGAACAGTATGCTTGGGAGTNATTCTGNTGGAGGTTTCCTTTCNACTG
TGGCGTGCTGACCCATTGGGTGGAGNCCCATTTGGNACAGNGGGCTACCCTTGCTCCGAG
GNCNGGCANGCTTGCTACTAGNAANCTTAGATGNGATCCCCCCGNGGNCTGGCNAGGGAA
CTINCGTATTATCNAAGGCCTTATTCCGGATANCCCGCTCCGTACNCCTANGGATAGGGG
GTGGGCNCCCCGGTTACCACCAANCATTTTNTGGTTTCNCCCTTTAAAGGATGNANGGGG
GTTTTAAAATATNGCTGCCGGCCTTTGGGCCGGTTAAAAATTCCAAATTGGGGTTCAANTA
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Sequence 1334

CCGCGGTGGCGCCCCCGGCAGGTACCAGGGTCCTGGTGGGATGGTGAACCGTGACGA GTACGCCATCAGGGTAAAGAACTCGTCCAGACTGTCAACTGTGATCCTGGACTCGCTGTA GGTGAGTAGCGAGTTCTTAGATCCTAAGAGACTGATGCATACATGGGGGAAAAACAAATAT AAAACCTGGCAGTTGTACCT

Sequence 1335

CGGGCCCGCCCGGCAGGTACATTTCCTTGTAGACTCTGNTAATTTCCTGCAGCTCCTGG
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TTGCGAAAGCTTTTANCNTCANAAAGCCGTTCATTACCTGAGGCCAGGGTGGTCTTTCA
AATAAGGGCCCCAAACAATTCAACCGGTNCTTCCAAGGGGTGGGCCAAGNATAAANGGG
CNTGGANCTTNTCAAGCTGGCTTGNATTGNCAAAGNTNTCCCTTTTTTTTNGGGTGCCCT
TACTACTNGGTAAGGGGCGNAAAAGGGCNAAATTAATNCCCTNGTTNCTTCTTGNTCGNC
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NGGAACCCTTTCAATTCTCCAACCAACNCTTTTTTTGGGNTACNTTAGGCAATNGNGGCCT
TGNNTTTCCCAAAATTGGTTTACCACANAAGGCCAAATTCNCCCGNCCTTTCAAGANCAA
TTTCNAAAACCGGTTTNAAGGTNAATTAAGGGGNNCTTTTTTTGGGANCANGGGAACCCCC
CNATTAATTTGNCCAACCTTTTGGGGGGGG

Sequence 1336

TTANCNGNAAGGCCCCGNGGGGAAGGCCAATTAAAAAAAGGTTGGTTAAAAAAAGGCCCCT TGGGGGGGGGTTGGCCCCCTTAAAATTGGAAGGGTTGGAAGGNCCTTAAAACCCTTCCAN CAATTTTA

Sequence 1337

Sequence 1338

Sequence 1339

Sequence 1340

CCGCGGTGGCAGCGCCCCGGGCAGGTACCATCACCCCTTCATGCTGGCCCTAAGCTT
TCTCCAGCAGTCCCACTTCCTGATATTCGTTCTCTTCAGCAGCCTAAAATACAGCTTTCT
TCTGTCCCCAAAGTAAGCCGCTGTGCTCATTGCCCTAATGAACCCTCCACTTCGCCAATG
CGTTTTGGTGGTGGTGGTGGCGGTAGCGGAGGNACCTCGGCCGCTCTAGAACTAAANGGA
TCCCCGGGCTGCAGAGAATTCGATATC

Sequence 1341

CGCGGTGGCGGCCGAGGTACCAACATGTCCCGTGGTTCCAGCGCCGGTTTTGACNCGCCA
CATTACCATTTTTTCACCCGAGGGTCGGCTCTACCAAGTAGAATATGCTTTTAAGGCTAT
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ANNTANATNTGTTCACCACCAGNAAAGAAAAAGTTACCCTNGCTCCNGGNGCGGGCCCGC

TTCTTANGAAANCTTATGNTGGGATTCNCCNCTCGGNGCCTTGCCAAGGGAAATTTTCTG
ATTATTTCNNANGNCTTTTANTTCNGGAATTANCCCGNTCGGATCCCTNCGGAGGGGGGG
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GAAGGGGGGTTTTAAAATTTTTGGCCTGGCNGGCCCTNTTGGGGCCGGTTAAAATTNCAA
TTGGGGTTNCAATTAAGGNCTTGGTTTTTNCCCCTTGGTGGGTTGGNNAAAAAATATTGN
GTTTAATTTCCCCGCCTTTCAACCAAAATTT

Sequence 1342

Sequence 1345

Sequence 1346

CCGGGCAGGTACCATCACCCCTTCATGCTGGCTCTAAGCTTTTTCCAGCAGTCCCACTTC CTGATATTCGTTCTCTCAGCAGCCTAAAATACAGCTTTCTTCTGTCCCCAAAGTAAGCT GCTGTGCTCATTGCCCTAATGAACCCTCCACTTCGCCAATGCGTTTTGGTGGTGGTGGTG GCGGTAGCGGAGGTACCT

Sequence 1347

GGAGCTCCCCGCGGTGGCGGCCGCCACGCTGGTTTTGCATCTTCAGGAGACGCTCGTAGC
CCTCGCGCTTCTCCTCGGCCAATTCGCGGAAGAAGTGGCTCACGCCTTCCAGAGCCACAT
CATCGCGGTCGAAATAGAAGCCCAGAGAGAGAGGTAGGTGAGGAGGCCTGCAGGTACCAGC
TGCCATCTGTCAGTTAAACTTCAGAACACACACATACCATAGGGATGAAGATAAGAAAGGAA
TGATTGTGACTCTGGATCAAAATGCTCCCAGTTCCTGAAGGTGCATGATTTAACTGTGAA
TGCCAACTGAGATCCTAACACCCTATACAACCAAAAGATGAACTAAGTCTCTGAACTGGT
AACTCATAAAAGACAAATTCCCACAGTNCCCTTCGGGNCGGTTNTAGNAACTTAGTGGAT
CCCCCCGGGG

Sequence 1348

CCGCGGTGGCGCCCCGGGCAGGTACAGATCTCTGCAGTTACAGGAACATCGTCTGCT
TCATGGTAAATGCAATTTCCTGTTCAGAAACCACACTAACATTACTTCTTTCAGTATTTC
TGCCTCAAAGTTGGTTTAAGATTATCATCATTATAAGAAAAATTTGTCTAGTGCTGGTCA
AGGAAATGGGTCTGTGTTTCTTTGGCATGAGCTTTTGGAGTGCTGTATTTTGGAGGAGGGG
TAAGGCAAGTCAGATCCACTACTGCGTATCATGACGCAGATGCACACAGATGCA
CATGCTCGAAAACAGGCACCTGGAGATTTTAGNAAAATTCATTTGGGGGAAGATTNGCCT
AACTTTCCTTTCTACTTCAGTGGAATGAATTACCATTTCT

Sequence 1349

GGAGCTCCCGCGCTGGCGGCCGCCCGGGCAGGTACCACACTCAGGGCAGTTTCCAGCTC CTCTCACAAACAGTAAATCTACACAACTTTCACAGCCAGGTCAGCAACTGGTTCAAGAAC CGCCGGCAGCGCGACAGGAACCCCTCCGAGACCCAGTCCAAAAGGTGAGCGCCAACTTTC CTCCTCCCCGCGTACCT

Sequence 1350

Sequence 1352

Sequence 1353

CTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGNCATGGTACCACGGGCCT GGGCACTGCATCTTCCCAGAGAAGCAGACTCCACAGGGGCCTCATGACCATCTTTCTCTG GAGAGGCAGGCAAACTCCCTCGACAGCCAAAATCCAGAACCTCCCCCGCGTACCTCGGC CGCTCTAGAACTAAGTGGATTCCCCCNGGGCTTGCANGGAAATTTCGATATCAANGCTTA TNCGTTACCGTNCGNACCCTCGAAGGGGGGGNCCCGGTACCCAGCCTTTTTGT Sequence 1354

Sequence 1356

Sequence 1359

Sequence 1360

Sequence 1362

Sequence 1363

Sequence 1364

AGGTACTCAGAGTGAGGATTTTCTGCAACCTGCGTTTGTCCCTCCAGCATCTGCTCTGGC TCCATGGCGGACCCTGCAAGTCACAGTCCCCGGATACCAGTCTGGGCGCCGGGAGCACCA CGAGCAGTAGAGCAGCAGAGTGGGACAGTCCACGACTGGGCGCCTACATGGGGTCTGGAA ACTCTACGACAGTCCCAAGTACCTGCCCG

Sequence 1365

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Sequence 1366

CGNGGTGGCGGCCCGGGCAGGTACTGTTTACTACACACTTAAAAACCCGAGTGTCNA GTGCCTTTAGGGGAAGAACACTTCTGCCTGCATGAAAATGTCTTAAAAGTGAAGGAAAAT TTGAAGAACGCTNTTGATCAGAAGTCCAGACTGTAAACATAATC

Sequence 1367

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CNNCAGACNGCAGGCNGCNGNNNGTGAGAGNGAACGGGGNCCCACNCCCANANACACNGA ACCNGGCNGGGANACCAGNGGCCCNGGNGGANGCACCANAGANGAGGAGCCNGNGAGCCA GGCCTGGTTNCNGCGGGGACCNGCCCG

Sequence 1368

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Sequence 1370

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TGATTCACCTTCTCCTGCAGGTGACCATTGATGGCAGGAACTACATTGTCGATGCTGGGT
TTGGACGCTCATACCAGATGTGGCAGCCTCTGGAGTTAATTTCTGGGAAGGATCAGCCTC
AAGGTGCCTTGTGTCTTTCCGTTTGACGGAAGAATGGGATTCTGGTATCTAGACCAAA
TCAAGAAGGGGAACAGTACCTCGGCCCGTTCTAGAACTAGTGGATCCCCCCGGGCT
Sequence 1371

Sequence 1373

Sequence 1374

AGGTACCTGNAGGCCTCCTACACCTACCNCTCTCTGGGCTTCTATTTCGACCGCAGATGA TGTGGCTCTGGAAGGCGTGAGCCACTTCTTCCGCAGAATTGNCCGANGAGAAGCGCNGAG GGCTACGAGCTGTCTNCTGAAGATGCAAAACCAGCNTGGTCGGCCGCTNTAGAACTAGATGANATCCCCCGGGCATGCAGGTAATTCGATATCAAAGCCTT

Sequence 1377

CCGGGCAGGTACCAAAATGGTTTTGAAGTTAAGGGNGCTGCTTTCTCTCTTCATTCCTGT GGGGGCCCCAATTCTNCATAATATTTTGCAGCTGAGAAGTATGTCTTTTTATTCATTTTT AAATTTTCATTTAAGTGACAATCAGTTGGGAGCAAATTAAATCCTCCCTTAAGGTGAAAA AAAAAAAAACAAAAGTACCTN

Sequence 1378

Sequence 1379

CCGCGGTGGCGCCGAGGTACTTTTTCCTAGTAGTGACCCAGTAAATATCTNTNCAACAA
ACTTGGCTTTGCTGGTGTGCAAAGTGTAATATAAGGAAAATTAGTGACATTTTTTTGCCT
TTTAGTGTGTAACNTGGGAATGTATANGTATAGAAAACAGAGAGATAGTTATATTTTA
ACAACTTGAAATTCATAGGTGTTAATAGATTCCTNTTTTTTGAAATTAAATATCTCCTAGG
ATTTTGATCACTTACAGTGTTGTATGCACTACCTTA

Sequence 1380

Sequence 1381

AGGGCGAATTGGAGCTCNCCGCGGTGGCGGCCGGCCGGGCAGGTACTGTGTATCATTGCA GNCTTGCTTTTTTGAGTAATGGATTCCTAGATTCTATGAGGATACCACAACCACTTTTAA AGAGGTTTCTAAGGNCAGTTGCAGTGCTTACGCCTGGGAGACCAAGGTGGGAGGATCACT TGAGCTCAGGAGTTCGAGACCAACTTTGTCNTT

Sequence 1382

Sequence 1383

Sequence 1385

ATTGGAGCTCCCCGCGGTGCCGGCCGAGGTACAAAGAAATGCATGAACTGGCAANTTATT
TGTGACTGCAACAGCCCGTGCGTGTTCAGGAGTGTGTCTTCCAATCTGNCCTAAGGCCCA
AGCAGCTGCAGCCTTAATATGATCTTCCGGTTCTTCTGACAAGCANACTGACAACTGGGG
TACCTGCCNG

Sequence 1388

CTTNGGCGCCCCGGGCAGGTTCTTTGGCCTCTNTGGGATACGAAGTTTTTCANNCAG GNTCACAACACGAGGCAGTTCCAGATTTCAACTGCCCATCAGATGGCGGGAAGATGAANA CAGATGGTGCAGCCACAGTTCGTTTGATATCCACTTTGGTCCCAGGGCCGAAAGAAGGCA GACCAAAATATTGCTGACAGTAATCCCGCGTACCTNGGCCGGACCA Sequence 1389

Sequence 1390

CTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGANGTCCNNNNACACCCNNNGTGC ANNGGTCTTGCGTNGCCNATGCCNCCACCATTGTCCANAAGACTCAGTTAACATTATTTG CAGTACAGACGGTTATTGATCCACGATGATAGAAGAGGAT Sequence 1391

Sequence 1392

CCGCGGTGGCGCCCCGGGCAGGTACTGTGCAATGCCTCAGGTTGCACCTGACTTATA
TGCTGAACTACAGAAGGCACATTTAATTTTATTCAAGGGTGATTTGAATTACAGGAAGTT
GACAGGTGACAGAAAATGGGAGTTTTCTGTTCCATTCATCAGGCTCTGAATGGCTTCCAT
CCTGCACCACTCTGTACCT

Sequence 1393

Sequence 1394

CGAGGTACTGTCGTCTCCCAACTCCCACCTACAGGGCCCGGGAATCCTAGGGAGCGGATA
AAGGCCTGGGAGAGGGAGCAAGATGGGCTCCGCCACGAGATCCGGCTGAAGTCCGGCTCG
GCGCCGGCCTCAACTGCAAGAGGAAGGCACTCTCTCTCCCCAAGCTGAAACACCAGAAGA
GCCACACT

Sequence 1395

GACTTTGTTTGTTTTTTTTTTTTTTCACCTTAAGGGANGACTTNATNTNTTNCCNTNT GACCGCCACTTAAATGAAAATTTAAAAATGAATAAAAAGACATACTTCTCAGCTGCAAAT ATTATGGAGAATTGGGGCACCCACAGGATGAAGAGGAGAAAGCAGCTCCCTAACTTCAAAA CCATTTTGGTACCT

Sequence 1396

Sequence 1397

Sequence 1398

ACTACTTAGGGCAATTGGAGCTCNCCGCGGTGGCGGCCGAGGTACCGCGGGAGCTTCTCC
TTGCCAGTTTCTCCCAGCAGGACCCTCTTCTTGTTTTGAAAGATGGTCGGCTGCTTTTGG
TAGGCACGCTCAGTCTGAATGTCCGCCATCTTCC

Sequence 1399

Sequence 1400

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Table 1

nnnnNGATATCAAGCTNATCGATNCCGNNAGACCTCGAGGGGGGG Sequence 1401

Sequence 1402

AGGGCGAATTGGAGCTCNCCGCGGTGGCGGCCGAGGTACGCGGGGAGGAACTGCTCAGTT AGGACCCAGAGGGAACCATGGAAGCCCCAGCTCCACTTCTCTTCCTCCTGCTACTCTGGC TCCCAGATACCACCGGA

Sequence 1403

Sequence 1404

Sequence 1405

Sequence 1407

Sequence 1408

Sequence 1410

GGGGGGGTAAAAAAAAAAAAGGGGGTTTTTTTNGNCCCCCTTTTTTNCCCCCCCT Sequence 1413

Sequence 1415

Sequence 1416

Sequence 1417

CCGCGGTGGCGCCCCGGGCAGGTACCAAAATGGTTTTGAAGTTAGGGAGCTGCTTTC

Sequence 1418

Sequence 1420

0

PCT/US01/00798

GGGGGGGGGGTTTTTTCNCCCCC

Sequence 1422

Sequence 1424

Sequence 1425

Sequence 1426

Sequence 1427

Sequence 1428

Sequence 1429

Sequence 1430

Sequence 1431

Sequence 1433

Sequence 1434

Sequence 1435

CGGCCGAGGTACTTTTTTTTTTTTTTTTTTTTTTCACCTTAAGGTNNGATTNAATT
TGCTCCCAACTGATTGTCACTTAAATGAAAATTTAAAAATGAATAAAAAGACATACTTCT
CAGCTGCAAATATTATGGANAATTGGGGCACCCACAGGAATGAAAGAGAAAGCAGCTC
CCTAACTTCAAAACCATTTTGGTACCTGCCCGG

Sequence 1436

TCATACTATAGGGCGAATTGGAGCTCNCCGCGGTGGCGGCCGCCCGGGCAGGTACTCCAG GCGAGAGGCGGACGCGAGTCGTCGTGGCAGGAAAAGTGACTAGCTCCCCTTCGTTGTCAG CCAGGGACGAGAACACAGCCACGCTCCCACCCGGCTGCCAACGATCCCTCGGCGGCGATG TCGGCCGCCGGTGCCCCNAGGCCTGCGGGCCACCTACCACCGGCTCCTCGATAAAGTGGA GCTGATGCTGCCCGAGAAATTGAGGCCGTTGTACCGTATATAAAAGACAATTGCTCACAA TGATAGCACTGAAGCACTGAGAGATATCAAAGTACCT

Sequence 1437

CTATACNGCGAATTGTTTTCCCCGNGGTGNCGGCCGCCCGGGCAGGTACACGGGAGATGA AGGTGCGCATCCTCTCGNNCGTAAGAAGCCTCTGGACATTGACTACATGGGGAGGAAC AGCTCCGGGAGAAAGCCCAGGAGCTGTCGGACTGGATCCACCAGCTGGAGTCTGAGAAGT TCGACCTTGATGGGCNAAANCCTGAAACAGCAAGAAAATATGAGATCAACGTGCTGTACC TCGGC

Sequence 1438

Sequence 1439

Sequence 1440

TATCACTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACACAAACTGTT CAATCTTCTCAAAGTGATGGACTCGGAAGATGCCACGGGTGTCACGGCCATGGGAGCCCA CCTCCTGACGGAAGCAGGTAGACAGGCCAGCATACTTGATGGGCAGGTCCTC Sequence 1441

CTATCACTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACGC GGGGATCCAGAATACATTTCCAACAAGAGCACTGGCCAAGTCAGCTTCTTCTGGAGAGTC TCTAGAAGACATGATGCTACACTCAGCTTTGGGTCTCTTACTCGTCAAGTTTCT TCCAACCTTGCCATTGCAATAAAAAAGGAAAAGAGGCCTCCTCAGACACTCTCAAGAGGA TGGGGAGATGACATCACTTGGGTACCT

Sequence 1442

Sequence 1443

Sequence 1444

CTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCAGCAGAAACCTGGCCA GGCTCCCAGGCTCCTCATCTATGGTGCATCCACCAGGGCCACTGNA Sequence 1445

ATAATTGCGCGCTTGGCNGTAATNCATGGTCATAGCTTGTTTTCCTGTGTTGAAAATTGT
TANTTACGCTCACTAATTTCCAACACAAANCAATTACTGNAGCNCGGGGNAGTCATTAAT
AGTTGGTTAAAAAGNCTCTGNGNGGNTGNCNCTTAAAATGGAAGNTGCAGGCCTTAAACN
TCAACCATTTTANATTTGGCNGTTTTGACTGCNTTTCAANTNGTCCTCGACNTTTTTCC
CAAGNTNCCGCGGNAAAAAACCACTTGGTTCCCNTTGNCNCCAGTCTTGGTCAATTTTAT
ANTGNAAAATTCNGGGNCCCAAAACTGACNGTCCGTGNGGGGAAGGAAGGGNTCGGGGTT
NTTTGGCCGGTNTATTTNGGGGGGGCCNGCCTTACTTTTTCCCGGNCTTNNCTCCTTCGGN
NTTCCAACTTGG

Sequence 1446

CCGGGCAGGTACACAGTAAACAGCATTCCTCACTTCGCTGAACAGCANNAGGCAACTCGT TTCTAAGTTCCAAGCTCACTCTTCATAGAGNCTATCCACCTTGGGCTNG Sequence 1447

Sequence 1448

TACCAGAGGCCCTGGTGGAGGCACCATAGATGAGGAGCCTGGGAGCCTGGCCAGGTCTCT GTTGGTACCTGCCCGGGCGGCCGNTCGACTGTTGGACTTGAACCAGCGCGCGTTCAAGAA GTTTGCCGGGCAACCGCACCAGCGCCTTNGNCGAACTTCGACCGGCCAGCC Sequence 1449

Sequence 1452

Sequence 1453

GGAAGCATNAAAGTNTAAAAGCCTGGGGGTGC

Sequence 1454

AGGTACTCCATCGCCTGCTTCAGCTTCTGCAGCTCCCTAGTGGCCCCACAGCTGCGGCCGCCCTCTTCCCCCATGATGAAAACATCTGAGACTCAGGGCTAAGCACCTTGCCCA

AGGCCACACAACAAGTAGGTGATGGAGAGTGTTGGCGTGTACCTGCCCG

CCGCGGTGGCGGCCGAGGTACCANNGACCTCTAACTCCCCCTGACACAGAGCAATTAGAC TCCCATAACAATGGTATCAATTATACCACTCCATTGGAGGGACTTCCTTTATGTGTCACC CAGGATACATTGCTCAACTGCAGTTGCCTTGCANTTTGATCCCAAGCATGGNTGAGTTAC CATAAAAAAATTATGTACCT

Sequence 1456

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Sequence 1457

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Sequence 1458

CCGCGGTGCCGCCCCGGCCAGGTACAGATGTCACCGGCAGCATAGATATCAGGAAGG
GATGTGTGCATATGATCATCACTTTCAGGCCACCATCTTCCCCTAGATCAAAACTGTTA
CCATGGAGAAAAGGTTCTACATTTGGTGTAACTCCTGTANCACTGACAATGAAAGCGCAG
CCATATATCTTTTCATTGGTCAATTCCACATAGACAGGCCACATCTCTGTATCGGCTGTA
ACTGACTTATGGTCTCTTGGAAAAGTGAAGGACTTTTTCTTCAAAATTCTAAACTCATCC
TGAAGGTAGATTTTCTTTACTTCACACATAGTTTCAAGGTGAATCTTATGAGAAAACTCT
TTTGTTCCTTTAAGATTCAAGCCTTCATGCCAAATCTTGG

Sequence 1459

TCGAGGCCGAGGTCTTGCGGATCTGGCGGACCTGCTGGTGCTGCGCATAGGATGTCTTTC
TAATCTGGTTGTTACGTTTCTTAGTGAAACCAACACAGAAAAGTCGGAGCAAAATA
Sequence 1460

Sequence 1461

TAGGGCGNTTTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTATGAATGTAATTCATAATT
TAAAAGGAAAACTAAAAACTATTTTGATTTGGGAAAATGAGCCTTAATTTGTTAAACCTA
TACACTGAGAACTAGCCTCAGGCTTAATATTCTCATTGCATTTGCAAGATCTGAGCAAAT
AAGATTAAGTAAAACAAATCAATTGTATATATAATTGACCTTTTTGTGGAACATGTAGTT
TATAGAAAGTATACTCTAAAGGGAATTTGCCGAAGACCTTTTACTGATTGAACAGTTGTG
CTACAATCAACTTTTCATAGTACCTCGGCCCGCTCTAGAAACTAGTGGATCCCCCCGGGC
TGCAGGAATTCCGATATCAAGCTTTATCGATACCGGTCGACCTCGAGG

Sequence 1462

Sequence 1463

CGGCCGCCGGGCAGGTACTCAGTGGATGACGAGTGCTTGGTTGAAATTGTTGAAAGGCC TGTGTTCTGAAATACCTGGGCCGTGTCCAGTGAGGCCNAGGAGAATTTTTATNGAGCATC TTTTGCCAATGAANAAGAANATTAAATATTGACCACTTACCTTGATCCCAAACGCTCCTG ACTGGAAGANTGGCACCATGNCGTGTTTTTATTNGAAGCTAAAGGCNANTAAAANNGTAA AGTAGTGCTCATTCANAANNTATNTTNGGNAAANTTTGTCNCNNANTCCAAANAAACTTT ACCANANGCAANATTTNACCTTTCCCAA

Sequence 1464

Sequence 1465

CCGCGGTGGCGCCCCGGGCAGGTACTGAGATCACTTGCACTTTTCCTCATTTCTTAA GAAAATCCAGTTTGCTTGCCATGACTTGTTTAGCGTTAGGTTTACAAAGCTTGTTGTTGA ATGTTGAATATTTGTCCAAAGGAGTTTGACAAAATAGAAGCTGCTTGGTCCCTGTTCTGC CTGCTAGGTCATAAGGATGAAGGCCATGTGGCTGGGGTACCT Sequence 1466

Sequence 1468

Sequence 1469

Sequence 1472

CGGGCAGGTACTTACAAANTGCCCCATTCTNTTCATCTGAAAATGTCCCCGAGCCTTTTG
GAAACAGGNGCAGGGCATNCANANTNTTCCCANTTTTTATNGAACTTGANGNACGGTTNC
AACNANAANNNCTTAATTTCTACANACATCTTTNTTGGGTNATTTGTTACCGAAGNTCC
TCCTTATTTGAGACCCCACCTAGACACCGACCTTGNANATTGGAACAAGTAAGCCCCTNT
NCNTTCNTACAATTGNAAATGGTANCGTGGGAAGAAGCCTTGGTTNGAATTTTAAAACC
CCCTGANTTNATNGTTGNCCCATGGNACCCAGGGGAACCAATTGGGTTTTTTTTAANAAA
AAA

Sequence 1473

Sequence 1475

Sequence 1476

Sequence 1477

AGGTACTTCAGGGAAATACCACCTCCACAAACGTTGAGCCAATTCAGGGGCTGCCAGTAG
AATCCTAAAGAGTGATGTCTCCGGTTCATGTGAACACCATCTGCANTCCACACCCCGCTT
TNAGGGACAAATTNANNGCCATTAAGNGNNAAGAACCATTGCTTCAAGCCAGAAGCTNG
TCCCCCTTTTNATCCCANTCCCCNAGTTTCACTCACCCCCTTTAAGNCCTCTGGAATATG
GGNGACCNAGTGCCGGAATGGGCCTTCNAATTAAGNCTCNACGGGTAAANGGGGCNTGGC

TCCTNNNCCCNTTCAAGNGGCNTTATNCTCCCNAAGATANANCNCCNAAANTTCTATANG GGGGGGGCNAATTTAACCGGNCCGNGGCCTTTCNANNTCCCCCAACCAACCNTTTTTTGG NCAANCCTTTTCAATTAAATTTTTCCCCCCGGTCTAATTGGGCCTTTTCCCCCGNCCTTT TAAAANAATTGGTTAANCCCCTT

Sequence 1479

Sequence 1480

CCGCGGTGCCGCCGAGGTACTGTGGAGCTGTTGGGACTGGGCAGGCGGCAAAGATCTGC
AACAACATGCTGTTAGCTATTAGTATGATTGGAACTGCTGAAGCTATGAATCTTGGAATC
AGGTTAGGGCTTGACCCAAAACTACTGGCTAAAATCCTAAATATGAGCTCAGGACGGTGT
TGGTCAAGTGACACTTATAATCCTGTACCTGCCCGGNATNTTAATGAACCGNTGCATGCA
AATCTTNTTTACTTCATNTCCTGTCAGGGCATACTTAANTNTGTTCCTCAGGAAAATGAT
GAGGGGGAGACACTNTCTNAACTTGNGGGGACCNGGTGGATGGACG
Sequence 1481

TACCAGTGGCCCTGGTGGATGCACCATAAATGAGGAGCCTGGGAGCCTGGCCAGGTTTCT GCTGGTACTGTTAACAACCGGTATTAGAAATTGAGATGTTTTTATTTTGACTATTTGAGA GTAACATTGTAGATAATGTTCCAAACCATCATCAAAAAATGCAGAGCAAACTTTTCTGTAT ATAAACTGTACCTGCCCG

Sequence 1483

Sequence 1484

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Sequence 1485

Sequence 1487

Sequence 1488

AGGTACAGTGGTTAAATAATTGACTCAATGACAAAAGTGGGATTGGAGTCCCAACAGTGT GGACATGCTTTGGATTGAATGTTTGTGTCTTGCCCCATATCCCAATGTTACAGCCC TAACCACCAATGTGATGGTATTGAGATTAGGGCCTTGAGTACCTGCCCG

Sequence 1489

Sequence 1490

TACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACATTTTGTTCCACCAAG
TTATCCAAAACACCAGTGAGGAAATCTTTGCCCAGGGATTCCAACACCTTAAAGTGGGCT
TTTTTTTGTGGGTTGGCCTTCTGCCATAGGGAACAGCCTCCGTCCTTTTTTACAGCGTTG
GAAAACCCCGCGTACCTGCCCGGGCGGCCGCTCGAATCA

Sequence 1491

Sequence 1493

Sequence 1494

Sequence 1495

ACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTGGAGGAAGTGAAGTCC CTATGCTGACCCCAATACTTGCAGAAGGTGATTCTGGCGGCCCCTTGATAGTTCACAAGA GAAGTCGTTTCATTCAAGTTGGTGTAATCAGCTGGGGAGTAGTGGATGTCTGCAAAAACC AGAAGCGGCAAAAGCAGGTACCTGCCCG

Sequence 1496

CACTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCAACTGGCCTCAT
CCTATATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAACGAACTGTGGCTGCACCA
TCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTG
TGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACCTGCCCG
Sequence 1497

GGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCGCGGGAGCTTCTCCTTGCCAGT
TTCTCCCAGCANGGACCCTCTTCTTGTTTTGAAAGATGGTCGGCTGCTTTTGGTAGGCAC
GCTCAGTCTGAATGTCCGCCATCTTCCCGGCCGCTCTAGAACTAGTGGGATCCCCCCGGG
CTGCAGGAAT

Sequence 1498

ATCATACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGGGCCATT ACTGCAGGAAAAGGTCCCGGAGAGCTAAGCAGTCAAGATGTGTGACTTCACCGAAGACCA GACCGCAGAGTCAAGGAGGCCTTCCAGCTGTTTGACCGAACAGGTGATGGCAAGATCCT GTACGTGCCAAAGCATCCTCGTGCGACCGCGAGAGCCCGGGGAGCGGGGGCTTGC Sequence 1500

TACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTATATCAACCAGAGCA
ACATACATGAATAAGCCAGCAGTAAGTGCAAATATCCACATAGAAACATTTTCAGCATAA
TGACCAATGAAAATTCCTGTTGCCATTCCAAGATACGCCAGCATGGCTGACAATGCATTA
TAAAGGACAGCCTGCTTAACGGTCATGCCAGCCTTTAGTAGAACAGCAAAGTCACCTAAT
TCATGAGGCAACTCATGACAGAACACAGCAACTAGCTCGCCGGGCGCCCCGG
GCAGGTACAAGGGATTGATTTAAACCAAATTCGAGGACTTGGGTTTGATGCCACCGTGTT
CTCTGGGTTGTTTTGGATAAAGCAGTTTCACCCATTACCAGTCAACCAGGAAGGGGGATT
CCCATCGAAACGTCATCATGTGGCTGGACCATCGA

Sequence 1501

Sequence 1503

Sequence 1504

Sequence 1505

CTTAGGGCGAATTGGAGCTCNCCGCGGTGGCGCCCCGGGCAGGTACATTCAGGACAA
GGATGGCGCTCCAGTGGCCACCAATGCCTTCCATAGTCCCCGCTGGGGTGGCATTATGGT
ATATAATGTTGACTCCAAAACCTATAATGCCTCAGTGCTGCCAGTGAGAGTCGAGGTGGA
CATGGTGCGAGCGATGGAGGTGTTCCTGGCACANGTTGCGGTTGCTCTTTTGGGATTGCTC
AAGCCCCAGCTGCCTCCAAAATGCCTGCTTTCAGGGGCCTACGAAGTTGAAGGGGCTAAT
GACCTGGGAGCTAGACCCGGCTGCTCTGGGCTCAGTGGGAGAACCTGGCCACAGCC
ACCACCACCCTTACCTCCCTGGCGCAGGCTTCCGGGCCAAGATCAAGCAACATTTGTCATT
AAGGACGACGTGGCATCTGAGGTGTACCTCGGCCGCTCTAGAACTAGT
Sequence 1508

CTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCACCAGGGCCACTGGTA
Sequence 1510

TAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACAGATGGGGGTCTCACTACAT
TGCCCAAGCTGTGCCAGAATTCCTGGATGCAAGCAATCCTTCTGCTTTGGCCTCCCAAAG
TGCTGGGATTACAAGCATGAGCCACCATGCCCAGACAAAGCCCTCAATTTCTTACATATC
GATTTAAGGGCCTGAATAAAACCAACACATTAAAAAGGAAAAAGAATAATTCACATACCAA
GCCGTGAGTAAATTCAAGACTGAGATGATATAATCGGTACCTGCCCG
Sequence 1511

Table I

AATTGGAGCTCCCGCGGTGGCGGTCGAGGTACATCATTTCCAGAGCAGCACTGGCAGC
GAGATAGGGTTGGAGGAGAAGTAGCGCCGGGACTTCCGGATGGCAAACTTCTCTGTGGGT
AGAGATTTCCCAGCAATCTTGAGCTTCAGGCCTGGCACAGCTCGAAATAATTCCACTTCG
TCGTCCCCGAACGGCTTGTGGTCCTCCTTCCCAAACATGCTGAGGTAGGCGGCCTTCATG
TAAATGTAGGTGGCCTTTTTAAGTCAGATCATGTCAGTTCCTTCTGGAAATCTGGTTATA
TTCCATCACACTCAGGAGACATCTCCTACAATTTCCTTGACACCTGCAGCACTCCAGCCA
CACGACGGCCCCCGCGTACCTGCCCG

Sequence 1514

Sequence 1515

CCGCGGTGGCGCCGNCGNACTCATTTACCCGGGGACAGGGAGAGGCTCTTCTGCNTGTA GTGGNTGTGCACAGCCTCATGCATCACGGAGCATGAGAAGACGTTCCCCTGCTGCCACCT GCTNTTGTNCACGGTGAGCTTGCTATAGAGGAAGAAGGANCCGTNGGAGTCCAGCACGGG AGGCCNTGGTTCTTTCCGCGTACCTCGGCCGCTCTAGGAACTANTGGATCCCCCGGGCTG CACGGAATTNGAATATCAAACCTTATCGATACCTTNCGACCTCCNNN Sequence 1516

ATAGGGCGAATTGGAGCTCCCGCGGTGGCGGCCGNCNGGCCAGGTACAGCCCACANANG GCTGATNGGCTTTTGNTGNTTNTTCTNGGAANATANTGATGAGTTCCTCNAAACNCNTTA ATTTTACCTCTTCCGGGACATCATCCTT

Sequence 1517

CCGCGGTGGCGGCCGAGGTACACTNTTNGTCAGGGGACCAAGCTGGAGATCAAACNAACT GNGGCTGCACCATCTGNCTTNATCTTCCCGCCATCTNANGAGCAGTTGAAANCTGNAACT GCCTCTGTTGTGTGCCTGCTGAATAACTATCTATCCCAAAAAGGCCNAAGTACCTGCCCG GGCGGCGGCTCTATANCTANTGGATC

Sequence 1518

CCGCGGTGGCGGCGAGGTACGCGGGGGGGAGCACTGCTCAGTTAGGACCCAGACGGAACCATGGAAGCCCCAGCGCAGCTTCTCTTCCTCCTGCTACTCTGGCTCCCAGATACCACTGGAGAAATAGTGATGACG

Sequence 1519

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Table 1

TTGCTTTACATAATTGAGTGTTTTTCAAAGGCATATAGAAAAGAAAAAATAGGCTTTTAT ATGTACCTCGGC

Sequence 1520

Sequence 1522

GCCGGGGAGAGGCGGTTTTGCGGTATTGGGCCGCTCTTTCCGCTCCTTCGCTCACTTGA CTTNGCTGCGCTCGGTCGTTCGGGCTTGCNGGCGAAGCGGGT Sequence 1523

CCGCGGTGGCCGCCCGAGGTACGCGGGGATCCAGAATACATTTCCAACAAGAAGCACTG GCCAAGTCAGCTTCTTCTGAGAGAGTCTCTAGAAGACATGATGCTACACTCAGCTTTGGG TCCCTGCCTCTTACTCGTCACGGTTTCTTCAACCTTGCCATTGCAATAAAAAAGGAAAAG AGGCCTCCTCAGACACTCTCAAGAGGATGGGGAGATGACATCACTTGGGTACCTGCCCGG GCGGCCGCTCGACCGCCTGGACCAACTTGTCGGAAACCACCTTTCTGATGCCGCCCACGG CAGCG

Sequence 1525

Sequence 1526

AAAAAGGCCAGCAAAAAGGGCCAGGAACCCGTA

Sequence 1527

GGGCGAATTGGAGCTCNCCGCGGTGGCGGCCCGAGGTCAATATAGGGCAGACAGTTTGCC TTCAGAAATTCAGAAATGCAGCTTTTGAGGGAGGTCAGCATCATTGGTCTCAGCTACCAT TTTCCTGCAGGATGTTNATAAATAGTTCCTGGCAAAGGAGGTTGCGTATAGGGTCCTACA

Sequence 1528

Sequence 1529

Sequence 1530

Sequence 1531

Sequence 1532

Sequence 1534

GAGCTCCACCGCGGNGGCGGNTCGTGGCACTCATTTACCCGGAGGCAGGGAGAGGCTCTT

TCATACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTGGGGTTGGGGAG
AACCCGTTTTGATTACAAGCAGATAATTATCTCAGTGAGATGGGGGTTAGTTCAAGGAAG
TAAGGAGGGGGGAGGATGTGAGGAAGTTAGAACAACCCAATGCTTATTTGATGGGCTGAA
TAAACTATTCCAGGACTGAACTATTTTTTGAGCACTGTGAGGTGGCACAGTAATTACCTGC
TTCAAAATCAACTGATACCAACATTTTTTATCTTTGTATCTTATCTCTGTACCTGCCCG
Sequence 1536

ATCTTTTAACTAAANGTAATNGTCACCATAATCTTATAGACAAAGCATTGAGGTTTATTG
AACTAATGCTGAAGGTAGTAAGTGGAGGAGCCAGGATGAGGTCAGAATCTGAGATTNTAA
CCATGCCTATGCTGTCACTTCTTACACTNTAAAATACCTCCATGCTCNTGTGGACACCTA
NGAACAANTGAATATTTCTATTCTTGTCCCAGGAATNTCAAAACATTAAACATGTTANACT
GTATTTTNGNTTACCATAANCCTTTCCAGGAGGAACAAGCACTAAACACAGTCTCTGGCT
TAGGATTTGGATGAACATATTCAAAAGCCATCTGCTTCCCAGCAATCATAATCATACCCT
TTGCTTTTGGCCACTATCACCAAGATCTCCANTAGTACCTCGGCCGCTCTACAACTAGTG
GATCC

Sequence 1538

CCGCGGTGCCGCCCGAGGTACCTATGATAATCATGATGGAGATCTGGGGAGGGGAGAAC
GTGGAAATGTCCTTCCGGGTGTGGCAGTGTGGGGGGCCAGCTGGAGATCATCCCCTGCTCT
GTCGTAGGCCACGTGTTCCGGACCAAGAGCCCCCACACCTTCCCCAAGGGCACTAGTGTC
ATTGCTCGCAATCAANTGCGCCTGGCAAAGGTCTGGATGGACAGCTACAAGAAGATTTTC
TATAGGANAAATCTGCAGGCAGCAAAGATGGCCCAAGAGAAATCCTTCGGTGACATTTAN
GAACGACTGCANCTGAGGGAACAACTGCACTGTCACAACTTTTCCTGGTACCTGCCCG
Sequence 1539

CGAGGTACGCGGGGCAGGTGATGTTTGTTTTCACGATGGTCTTCAGATGCCCACGTGGGC ACTGCTGAGAAAGCCACTTGGTAAAACTGATGCCGGAAATGGGGCTTTTTGGGATCCCTG CTCAGCTGCTTCTGAGTCCCAGCATGCCCTGGTTACCTATGGCCCTCTTTCCCATGGGAC CTGACCTATGATCGGCCCCGCTCCTAGGCGTGGTGACCAAGATGAAGATGCAGAGGACC ATTGTCATCCGCCGAGACTATCTGCACTACATCCGCAAGTACCTGCCCG

Sequence 1540

GGCCGCCGNGCAGGTACAGCATCNCTGGTGGTTTCAAAGAACGTAGTCATTCTTCTCAC TGCAACANTGTANGATAAGCANGGNAGATCTGTTATTTCCAAATTAAAGGTGATTAANAT ATATGGAGAGAGANCATGGCATGTGAGGTTTATAGGGCTAGANACTGNACANCCATGTAC AACCCANATT

Sequence 1541

TTAACTGGACAGGTCAATTATCTGAGCTGTGAAATCATTGTCTGGCACTACAGTTGAAT

CCGGGCAGGTACGCGGGGAGACCAAGGGCTAAAGCTGGGAGGTGAGTCTGTCACCTTGA GCCGGGCGAGCGCTGTGGGCCAAGCAGGGGTTGCAGGGCAGTAGGAGTGCAGACTGAAAA AATGCAGACCGCCGGGGCATTATTCATTTCTCCAGCTCTGATCCGCTGTTGTACCT Sequence 1543

CCGCGGTGCCGCGCGAGGTACAGAAGGGCCATGCTGTTATTACTCTTACACAAGGAGGCA GCCCTCGAGCCACAGGGTCCAGCTGTTGGCTATAATAGCCTACCGGTCTCTGATGATCAC CATGTTTCTGGAATTCAAGCCAGGAAGAAGCAGCAATCTGTCTTCTGGATTAAAACTGAA GATCAACCTACTTTCAACTTACTAAGAAAGGGGATCATGGACATTGAAGCATATCTTGAA AGAATTGGCTATAAGAAGTCTAGGAACAAATTGGACTTGGAAACATTAACTGACATTCTT CAACACCAGATCCGAGCTGTTCCCTTTGAGAACCTTAACATCCATTGTGGGGATGCCATG GACTTAGGCTTAGAGGCCATTTTTGATCAAGTTGTGAGAAGAAATCGGGGTGGATGGTGT CTCCAGGTCAAATCATCTTTCGGTACCTGCCC

Sequence 1544

Sequence 1545

NCCGCGGTGGCCGCCCGGGCAGGTACTGCTTCTATAAGAACGTGGTCCTGTATATTA TTGAGCTTTGGTTCGCCTTTGTTAATGGATTTTCTGGGCAGATTTTATTTGAACGTTGGT GCATCGGCCTGTACCT

Sequence 1547

CACTCCTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACACCTCATTGAGG
ATCTAATGGACCCCTATCTTCAGCATGGGGAACAGGGTATAATGTTCACCACCTTGAAGG
ATCTAATGGACCCCTATCTTCAGCATGGGGAACAGGGTATAATGTTCACCACCTTGAAGG
CATGTTACTACCAGAGTTCAGCGTGAGAAGCTTAACTAGGCTGCATAACAGCTTTGAAAAC
TGGATTATCTACTACAGAGTGTTATAAACACCATCTGGAGTCTTCCTGTAGTNGGCAAAAA
AAGAACAAGTGTTGAAATTTGGAAGGGGACTTTGTGTTATTTNAGGTTGTTAGAATGAGC
CTTACCAATAATAAGAAGCCCTTGAGCCCAGAAAAAAGGACTGTTTAGTTTAAAGGGAGG
ATTGAAAGGNAGNGTAAAAAAATCNNATTAGACCAGTTNTTGGCCGCTCTAGAAACTAGG
TGGGATCCCCCGGGCCTGCAGGGAATTTCGATNTCCAAGCTTATTCGATTCCGNTCTGAC
CTNCNAGGGGGGGGGCC

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Table 1

Sequence 1548

CCGGGCAGGTACCACAAGCTGTGTGTCTTTAAGCAACAGAAATTTCTTCCCTCACAGTTG CGGAGGTCAGAGAAACAAGGTGTCTGCAGGACCAACCTCTCCTCTGGATGCTCT AGGTGAGAATCTTTTCCATGCCTTTCTCTTAGCTTCTGATGTTGCCGTCAGAACTTCAGA TGGTGTTCCTTGGCTTCTGTCAATATTAATACATAAATCCTTTTCAGTCTCAGCTTCTC CTTCACATGGTCCTCCCCCCCGCGTACCT

Sequence 1549

Sequence 1550

AGGTACCAATTCTTCTTGAATGTCTAATTGAATTCAGCTGTGAATCCTTCTGGTTTTAG
CCCTTTTTTGTTGTTGTGGCAACTTTCTTTTTATAACCAATTCCATTTAGCTGCTTGTTATT
GGGCTGTTCATGGTTTCTACTGATGTAAGACGGTTGTATATTTTGAAGGATCT
ATCAATTTCTCTAGATTTCCTAGTCTGTATGTGTAAAGGTGTTCACAGTAGCCTTAAAT
AATTTTTAAATTTTTGTGGTATTGGTTGTAATATGTCCAGTTTTATTTCTAACTGAGC
TTATTTAGATTTCTCTTTTCCTTTTCTGGACTAATCTTACTAAGAATCAATTTGGTTAAT
CTTTCAAAAAAATAGCTTTTGGTTAATCTTTCCNATTTTTGGTTCCAATGCCATCCCG
CGTACCTGCCCGGGCGGCCGCCCGGGCAGGACTCAAGGCCCTAATCTCAATACCATCACA
TTGGTGGTTAGGGCTGAACATTGGGAAATNGGGGCAAGACAAACATTCAATCCAAAGC
AAGCATGTCCCCACTGGTNGGGACTCCAATCCCCTTTTGGCATTGAGTCATTAATTAACC
ACTGNACCTCGGNCCGTCTANAACTAGTGGANCCCCGGGCTGCAGGAATCNATATCAGCC
TAATCGATNCCGNCNACCTCNANGGGGGGGCCCGNNCCCACCTTTTGG

Sequence 1552

NACCTGTCCGTGCCAGCTGCATTAATGGAATCGGCCCAACCGCCGCGGGGNAGAGGCCGG TTTTTGCCGTATTTGGGCCGCTTCTTCCGCCTTCCTTCGCTCACTTGACTTCGCTT Sequence 1554

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Table 1

CAATTTCCACACAAACATTACCGAGCCGGGAGCATTAAA Sequence 1555

TTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGGGCTGAAAAGTGCG CCCTACGAAAGGACGGTCGACTCCGGCGGGGCCCAGGTGCCAATGGGTCATGTTTGGTTA GAAGGTGACAATCTACAGAATTCTACAGATTCCAGGTGCTATGGACCTATTCCATATGGA CTANTAAGAGGACGAATCTTCTTTAAGATTTTGGCTTCTGAGTGATTTTTGC GTGCCAGCCTAATGGCCACAGATTTTCTGATGATTAGTAAGCATTTATTCTTTTGACTT GATTATTTGTCTCCTTTTCATGTGAATTTTATTACTTCCCGTTTTAAACCCGTGGTACCC TTGCCCGGGGCGGGNCCGCTTCTANGAACTTAGGTGGGAATTCCCCCCCCGGGGCCTGC CAANNGAAATTTTTNGNATTATTCCAAAGGNCTTTTATTNCGAATTANCCCCGNTCCTNA ANCCCTTCTGAAAGGGGGGGGG

Sequence 1556

TAATITGCTCCCAACTGATTGTCACTTAAATGAAAATTTAAAAATGAATAAAAAGACATA CTTCTCAGCTGCAAATATTATGGAGAATTGGGGCACCCACAGGAATGAAGAGAAAGCA nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnGTTAAATTGCCGCCGCCTTGGG CGGTAAATCATGGGTCATAGGCTGTTTTCCTTGTGTGAAAATTGTTTATCCCGCTCACAA

Sequence 1557

TCCCCCGAACTTGATCAATGTATACAATGCTTACACATTCAAATATGTGCAAGATTCAAC AAGGAACACTCTCCACTGCTGTGCTTGAAGTACCTCGGCCCGCTCTAGAACTAGTGnnnn nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnCGCGCTTGGCGTAATCATG GGTCATAGCTTGTTTCCTGTGTGAAAATTGTTAATCCCGCTTCACAATTTNCACCACAAA CATACCGAG

Sequence 1558

CTATCACTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGGTCC CAGCTCCTGGCTGACTTCTAGTCTTCTGGTTGAAGCTGCGCCTTTAGATGACACGACCCT ACCCACCCTGTTTCCAGCGGATGCCCGGGCCTGGAGCCCACAGAATTCTTCCAGTCCCT GGGTGGGGACGGAAAGGAACCGTTTCAGATTGAGATGGCCCATGGGCACCACCACGCT CGCCTTNAAGTTCCAGCATGGAGTGATTGCAGCAGTGGATTCTCGGGCCTCAGCTGGGTC CTACATTANTGCCTTACGGGTGAACAAGGTGATTGAAGATTAACCCTTACCTGCTTGGCA CTAGTGGGATCCCCCGGGCTGCAAGGAATTCGAT

Sequence 1559

CCGCGGTGGCGGCCGAGGTACCCATTCCCTTGATGTCTACAATATCACCTTTCTTATAGA TTCGCATATATGTGGCCAAAGGAACAACTCCATGTTTTCTAAAGGCCTAGAGAACATATA TCGGGTGCCTCTCCTTTTCCCTTTGTGTTCGTCATTTTGGCGAATTACTGGAAAGATGG nnAGTGAGGGTTAATTGCGCCGCTTGGCGTAAATCATGGTCATTAGCTTGTTTCCCTGTG GTGAAAATTNGTTATCCCGCTTCACAAATTCCACACCAACCATTACCGAAGCCCGGGGAG CATTAAAAGTNGTTAAAAGCCCTGGGGGTGCCC

Sequence 1560

TANGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTTCAATGATAAAACCATTGA

Sequence 1561

Sequence 1562

Sequence 1563

Sequence 1564

CTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACAACTGAGCACATAGC ACCAGAATATTGGAACAGATGCTTCTCCAAAGCCAAGGGTTGCCTTACATTTAGAGTGGG AAAAGAGGAAAATGAGTTAGCAGAGGAGCAGCGGGGAGGGGGGGTAAATTACAGGACATAA TTTGCTTCTAAAAAATTTTGTGTTCGTGTTGTAGTTATATAATTAACTTTTCTATTGTACC TGCCCGGGCGGC

Sequence 1565

CGACTNCTATAGGGCGAATTGGAGCTCCCCGCGGTGCCGGCCCCGGGCAGGTACGCGGGGGGTTCCCAGGATGGTGATCCGTGTATATATTGCATCTTCCTCTGGCTCTACAGCGGGAAGAGATGGATCAAGAAGATGAAATAGAAGACTCCACCAATCATCCCCTTCACACGAACACCAATTTAACAACTATCTACATGCACCAACACAAAAGCTTCATCAATTTAACAACTATCTAC

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Table 1

ATGCACACACACAAAACCTTTGTAAGAACTCAAAATCAGATTAAGAAGAAACAACAAGAT GTGCTTGGTTTCCTAGAAGCCAACAAAATAGGATTTGAAGAAAAAGATATTGCAGCCAAT GAAGAGAATCGGAAGTGGATGAGAAAATGTACCT

Sequence 1567

CTATACGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCGTTTTTGTTGGTTTTT
TTCTCCCTCAAAGTGAAATGNNAGACTATTGTAGGGTTTTGAGCCAAGGAGTGATATTAT
CTGAATTCTGTTTTAAAAGGNTCATTNTGGCTCCTGTGTGGAGGCAGGGTAGCTACTTAN
AAACCAAGCCATCTCAGCCTCCCGATTTGTAAGAGATGTGGTCTCACTATGTTGCCCAGA
CTGGTCTTGAACTCCTGGCCTCATGTGATCCTCCCACCTTGGCCTNCCAAAATACTAAAA
TGATAGATATGAGCCGCCACACCTGGCCATAAGCTTCAGCCTTGAGCAGATACTTTCTAA
ACACTTTATATAGGGAAAAAAAACTAATTCTTTGCGTAGCCCAAGGTGTTCATTTTTGCC
GAGAATAACCGTAGCCATANGTGTTTACAATTACGTGGGTGGTAATTT
Sequence 1568

Sequence 1570

CGAGGTACCATCATGGCTTGAGTGCTCTGAAGCCCATCCGGACTACTTCCAAACACCAGC
ACCCAGTGGACAATGCTGGGCTTTTTTCCTGTATGACTTTTTCGTGACTTTCTTCTTGG
CCCGTGTGGCCACAAGAAGGGGGAGCTCTCAATGGAAGACGTGTGGTCTCTGTCCAAGCA
CGAGTCTTCTGACGTGAACTGCAGAAGACTAGAAGACTGTGGCAAGAAGAGCTGAATGA
AGTTGGGCCAGACGCTGCTTCCCTGCGAAGGGTTGTGTGGACCTTCTGCCGCACCAGGCT
CATCCTGTCCATCGTGTGCCTGATGATCACGCAGCTGGCTTCACTGCACCGCCAT
CTTTGGAGACTGCTCCATCAGTGCCGAGGTGTGTGGGCACCAGGCTTCACTGACTCACAT
TTTGGATTGCATACTGGAAAAGAACCAATCTTCTTGCTAGTAAACCAGCAACCCGGCTGT
ATACAGTGGTGACCCAAGCAATGGATATAAACCTAAAAATCTGANGGAAGGAAGGGTNG
AATACAGTANTTCTTGGAATCTGAAGTCTNCTATTTGATCAAGGTTATTTCCTG
Sequence 1571

CGCGGTGGCGCCCGGGCAGGTACATGATACATGACCCCAGGTTCCAGTGTAGAACC TGAGTCCCCCATCCCGGGCAGGTACATTGATATGTCTTGACTCTCCTGTCTACT TTTGCACACACCCTTAATTTTTAATTGGTTTTCTTGTAAATACAGTTTTGTACACTTTTG GTCAGGGGACCAAGCTGGAGATCAAACGAACTGTGGCTGCACCATCTGTCTTCATCTTCC CGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACT TCTATCCCAGAGAGAACAAAGTACCTTGGCCGCTCTA

Sequence 1572

WO 01/51628 PCT/US01/00798

Table 1

Sequence 1574

Sequence 1575

Sequence 1576

ATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTGGTGCACACCCCCACTCC CACGGTGTGGGTAGTGCCGTGAATTGGAAACCGCAGATACCCTGGAGGCCTGGTAGGCAG CTGACTGCCCAGCACTGGGCAGACTGATAGTCCGTAAGTCTGATGGCAATGACNACCTAT AGTTCTGAGGAAAAGGAAGGTGGAACTCAAAATTTCCTTGTGCTTGGACTTGAGAAAACT GNAATCTTGAAGGTTTGGCCGAAGTT

Sequence 1578

Sequence 1579

CCCGTTCNACCTCGAGG

Sequence 1580

CTATCATACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACAGG
AAAGAGAGAGCCTTCTGGTGAAAATCAAAGTCCTGGAGCAAGACAAGGCAAGGCTGCAGA
GGCTGGAGGATGAGCTGAATCGTGCAAAATCAACTCTAGAGGCAGAAACCAGGGTGAAAC
AGCGCCTGGAGTGAGAAACAGCANATTTCAGAATGACCTTGANTCAGTTGGAAGACTC
AATTATTCCCGCAAGGGAGGAAGCCTACTAGGAAGNATAGAATCGGAAAGAGAAAAGAGT
GAGAGAAGAAGAACAGTCTTAGGAGTTGAGATCGAAAAGACTCCAAGCTGGNGATCCA
AGAAGAATTTGTAGNAGAGGTGCAGGCGTTTANGCTTGGAGGGATTTCTTCCCCAGGGAG
GACCCCCAGACCNCCANTTTTTTGNAAAACCAGGAAA

Sequence 1582

Sequence 1583

Sequence 1585

GACTNCTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGAGCGGCCGCCCGGGCAGGTACC
TATGATTGAAAACAGTAGTTGGTCTATGACTTTTGAGGAGAGGGAGAACCGAAGATTACA
GGAGGCCAGCATGAGGTTGGAACAAGAGAATGATGACCTTGCCCATGAACTAGTAACAAG
CAAAATTGCTCTACGGAATGACTTGGATCAGGCAGAAGACAAGGCAGATGTGTTGAATAA
AGAGCTCCTTTTGACCAAACAGAGGCTGGTGGAGACTGAAGAGGAAGAAGAAGAAGAAGAAGAAGAAGAAGAACAGCTAGAAAAATTG
GAAATAAAGAAAGACTACAGCTATCATTGCTTGAAGTTATAAACAGGATCTTGTTCCGCA
GTTTGAAGTACCTCGGCCCGCTTCTAGAAAACCTAGTGGGATCC

Sequence 1586

Sequence 1588

Sequence 1589

Sequence 1590

AGGTACCTAATGAAACCCGTCTTTGGCCTGTGGCTGAGACGCCATCTGTAGGCGGTGAAA
TCTTTCCAGCCTATGTGACGAGGGTCATGCCACAGGGTGCGCACCTGAAGGAAAAGGAAA
AGGAAAGGTTGAAACACAGCTCCTTCAGGTGACAGAACAGATGTCCCATGGTGACCAAGG
ACCCCAGCCTCCATTGACTGTAAGAAGATGAACCACAGGCAACAATTAAGATCAACTTTC
AAATCCCTCCCTTGTCATAGACTCTCCTAAGCCCGTTCAAGAAACCTCTGCTTCTCTGAC
ACACGGAAAGAATGCTGGGGAAGAGGGTGAGTTTGTTTTTCATTAAAAGA
Sequence 1591

CTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTACNTGCNCATCAATGT ATGATGATGACTATTTGGCTTAAATGGGATACAATATTCGACCACGCTCAAGAACCTTNA

Table 1

GAAGCTTGACTGAAATTTCTAANACTGATATTTCTTACTGAAATGTGNCCTTTGGGTTTN AANCTGAGGTTNCTATNGTTTGCTTNCNACAGACATATGTTTGACATACAAAATATGGTA AAGATCCACTACTTNTGCAGAGGTATATTGGCCATATTATTCCCTTATNGGCCTGGATTN CCTCATCAATAGCACAATTCATTCAAA

Sequence 1593

CCGGGCAGGTACTACAATGAGACAGTTGGATCCATTTTTCCAGGGTTAAGCCTGCAATAC CTGAAGCTCCAGACCTGAAACCCAGAGCTCCTGCCAGCTGCTATGCCTGTGAACCTGTGG AAGACCTGAAGTACCT

Sequence 1594

TCCTGTGTGAAATTGTTATTCCNGCTCACAAATTCCACACAAACATTACCGNAGCCCGGA GGAGGCAATAAAAGNTGTTAAAAGCTCTGGGGGGTGCNCTAATTGAAGTTGAAGCCTAAA CATCACCATTTAAATTTGCCGTTTTNCGACTTCACCTTGCCCNGCCTTTTTCNCAAGTTC CCGTNGTAAAAACCCNTNNTTCCGTTGGCCCCAGGGCCNTTGCCAATTTTAAAATT Sequence 1595

AGGTACCTCATTACTGCTCCCCATGTGGCCTCCTTACCCAGGAAAATTATGAAAGTCTGA
ACTCAGTCTCTTTNGACACCATCTCAACAGGAGGGGAAGGGGCACCTCATTATTGCCTGG
CAAGGGAGGAAGTCTAGGTTCCTCACTCAGTCTTTGCTGGTGACACAGGATTCTTTGGGA
GGCCACTTCACCAGGCTCCACCCATTCAGCCCAGCAGGCCGTGCTTGGTTTGCGCTACTG
GCCTGGATCCCATATCCTGGGTAAAATGGTGAAGGGTGTGTGCAAGTGGGTGTGAGGT
CTGACCACAGTGCACAGCCNGNCACACAGGCTGCTTGCAGTTGGGGCTGGGCAGGCAGCT
CCAGATGCCAGCACAGATGCCTCCTTCATGTTGAAAGCNTGCCNGCTGGACTAGGC
Sequence 1596

CCGGGCAGGTACTGGGCGCAGATGGGCGACCGTCACAACACTACGGTCCACTGGACATGT CTGTTGCTGAGAGAACCACTGGGTGATGCAGGCGTTGCANAAAGCATGTTCACAATGAGG TGCCTGGTAATCGTGAGCTTCTCCTCATACTTGCCCCAGGATGATACAACTGACTCTGGT CTTGGCAAGGNTGAACCT

Sequence 1598

Sequence 1599

AGGTACATGTGTAGAAAGCAGTGGGAACTGTGATTTGGCAACATGTCAGCTTTAT AGTTGCCGATTAGTGATATGGGTCTGATTTCGATCTCCTGATGTAAACCATGCTCAC CCATATCCCACTATACAAATGCAAATGGTTGCCTGGTTCCATTTATGCAAGGGAGCCAGT ACCTGCCCG

Sequence 1600

Table 1

TGGATGCACCATAGATGAGGAGCCTGGGAGCCTGGCCAGGTTTCTGCTGGTACCTGCCCG

Sequence 1601

AGGTACGCGGGAGATGAAGGTGCGCATCCTCTCCGAGCGTAAGAAGCCTCTGGACATTGA
CTACATGGGGGAGAACAGCTCCGGGAGAAAGCCCAGGAGCTGTCGGACTGCACCA
GACTGGAAGNTCTGANAAAGTTCGACCCTNGATGGGCGAAAGCTTGAAAACAGCNNGNAA
ATATTGNAANATCAAACGGTNCCTGGTACCCTGCCCNNGGCCGTGCCCGCTTTTTAANA
AAACCTTANNNNNGGNANTTCCCCCCNCNCGNGGNCTTTGNCCACTGNGAAANTTNCNNA
ATTANATTCTNAAAGCCTTTTAAATNCCGAAATTNCCCCGGTNCNTACCCCNCTTCGCTA
NGNGGGGGGGGGGGGGCC

Sequence 1602

GACGGAAAGCTTAGATATGCCAACAACAGCAATTACAAAAATGATGTCATGATCAGAAAA
GAGGCTTATGTGCACAAGAGTGTAATGGAAGAACTGAAGAGAATTATTGATGACAGTGAA
ATTACAAAAGAAGATGATGCTTTGTGGCCTCCCCCTGGATAAGGGGTTTGGGCCCGACAGG
GAGNCTTGAAATTGTAATTTGGGGGATGAAGCACATATCTTTTTACCCACCATCAAAAAA
ATTAGGGTNTCTCTTTATTGGATGGTAAAATCCAGTCCAAAGGGATTCCTGGAAGGCCCT
TCGNAGGTATTTTTTACTTATTTTGGGTTACCCTCGNGGCNCGGCTTCTTAGAAACCTAG
GTGGGATTCCCCCCGGGGCCTGGCAAGGGGAATTTCCGAATANTTNAAGGCTTTATCCG
AATACCCGTTCGAACCCTCNAAGGGGGGGGGGCCCCCGGGTTACCCCCNAGCCTTTTTT
GGT

Sequence 1603

ACTATAGGGCGAATTGGAGCTTCNACCGCGGGGGCGCCGCCCGGNCAGGGTACTCCTTC
GTNATACCCATCTGGGCAGTCCAAGACACCATTGCACAGCTGGGATAAATGAACACATTT
GTTGGTACNCGGGATGATAATGTCCCGATCACCTTCGGCCAAGGGACACGACTGGAGATT
AAACGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGNTGAAA
TCTGGAACTGCCTTTGTTGTGTGCCTGCTGAATAACTTNTATCCCAGAGAGGCCAAAGTA
CCT

Sequence 1604

Sequence 1605

Sequence 1606

Sequence 1607

GGGGGCGGCCGAGGTACCANAACTTCTATGCACACCTCCCTGAGAGTCTGGGAACCTTCA

Table 1

CCGCTGACCTGTGAGATGTTCCCAGCAGGCATTTATGACACCAAATATGCTGCTGAGT
TTCATGCCCGTTTCGTGGCCTCCTACTTAGAATATGCCTTCCGGAAATGTGAACGGGAAA
ATGGGAAGCAGCGGGCAGCTGGCAGCCCACGCCTTACCCTGGAGTTCTGCAACTATCCTT
CCAGCATGAGGGACCATATTGATTACCGCTGCTGCCCCCAGCAACCCACCGTNCTC
ATCCCACCAGCATCTGTGACAACTTCTCGGCTTATGGCTGGTGCCCCCTGGGACCACAGT
GTCCTCAGTCTCACGATATTTGACCTTATCATTGACACTGATGAGGCTGCGGCAGAGGAC
AAGCGGCGACGG

Sequence 1608

TGGCCCGAGGTACGCGGGGGAGGAAGGACCTGGTAGTTTTGATGACCGCTGTCCTA GCAGATACTTGCACGGTTTACAGAAATTCGGTCCCTGGGTCGTGTTC

Sequence 1610

CGCTCACTTGCCCGCTTTCCAGTCGGGGAAAACCTGGTCGTGCCAGCTGCATTAAATGAA ATCGGCCAACGCCGCGGGAGAAGGCCGGGTTTTGCGGTATTGGGGCGCTTCTTCCCGCT TTCCTCGCTT

Sequence 1611

GTGTGCCACCGCCACTACCACTGATATGCCGAGACCCACTCCAGCCCCTTNCNTGGAGTA
NNGGCCGGNACCCAATTCATAGACATAATTTATCCANATAAGGTGAANTCTCAGTAGGGC
TTGTTNCNCTCTGAGCCCGCTTCTNAGNNAACCNTAAGNNGGNATTNCCCCCTCCGAGAG
TCNTGGCAANGGTAAANTTTNCNNATTANNTCCNAAAGCCCTTTTAATTCCGGAATAAAC
NCAAATTCNGGACNCCTTTNNTAGNGGNGNGAGGGGNGNCTCCCGGGTNTAACACCCCAAG
GACATTTATTTGGATTTCCCCCCTTNTATTANGGTTGGAAGNGGGGTNTNAAAATTTTNG
NCCNGCCCGGCCCCTTTNGNGNCCCGTTTAAAAAAANCCAAATTGGGGGGTCCCAAATTAAG
CCTTTGNTTTTATCCCCTTTGATNGGTTGNAAAAAAATTA

Sequence 1612

AGGCTCCCGCCCCCTNACNGAGCATTTCACAAAAAAATCGNAACGCTCCAAAGTTCAAGGAAGGTTGGGCGAAAAACCCCCGACNAGGGACCTATTAAAAAAGAATACCCCAAGGCCGTTTTTTCC

Sequence 1613

CCGGGCAGGTACTGGGCTCTGACCACTATTGGTTTTGAGACCACGATGTTGGGAGGGTAT GTTTACAGCACTCCAGCCAAAAAATACAGCACTGGCATGATTCACCTTCTCCTGCAGGTG ACCATTGATGGCAGGAACTACATTGTCGATGCTGGGTTTGGACCGCTCATACCAAGATGT GGCNAGCNCTCTGGAAGTTAATTTTCTGGGGNAAAGGATCANGCCTCAGGTTGCCCTTG TGGTCCCTCCGTTTTGACCGGGAAAAGNANGAANTGGGATTTCCTGGGATATTCCTANN

Table 1

GAACCCAAAAATTCAGNAAAGGGGGNAACCANGGTTNCCCCTTNGNGGACCCCGGCCTCC TTTANNANACCTTAAGGTNGGGGAATTNCNCCNCCTCCGGGGGCCCTTGGCCAAGGGGAA ATTTTTCGGAATTATTTCAAAAANNCTTTTAANTTCNGAANTTATCNCCAGTTTCTGAAN CTCTTNCAAAGGGGGGGGGGGCCC

Sequence 1615

CGAATTGGAGCTCCACCCGCGGTGGCGGCCCGAGGTACATCCAGAAATAGATCCAAGAAA TGGGGTGGTTGAGTGGGTCCGCACGAAATGCTTGATTATGTCAGCAACACCCCAACACTGT CTGTTTTCCATTTGNTGGTTTTAATCATAAAATTGTCAAGTGATNCNNGTTTTTAAAAAN AAAAAAAAAAAAAAAAAAAAAAGTACCTGCCCG

Sequence 1616

Sequence 1617

CCGCGGTGGCGCCGAGGTACAGGTTTGTAGCCTAGGAGCAATAGGCAATATCATGTAGC CCAGGTGTGTAGTAGACTGTCTCATCTAGGTTTGCGTTAGTGTGTCTATGATGTTGGCAC AAGGACAAAATCACCTAACAATGAATTTCTTGGCAGGTGTCTCTGTTAAGAAGACATGAC TCCAGTACCTGCCCG

Sequence 1619

Sequence 1620

Sequence 1621

Sequence 1622

ACTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACANGACTCCAAGTCC
AAAGCAAATACCCATGGCATGAACAAATAGGATGCCTAAGATTCTAACATTTGCTTCGGC
ATGGCTTTCCTCCTCACTTCCCTACCTCACAACAAGAAAAAATTTCCTAGATGGGACAAT
GGCAAGATATTGTGCTAATACATTTCATAGGATTTCTAGATGCTGGGCTATAACATCCAG
GTTGCAATTTGGTGACGGATTTTTTTATTTCTATTGCAAATGGACTACACTCCAAACACA
AAAAGATTCTTGCCATAGCATCCAAACATCCCTATGTAGACCCACACTTCCTCTCAATAC

Table 1

AGAAAGAGAATCACTCAGAAAGGACAAAGCTGGCAGACCAAGAAAGGAGGCAAGGGTAAA CTCTGTCACTGGCCAATTNTCTAAAACAAAAAT

Sequence 1623

Sequence 1624

Sequence 1625

ACTATAGGGCGAATTGGAGCTCNCCGCGGTGGCGGCCGAGGTACCAACATGTCCCGTGGT TCCAGCGCCGGTTTTGACCGCCACATTACCATTNTTTCACCCGAGGGTCGGNTCTACCAA GTAGAATATGCTTTNAAGGCTATTAACCANGGTGGCNTTACATCAGTATGCTGTCACCAG GGAAAGACTGTGCAGATNGTTGTCACACNNTAATTAAAGTACCTGCCCGGNCTNGACGAN CTATAANANGTGCAATNCGGAGCACNTTCACTGNNATGTTNCGCCGGAAGGCCTTCCTCC ACTGGTACCTGCCCGGGCGGCCGCTCG

Sequence 1626

GGGCCTGAGGTTTTACTCCNNAAAAGCANAGGAGGTGGCAACCTTGGCTTTGGGGTTTTGGCAGGCCCANGANAGGCAGNGGAGGANAAGCTCAAAGCCGGGTTTCATGTTTCACACCAAAGGCCCANGAATTGTGGGGNAGAAGGACCAAATCCCAGATNCCCCTTGTTTAGCACANCAATTTAGGNTTCACNAAAATTGTNNTNTTTTGGGCCAAAAAAAACCATGTTGGACCACNCTCATCCCATGGANTANATTTTGTACTTTAGATTCTCAAAGGAAAAAGA

CTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACACGCCTTGTTTCAAACT GTTCACTGTGATCTGTGGGTCTTTGAGTTTCAGTGAGTTTGCTGAAATGTCGAAGAAGTA GTTCCAAACTTCAATGTTCAATGAAATTTTTGTTCAAGTTTGAAATGGAGAGAGCAGCTT TAAAAGGTACCTGCCCG

Sequence 1629

TCTAAAGGAATAAGCTTGCGGCCGCTTAATTAATTTTTAGGCACATGTAGGGTGATCCAA ATTGGTCTGGGGTCAGGATTTGGCCCACAAGTCTATCAGTTTTAG

- Table 1

TTTTGACTTTAGGTTTCTTGAAGGAAGGGACCAAGCCTGCTTTTTGTCATCATTATATCC
TCACGGCTTAAGGTGTTAAGCCCCTGNTNCAAAAGAAGCCTTGGTTACCAGGGNAAAANG
GCCACCNTTTGTNTTTGTCAAAAAATATGAATTGTGGTTGGGGAATTGGAAAGGGGGGAA
GNGGGTTAAGGGCCAANAANTGGGGAATGGAAGTTG

Sequence 1630

Sequence 1631

Seauence 1632

Sequence 1634

Sequence 1636

Table 1

CTTGTGGCTTTNTTTGGGTNACCTAAAGTAAGGGNTTGGAACCAANTTTATCACCAAGTT

Sequence 1637

Sequence 1638

CCGCGGTGCCGCCCGGGCAGGTACGCGGGGAATCATTTTGCTTCCAACCCCATTTA GCCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAATTGAAGAATGAACA AACATTGAGAGCAGATGAGATACTCCCATCANAATCCAAACAAAAGGACTATGAAGAAAG TTCTTGGGATTCTGAGAGTCTCTGTGAGACTGTTTCACAGAAGGATGTGTGTTTACCCAA GGCTACACATCAAAAAGAAATAGATAAAATNAATGGAAAATTAGAAGAGTCTCCTGATAA TGATAGTTTTCTGAAGGCTCCCTGCAGAATGAAAGTTTC

Sequence 1640

CTTAGGGCGAATTGGAGCTCCCGCGGTGGCGGCGAGGTACGCGGGGGAGGAACTGCTC AGTTAGGACCCAGACGGAACCATGGAAGCCCCAGCGCAGCTTCTCTTCCTCCTGCTACTC TGGCTCCCAGA

Sequence 1641

CGAGCATTNACAAAAAATTCNGACGCTCAAAGTCAGGANGGTTGGCCGANAACCCCGACC TGGGACCTATTAAAAGGATTACCCANGGGCCGTTTTCCCCCCCCTTNGGAAAAGCCTTNCC CTTCGTTGCCGCCTTCTTCCCTTGGTTTCCCGAACCCCTTGGCCCGGCCTTTAACCCGGG AATTACCCCTTTGGTCCCCCGCNCCTTTTTCNTTC

Sequence 1642

CTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGGTCTTCATCTTCCCGCCATCTGATGAGCAGCTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGTTGAATAAC

Table 1

TTCTATCCCAGAGAGGCCAAAGTACCTGCCCG

Sequence 1644

Sequence 1645

AGGTACACTTTNGCACCTGCAAATCTGTTTATTAATTAGACCATAGAATCTGTGTTTCAT
TGGTGGTCAGCTGGCCAATCTGATGGTCTTGTCATACACAGGTAAGAAGAAGAACAAAGAGC
CAAGAGTTTGTTTGGAGGCCGGAGTGAGCTTGACAGAACTAGATGAAATTGGCCACTGGG
CACTGGGACCCAGAAAGGCCTCATTGCCACAGAGTTGCAACAGAGTGTGGGGTCCCATTA
TCAGAATCCTTTCTATGGTGCATCCAATTGGCTATGACTCTCCTAAGAACAGCGCTGCAG
GAAAATGCAAGTTCACAGGATAATGAATGCACTGTTGCTTCTCT

Sequence 1646

Sequence 1647

TACTCACTATAGGGCGAATTGGTAGCTCCACCTGCGGTGGCGGCCGAGGTACACGGGGAC CTCANAGCTGAGCTGGGCATGAGNAGATGCTCAGTAAGTGGTAGCACAGGGTTGGTCCCT ACGGTGGAGGCCCCCTAACACCG

Sequence 1648

Sequence 1649

Sequence 1650

Table 1

GCTCAACTGGGAACTCTTTGAAGGCTAGGGCCATCAATTACATTTTTTGTTTCTTCCA
Sequence 1651

Sequence 1653

Sequence 1656

CCGGGCAGGTACCTGGTAATTTACAGAACGTTCGTTATCAGATTTGATAATTATATTA AGGTTGTAAAGAATGTGTATGCCAGAATTATAGGTAGTAGATCCTAGATTCTTAGGAAAA ATAGTTTCTTATAATCTTTTGAGTAGTGGAAATGGTTACTTTTACAATGGTTATGAACTG GGTCAAGGCAAAAGGGCCACTATATGTCTTCAGTCATCTTTCTATGCCTGAAATCCAGGA AACAGTGAAAATGGATGTTCCCTGGAACAGCCATTGCGATGCCATATGTTGGTCATTGGT GTCCTTAAAGTGTATCTCAGATAATTGTGTGTCTCCCT

Sequence 1657

TNACCGCGGNGGCGGCCGAGGTACAATTGATATAACAGCTTTGTTGCCACCCCAGGCTTT TCTGTGATGATGCCATGGGCCACATTCTGATCAAACTGCACACCCAGAAGGTGAAGTGTT GGCTCCAAGCGAGAAAAATTATTAAGTTTGGCACTTGAAACCCTGCTGTCCAAAAATTCT GAAAAATCATCCTGAAGTTCAAACTTGTGTAGAACTTCTCCAAGTAGATAGCCACTGGAA AATGCCTTTGCAAATGACTTGGGACTCACGGTCCGGGACACCTTCAACTCCTTGTTGAGC

Table 1

CACTGGCACAGGGATCTCCGACATGGTTCAGCCCGGTGCCTCATACCGCANGCGGGGGCT TAGAAA

Sequence 1658

TCCTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACACTTATAGTTGAGAGC
CAAGTCTCCCTTATCATTGGTGAATGAGAATGAGCTACTGAAAACAAAAGAGGGTCTTC
TACTCAGCCTCTACCCCTAATATTTATATCAGAAGCAGAGATTAACTGTCCTTACTCATT
CACACGTTAATGGAAGAAGGAAGTTTCCTAGAAAAATCCTCCCGCTCCACCCTGCAAA
CTTTATGCTTTTCTGTTACATAATCAGGCAGGGGCAAGACCTAAACTATTTTGAATTGGT
GGTGTTGAGGCTAAATTCTCTGCTATTGACAGAATTGAGAATGTGATCAATTTCAGAGTA
GCATGCTACAAATTTTGTCCCAATTTCAATGGGGAGAA

Sequence 1659

CTCCCCGCGGTGCCGCCCCGGGCAGGTCCCTNTGGTNGTNGCTCAGGAAGCTTTANA
NATATATGGCTATTTAATTTGCAAATAATACTTAGAACTGCAAAAACACGTTCACCTGGT
CTTGTTGAGAAAGAAATCATAAGTCCCCTGACTTAAACTCTCTCAATTGATGAAGTGACC
AGGATTACTCAGAGTGCAGTTATTGGCACCCCCGAAGCACCAGAGTCCAGGAAAGATGCT
TATCAATCTTTTGCCATTGGCTTCTACTTGCAGGTGCCTTCTCTACTATTCAATCATATA
CGATCATTGGAAAGACAAATGAACTCAAGAAAAGCAGCGAAACAGTACCTCGGCCGCTCT
AGAACTAGGTGGGATCCCCCCGG

Sequence 1660

CCGCGGTGGCGGCCGAGGTNCCCGGGGGATGCTGCCACCTAGGTTACTTGTAGGACCCTA
TACGGCAACCTCCTTTGCCAGGAACTATTTATAAACATCCTGCAGGAAAATGCAGTGAAG
TAGAAGAGACAGGGATATCCCAGAAGGTTATGCAAAACATCAAGAGAAGATGAGAGAGT
CTATATGTCAGAATACACATTTCCCACCTTGCCCAACAGTAGAAAAACATAAGAAGAGAA
AAACATTAAAAAATGACAAGGAAGTTAATGGAAGTCAGCAATGTGATGGTGTTTGGGAGG
TGGAGCCTTCAGAAGGTAATTAATGCCCTTGTAAGAAGAGGCCAGAGAGCTTGCGCACC
Sequence 1661

Sequence 1662

Sequence 1663

Sequence 1664

Table 1

Sequence 1665

Sequence 1666

ATACCAGGCCGTTTCCCCCTGGNAAGGCTNCCTCGTGGCGCCTCTCCCTGTTNCCGACCCCTTGCCCGNTTTTACCGGGAAANACCCCTGTTCCCGCCCTTTTTTTTTCCCCTTTTCCGGGGGAA

Sequence 1667

Sequence 1668

Sequence 1670

CCGCGGTGGCGCCGAGGTACACACTAGTTTTGTCATACCGTGAGGCAGTGTATTAAAGA GGAAATGTTCTGTCTTTGGGACCAGACAGACTTGTTTCCATAACCCTGATTGTCTAGCAC TTTATAGCTCTGAGTCCATGGACCACCACTTAGCCATCCCTACCATCAGTTTTTTGTAAA GAGCTATGTCAGGAATGTGGAAGGATTCAAGAGAGGGGCTTTTAAAGTGTCCATCACGACC TTTAACCCAAGGGGAATTAATGCAGGAACAGAAAACCCAAATACCACATGGTTCTCACTT TATCTGTAGGGAGCCTAAAACATTTGGAGGCCACCACCATGGGACCACCGAAGGGGGAGG CCAATTAGGACCCTACCTATTTGTAGGG

Table 1

Sequence 1671

GCGTTGGCGCTCACCTGCCGCTTTCCAGTGCGGGGAAACCTGGTCGTGCCCAGCCTGCA TTTAATGAAATCCGGGCCAACCGCCGCGGGGGGGAGAAGGCCGGTTTTGCCGTTATTGGG GCCGCCTCTTCCCGC

Sequence 1672

Sequence 1673

CCGCGGTGGCGGCCGAGGTACGCGGGGTAGATGGAAGAACTTGTGTGCTTAGACCT GACGCTGGGAGGAGATGCTGCCACCTAGGTTACTTGTAGGACCCTATACGGCAACCTCCT TTGCCAGGAACTATTTATAAACATCCTGCAGGAAAATGAGTCTATATGTCAGAATACACA TTTC

Sequence 1674

Sequence 1675

Sequence 1677

Sequence 1678

Table 1

Sequence 1679

TTCTCTTACTGATAGTAGGATATTTCTGCTTTAGTTATTGTCACCTTAAATATATTTTCA
ATGTTGAAATCCTCACAGCATGTTTGATGAAATCTAGTTTTCAAATTTTCTTAGGTATAT
TTCTGTCACGTTGGCATGATAACAAATGCAATAACCCAAAAGACCCCAAAAGCTAGTGTA
ATCCCTTTTGCAATCCAAGCATGAGGATTCATCTTCATGTTGACAGTGCGTGAATGTTCG
GTAGGCTTTGTCAAGCTTGCATACAATAAATTATATATGTCCCTTTTCTTTTAGGGTC
Sequence 1680

CCGCGGTGGCGCCCCGGGCAGGTACTTACAGGGGACCGCCAGGGGCCTCGAGAATCG
GTATCCTGAGTCCTCTTGAAGAGCAGTAGAGGTTGTTTCATTAAGTGCAAACACATTGTT
CTTAATTTGAAAACTGTGGGCAGAAACAGAAGCCCGAGACTAATTTTTCCATTGCTAACT
CTAGATTCTCGGCCACTGGAGTCTGAAGATACTCTCTTTGAGAATGCATATTATTTTGCT
CACAGCTAAAACATTTAAGTATCATAGCTGATCAGTGGAGTGAGATTAAAAAGGTTTCTT
TTTTGAATCATCAGCTAGAAGATGTACCCTCGGCCGCTCTAGAACTAGGTGGGATC
Sequence 1681

CCGCGGTGGCGGCCGAGGTACAGCAATGGCACACTCTATCCTAATAATGACATCCTGTAT
AATTTAGTATGCTCTGTATCTCACTTTAAATGTAGCATTAAGGATGAAGCAGTAGAAAAT
GAACGCCGGGCCTTTTAATAATGAGGCTCAGGTTTGCTATCTTAATTTCAGGAATTAGGA
ATGGGAGGGATGCTAAGGAGACTGTTTAAATTTTTAAAAAGTTCTCTCTATGCCTGATAC
AGATGCAAATTGCTTGCTCATTACATTCTTTCAGCCTTTTTAAACAAGTTTGCTAAAACA
ATCATTCTCTGGCATTAAGACAGCTTACCTGCCAAGCTTGGACATTTTCTATAACCCAA
Sequence 1682

Sequence 1683

CACTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACAGGGCTCTTGATA
TATCCTGGCCTTAAGTCTCAGGTTCTCCAACAAAGCTGGCAGCCTGTGGTATGCCTTCTG
GGGCCAGAGAGTGTGGCATGATCCGAGGTCCTCAATGAGCCCATCATA
TTGGCTTAACCAAAGCCAGTGGTCTTCAGGA

Sequence 1684

Table 1

TTTTCTTTTTTTTTTTTTTTTTAGTAAAAGG

Sequence 1685

Sequence 1686

TAAAGATACCAGGGCCGTTTTCCCCCTGGAAAGCTCCCTTCGTGCCGCTTCTCCTGGTTC
CGACCCCTTGCCCGCTTTAACCCGGAATACCTGGTTCCGCCTTTTTCTCCCCTTTCGGGG
AAAGCCGTTGGGCGGCTTTTCTTNAATAAGNCTTNAACGCCTGNTAGGGTATTCTTCAA
GTTTNNGGTGGTAAGGGTTCGGTTTCGGCTTCCCAAAGCCTTGGGGCTTTGGTTGTTGGCA
ACGGAAAACCCCCCCGGGTTTCAAGACCNCNGAACCCGGCTTTTGNCGGCCCNTTNATTN
CCCGGGTTAAACCTTATTCCGGTCTTTTTGGAAGGTTCCCAAACCCCCGGGGTNAAGGA
ACAACCGGAACCTTTAATTCCGGCCCCACCTTGGGGNCNAGGCNAAGGCCCCAAACTTGG
GGNTAAAACCAAGGGGAATTTAAGNCAAGTANNCCGGAAGGGGTTAANTGGTTNAGGGGC
CCGGGTTNGNCTTANCAANGAAAGTTTTCCTTTGGA

Sequence 1687

Sequence 1688

GACTCCTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACAGCATGGATAAT TTAGATGTGACTCTGGACAGAGGGATGGATCAGATGACTTCTTAAGTTATCTTCCAGTTT AGGAGTTCGTAAACTATACTTTCTCCTTTCCAGACTATCCTAGTAAGAAAATTCTCTTTT AAGACAGAGTAGAACTCTGGAATTCATCAGTTTTGATGTTTCTTAAAGTGTAATCTAAGA TAGTGCTCCTGTATTAAGTTCTGATGTCTGACCATTGTTCAAATAAAGAGTAAAATGCAA

Table 1

ATGACAGGAAATTGGCTGTGTTCTGAATCCTATTTTTATTTGGGATAACAATAAGCCTGT ATGGTCACTGGTGACCTTTTGATTTGCTGTTTCTGCAACCTCACACTTGCCTCAGGATTC TTCTTCCACTTCTTGCACTTTATATTG

Sequence 1690

GAATTGGAGCTCCCGCGGTGGCGGCCGAGGTACAATATAGGCAGACAGGTTTGCCTTCA GAAATTCAGAAATGCAGCTTTTGAGGGAGGTCAGCATCATTGGTCTCAGCTACCATTTTC CTGCAGGATGTTTATAAATAGTTCCTGGCAAAGGAGGTTGCCCGTATAGGGTCCTACAAG TAACCTAGGTGGCCCCGCGTACCTGCCCG

Sequence 1691

GAGAAGGCGGGTTTGCNGTTATTTGGGCCGCTCTTTCCGNCTTCCTCGCTCACTTGACTC
GCNTGCGCCTCGATTCAATTCGGGCNTGATGGCAGAAGCCGGCTATNCAGCNTCACCTTC
ANAAGGGGCGGNTAAATTACCGGGTNTTATTCCCACCAAGGAAATTCAGNGGGGNATNAA
ACCCCCAGGGGAAAAGTAACCATTGGTGGAGTCCAATAAAAGGGCNCACNCCAAAAATAG
GGGCCCATGTNNAANACCCCGGGGNAATAAAAAAGNGGCCCCGGCCNGTTNTNGGCCTTG

Sequence 1692

Sequence 1693

GGGGCCATTGAGACTGCCATGGAAGACTTGAAAGGTCACGTAGCTGAGACTTCTGGAGAG ACCATTCAAGGCTTCTGGCTCTTGACAAAGATAGACCACTGGAACAATGAGAAGGAGAGA ATTCTACTGGTCACAGACAAGACTCTCTTGATCTGCAAATACGACTTCATCATGCTGAGT TGTGTGCAGCTGCAGCGGATTCCTCTGAGCGCTGTCTATCGCATCTGCCTGGGCAAGTTC ACCTTCCCTGGGATGTCCCTGGACAAGAGACAAGGAGAGGGCCTTAGGATCTACTGGGGG AGTCCGGAGGAGCAGTCTCTTCTGTCCCGCTGGAACCCATG

Sequence 1694

CGGCCGCCGGGCAGGTACAAGGGAGACAGCATGCAGGGTGTGTTCAGAAGAGCTTGCTG
AGGTGCTCGGCTCTTAGCATTAAAAATGTGATGTTGGTATATCATCCTGATAGAAAACAC
TGCTTTCCAAATCCTAGTCACTTGGATGGGAGGAAAGTAAGAACAGATTCTTCCAACCAC
TACTGATTTGTTATAATTCTCCCCATTGAAATTGGGACAAAATTTGTAACATGCTACTCT
GAAATTGATCACATTCTCAATTCTGTCAATAGCAGAGAATTTAGCCTCAACACCACCAAT
TCAAAATAGTTTAGGTCTTGCCCCTGCCTGATTATGTAACAGAAAAGCAT
Sequence 1695

GGGGCCATTGAGACTGCCATGGAAGACTTGAAAGGTCACGTAGCTGAGACTTCTGGAGAGACCATTCAAGGCTTCTGGCTCTTGACAAAGATAGACCACTGGAACAATGAGAAGGAGAGAATTCTACTGGTCACAGACAAGACTCTCTTGATCTGCAAATACGACTCCATCATGCTGAGTTGTGTGCAGCTGCAGCGGATTCCCTCTGAGCGCTTGTCTATCGCATCTGCCTGGGCAAGTTCACCTTCCCTGGGATGTCCCTGGACAAGAGACAAGGAGAAGGCCTTANGATCTACTGGGGGAGTCCCGGGAGGAGGAGGCAGTCTCTTCTGTCCCGCTGGAACCCATGGTCCACTTGAASequence 1696

CCGGGCAGGTACGCGGGACAGTTCTCTTTCCTCCACTAGACTGAGCTCTTCAGAGGAAGA CTCACTTGGCTGAAACCATGATTTTACTTTAAACACATTGAAAACCTCTACTGGAGTGCA TTGTGTCTGGTGGGCTTCAACCTTAATTCTTAAGTATGTGAAAACACATCACCTATCTGG AGGTTTACACTTTCTGCTAATGACTTTATTTTTAAGCCCACCACCCTAACACAAATA

Table 1

Sequence 1698

Sequence 1699

Sequence 1700

TGGAGCTCCCCGCGGTGCCGCCGGCCGGCCAGGTACCTCTGGTTGTTGCTCANGAAGCTT
TAGAGATATATGGNTATTTAATTTGCAAATAATACTTACAACTGCAAAAACACGTTCACC
TGGTCTTGTTGAGAAAGAAATCATANGTCCCCTGACTTAAACTCTCTCAATTGATGAAGT
GACCAGGATTACTCATAGTGCAGTTATTGGCACCCCCGAAGCACCAGAGTCCAGGAAAGA
TGCTTATCNATCTTTTGCCATTGGCTTCTACTTGCANGTGCCTTCTCTACTATTCAATCA
TATACGATCATTGGAAAGACAAATGAACTCAAGAAAAGCAGCGAACAGTACCTNGGCCGC

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Table 1

TCTANAACTAGTGGATCCC

Sequence 1702

Sequence 1703

GGAGCTCCCCGCGGTGCCGCCGGGGGCCATTGAGACTCCCATGGAGACTTGAAAGGTC
ACGTAGCTGAGACTTCTGGAGAGACCATTCAAGGCTTCTGGCTCTTGACAAAGATAGACC
ACTGGAACAATGAGAAGGAGAGAATTCTACTGGTCACAGACAAGACTCTCTTGATCTGCA
AATACGACTTCATCATGCTGAGTTGTGTGCAGCTGCAGCGGATTCCTCTGAGCGCTGTCT
ATCGCATCTGCCTGGGCAAGTTCACCTTCCCTGGGATGTCCCTGGACAAGATTTTACTCC
CATAACCCAGGCAGAAGTACCTCGGCCGCTCTAAANCTAGNGGGAATCCCCCGGCCCTGN
GGNAATTTCNATNNANGCTTTTTANTNANNCCCNNCAAACCTTNTNNGGGGGGGGCCC
Sequence 1705

CCGGGCAGGTACAAGCTATCAAAGGCGGCAATTTTCTCCTGCAAGACTACGACAAGGATC CGTTTATTGCAATGGAGATCATAAATAGGTGTCTTAAATTGAATGGACTTGACCATCTCC CCAGTACTCTGCGTTGTTACCACTGCTTCCCGCGAACTCTGCGTTGTTACCACTGCTTCC CGCGAACTCTGCGTTGTTACCACTGCTTCCCGCGAACTCTGCGTTGTTACCACTGCTTCC CGCGAACTCTGCGTTGTTACCACTGCTTCCCGCGAACTCTGCGTTGTTACCACTGCTTCC CGCGTACCT

Sequence 1706

Sequence 1707

Table 1

TTAAATAGCCATATATCTCTAAAGCTTCCTGAGCAACCAGAGGTACCTGCCCG Sequence 1708

CCGCGGTGCCGCCCGGGCAGGTACGCGGGAGGCATGAGCCACTGTGCTCGGCCAAG
ATTCTCTTAAATTCATCTTTTGCTTTTATTTCCGCTTACCCTGCTTCAGACTAACTTCT
CACCGTCAATCACAGAATTGGTTGGATAGTTTGCTTTCTTGCTAATTTTGCCTTCTTTCA
CTTGTTCTCTATAAATTGTCCAGACTATCAGATAAAATCCAAATGTTTCATCCTTTGCAA
CTGCTCATATACTGTCTAACTTAGTGAAACAAACTGCTTTCATTGTTATTTGTTCTTCAG
AATACTACCTCCTAAGTAAATGGTACCT

Sequence 1709

ACTNCTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCGTTCCTCCAGTG CCCAGAGATGCTCTCCGCACCAAGCCACAGATGTGGAGGAGGCAGATGGCCTGTGAAAAC TGAAGGCAATTTGGAAGGCATTTTTAAATTCCGTGGAGCCACTGGAGAAATGTTTACAGG AATGATGCCTTAAAATTCCTCAGTGGTAAGATCTGAGTACCTGCCCG Sequence 1710

Sequence 1711

CCGCGGTGCCGGTCATTCTCCGCTCATTGCTGCAGGTGCTGATCCCCCGAG ACTGGCTGTTGCGCCTGTTTGGTCGCCGCCGGCCTGGGTTCCACCCTGCGTGGCGGGCTAT TCGCCTTGCCGGGGATGATGTGCAGTTGCTGCGCCGCTCCGGTGGCGGCCGGTATGCGTC GGCAGAAGGTCTCGGTGGGCGCGGCGTTGGCGTTCTGGATTGCCAACCCGGTACTGAACC CGGCGACACTGGTGTTCATGGGCTTTGTGCTGGGCTTGGGGCTTTACCGCGCTGCGGTTGG TGGCCGGGATCGTGCTGGTAGTGGGTGTTTCGCTAGTGGCGCAACGCATCGC Sequence 1712

Sequence 1713

Sequence 1714

TCGACTACTTAGGGCGAATTGGAGCTCNCCGCGGTGGCGGCGGCGTCACGCCACCCGAG

Table 1

Sequence 1715

TTAGGGCGAATTGGAGCTCCCCGCGGTGGCCGAGCGGCCGCCCGGGCAGGTACCTCTCCC
CTGACCTCCTTTGGCTAAAGTGCCTTTCAGATTTTATTACTATTGTTAACATTTCCAACA
GCCATTTTAACATTATTTTTACAAATTTGATGTGAATATTCCATATTAGAAATATGATTT
CAGAAGACAAAGAATTTGTTTGTGAAAATGCTAAGGACTGAAGCTGACAGAAATAACATT
CCTGCTTACAATGAACTTTTGCACGTATAGTAGAAAACCAGGAGCGTCCTCAATGTGCTC
CTTCACCCTATTGGCTGCATCTCCATGAGCCCCTGAGAAGGGAAATTAACACTACCTGCA
GAGGAGACAAGAGGCACCTGAGGACCCAGGAGGACCCACAATAAGTTGCTAAAATGAAAC
ATCTGTTACATTTGTGTTTAATTAGTAATATGTCTT

Sequence 1717

CTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACTTACAGGGGACCCGCCAGGGGCCTCGAGAATCGGTATCCTGAGTCCTCCTGAAGAGCAGTAGAGGTTGTTCATTAATTTGAAAACTGTGGGCAGAAACAGAAGCCCGAGACTAATTTTCCATTGCTAACTCTAGATTCTCGGCCACTGGAGTCTGAAGATACTCTCTTTTTTGAGAATGCATATTAATTTAGCTCACAGCTAAAACATTTAAGTATCATAGCTGATCAGTGGAGTTGAGATTAAAAAGGTTTCTTTTTTTGAATCATCAGCTAGAGATGTACCT

Sequence 1720

GAGCTCCCGCGGNGGCGGCCCGAGGTACACTTTCAAGACCAAAATGTAAATTTACAAAT GTGTCTCAGTAAGAAAAGTTACAGAAGCTGGGCCGGGCGCAGTGGCTCATGCCTGTAATC CCAGCACTTTGGGAGGCTGAGGTGGGTGGATCACTTGAGGTCAGGAGTTCGAAACCAGCC

Table 1

Sequence 1721

ACTNCTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCCTGATTAGTTNAA
TATAAAGACTCCGTAATTTTTACAATTTTAACAATAATTTTATTTCTTCAAGCTTGTTAG
NTNGGGATTGNATTAAAACTACAGTGTGTGACTTANAAAATGATAATGCTGCTTTATGGA
AAATGGATTATAGGTGGGTAAGACTTTCNTTTGCAAAAATTTGGGNAATTACCCATCAGT
NGTTAGGAACCCAGNTGAAGTCTANANGACAGATGATAGTATCTTATACTAGGTTGGGCT

Sequence 1723

Sequence 1724

ACTTAGGGCGAATTGGAGCTCCCGCGGTGGCGGCCGAGGTACCACATTTTCTTGATTCC
TACAATCTATTCTTCCTACAACAGCAACAGTAATTGTTTGAAATTATACATAAGACTTCA
TCACTATTTTGTTCAAAATTCTTAGGATTCTTCCCAATACTTTTAGGATAGGGCTCAATT
GCTTTATCATTGACTGCAAGGGCCCTGTGTCCTCTGAACCTGCATACCTATCCAAGTTTA
TCTCCAACACTATCCCACTGTATTACCCTACTCTGTCTACAAAGTCTTTTCTGTTCTTTG
AACAAACAAAATTTATTCTTACCTGAGGGTCTTGCATCCACACTCAGACCTTACTTGGTT
TTAGTTTTCAGAAAGGCCACCAAGGGACCATCCTATTTAAAACAGTCCCCATGGTTAGAT
CCCACCTCCGTCACCTTTTCCTAGTGAGTTTTCACCA

Sequence 1725

Sequence 1726

CCGCGGTGGCGCCCCGGGCAGGTACATGCCAGGCACAAGCTGGAGTCACAGATGCCA CACTGACTATCACATTGTCATACTCAGAGAGAGAAAGGTGTATACACCCAGTATTTT CTTATGTTTTCTCTATACTTCCATATCCCCACCCCCATTATCCCCGAGACATTTCCCAG TTGGGAAGTCAGTTGCTTATGGGAAACTGGCTGCAGGGGGATCAGCCCACCTGTAACACA

Table 1

Sequence 1727

Sequence 1728

Sequence 1729

CCGCGGTGGCGGCTGGATTCTTGACATTCATTAATATCTTGACAACTCAGCCCATCAGAG GTTCTTCGAAAGCCACTTCCACAACGGACCACAGCGATAAGATCCAATCGTATTGTCA CAGTCCTGACCAGCGTGGCAGGTATGCCTACCCAAAGCACACTCATCAATATCTTNGACA AGTTCTTCCATCTGCAGCTATGGTGAGGCCTTTAGGGCAGGAGCAGTAGTAAGTCCCCAT GGCATTGTGGCAGCTATGGGAGCAGGGATTCCCTGCTGCACATTCATCCTCATCAGCACA AAAAGGTCCAACTGAGTCTAAGGTAAACCCGGAGGGGCACTGATTCTGGCGATCTCCTTT GGATATTGAAGCATTGAATTTT

Sequence 1730

TTCACTCTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCAGGTTCAAATA
GTCAGCAGCTCATCATAATCAATGAGCGAGGACATAAAGTAGGAAAAATGCATCACCATG
GTGAGCAAGGAAAGCAAGTTATTGGAGGCACATGTTAACACATAAAATATAAAATTAATA
TGATCACACTGGAAAGGCTTGCCTGAGCCCACAGTTTGAATGCCTACAATAAGATGAGAT
GCACAACANAAAGCAAGAGAACCTGATCAAGTGGGTGACCTGGCCATGGGTGCTCTCATC
AGTGGGGGGACCCAAATGCTTATGTGGGACTCACCAGGTATCGAATTTANCCATTGATTA
GGGAGTGGTTTTGGTTGGTGGTGCNAGGAAAACTTTTNTTAATTCCAAATTGGAAAT
ACCAATTNGAAAACCTTTTAAAAAAAAATTAATTTGNTNAGGANTTCTTTTTACCACCCAA
GGCCCAAATTNGTCAATNTTTTGGCCGTTACCCTTGCCC

Sequence 1731

Table 1

Sequence 1732

CCGGGCAGGTACATGAAGGAGGGCACTANGGGGAGCTAANCAATTTGTGAGTTAGGTAGC CAAGATTCGTTGAGGTTGGAAGAATGAGGAAAGAAAGGGGATCTGTGGCAAAAATATGCT

Sequence 1734

ACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTTCATACTACTTTAAGT
TACCTCCTATTGGGGGCATTATAAATGGGTAAGCAGAGAACATCATGGAAAGACATGGAG
CTTAGTATATGCAAATGTTGAGTTACTCAGTGTAATGTGTGAAAAAGGAGTTTCATAAGT
TTCGGTCAGGGAAAGAAAGGCAGGGTCAAAAATTTCTGCTTGAGAAGTTTTGGGGAGCTT
GGGGAGACTTTAAACAGGGAGCAACACAGCGCCTCTGTACCTGCCCG
Sequence 1735

CTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGACAGTTTTGAGCACCTGCCTT
GTGCCTCAATGAATACTTGTTGGGTGATGAATGATATAAAATTCATCTTGACATTCAGCT
TAGGTTTGGAAGACAGTGTATGATTTCTTTACCATGGCCTTGACTCATCTTCTGAATGGT
CAGGCTAAGTGCTGCCTCCTTCTCTGTGTAGCCTATTCAGGCACCTGCTCACCTACCACA
ACCTGCCAGGCCCCTCCAGCTCTGGAAGCATGCTATGTGAGAAATAATCCTAATATCCAA
GTCACAGACAGTGGGTGGGCTTGGAAGTGCAGGGCCTGTGATCCCTTTGTGGAGTAGCTG
AATTTAAGAAGTTGACAGCAATTGTGTTCTATAATGAGAATGGTCCTGATCATCATGGAG
GAATAATAGCTGCCTTTTTATTGAGAAACTGTCAGGTACCTGCCCGG
Sequence 1737

TTAGGGCGAATTGGAGCTCCCGCGGTGGCGGCCGAGGTACGCGGGATCAAACATCTTGT
TATACTTTGTAAACATTTTCTTTTTTTTAAACCCCAGTTCCAGCCGGACGCCCCCAGACCT
CTGAGGTTCGAGGAGGTGGTGTTTCATTTGGGGCTTTGCATATTTGGTTGTTAGGTTT
TGCGAGANCCTTTTTNATTTNGCCCAGACGTCTTNATGCCGGNGGTGAAANTTNCACTTC
GGGCNCCCCTCCCCTGGAGNTCTTTTGTGTGCCGCNGGAANTTCAGTGGAAGATCCGGTT
TACTNAGCGATATAGGAGGGATNTATANCTNNNNANTTCNNNNNTTAANTNTATTTGTTC
CTTGCCCGGNGNCGNGCACNCNTNNACTGCCCGCTTT
Sequence 1738

AATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGATCAAACATCTTGTTATACTTT
GTAAACATTTTCTTTTTTAAACCCCAGTTCCAGCCGGACGCCCCCAGACCTCTGAGGTT
CGAGGAGGTGGTGTTTCATTTGGGGCTTTGCATATTTGGTTGTTAGGTTTTGCGAGAG
CCTTCTTTATTTTTGCCAGACGTCTCAATGCGGGGTGAAGTCCACTCGGCCCCCTCCCCT
GAGTCTTCCGTGTGCGCGGAATTTCGAGGAGATCCGGTTACTAAGGGATATAGAGGAAAAA
AAAAAANTTAAAAATTAAAAATTAAAAGGTACCTGCC

Table 1

Sequence 1739

CTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGGGTATGATGGAAG
GAAGAACTTGTGTGCTTAGACCTGACGCTGGGAGGAGATGCTGCCACCTAGGTTACTTGT
AGGACCCTATACGGCAACCTCCTTTGCCAGGAACTATTTATAAACATCCTGCAGGAAAAT
GCAGTGAAGTAGAAGAAGACAGGGGATATCCCAGAAGGTTATGCAAAACATCAAGAGAAG
ATGAGAGGAGTCTATATGTCAGAATACACATTTCCCAC
Sequence 1740

CTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCAACATACAGTTAAGCTA
CTTAAGTTGTAGTGACTTAGGACTTAATTATCTTATAGGATAAAATAAAAACTTTAATCC
TAAACATTAGCCATTGCATTAAATGCTTTAAAGGAACAACTGGCTTTGAGCTCTGTTCAT
CCATGCAAGGATTATACAATCTCAGTGCTCTAGCTAAATTGCTAATGTTTTATTACTAAT
GCACTGGTAAGCCTCTCATAGAAGATGGGTCTCTTGGATTTACACTGAAATATAACTTTT
CTCTTCCATATTATTGGAAGACCTTATTCTTCAGGCAGGAGCTTAGAAAGTCTAAATTAT
GCACCAGAGCCTTAATTATCTGATGGCAAAAACCACGATACTCTGGTCACTACCAAT
TGACAATNAGAGGACCCCAATTAAAAACTCTAGAAATATTGAGTCCTGAATACCAG
Sequence 1741

GGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACGAAAGATGATATACATGAAAATGA CTTGAAAATTCGTTTCTCTACTTTTTTTTTAATGTAACACAAAGTAAATGAGAATCTGAG TATTTTATCAAGTTGTTTCAATGAAGACAGAGTTGATTCAGAAGGTAATTCCCAGATTGG ATGGTATGAGTTTCCGGCAAGATTAGAGAAAGAGTTTTTCTATGTAATAACTGATATTTG TTCACATGCTTCCTCTTGATGGCTCATCAGGATTTTAGAGATAGAAAGGACATNTTATCC AACCGCTTTCATTTTCTTAAAGAAATTGGGGACCGGGCGCAGTGACTCATGCCTGTATTT CCAGCACTTCGGGAGGCCGAGGCAGGTGGATCCTAGGTCAGGAGTTCAAGACCAGCCTGG GTCAAGAATGATGAAACCCCCGTCTCTACCAAAAAAA

Sequence 1742

Sequence 1743

Sequence 1744

Table 1

Sequence 1745

Sequence 1746

CCGCGGTGGCGCCCCGGGCAGGTACAGCTGGACAGGGATATAAATCAGTGAACTCTG
AGAACACTTTTAATCCAAGCACCAAATAAGGCAGCATTTCCTGTGACTGCTGGACGCCAC
GGTTTAAGTGAGATGCCAAACATTCCTCATTTGGGAAAATGCGCAATAGTCCACAGAGAG
AACAAAATCAAAATGTGAAAAGTTGAATAAAAAAACACTCCTTTGGAAATAAAATAATTACT
CAGCATAAGTTAGCTGACCTCATCTTTGGGACTAGAAAAATAACAGTAAATAATAAAT
AGCTCCCGCGTACCT

Sequence 1748

AGGTACATCTCTAGCTGATGATTCAAAAAAGAAACCTTTTAATCTCACTCCACTGATCAG
CTATGATACTTAAATGTTTTAGCTGTGAGCAAAATAATATGCATTCTCAAAGAGAGTATC
TTCAGACTCCAGTGGCCGAGAATCTAGAGTTAGCAATGGAAAAATTAGTCTCGGGCTTCT
GTTTCTGCCCACAGTTTTCAAATTAAGAACAATGTGTTTGCACTTAATGAAACAACCTCT
ACTGCTCTTCAAGAGGACTCAGGATACCGATTCTCGAGGCCCCTGGGCGGTCCCCTGTAA
GTACCTGCCCG

Sequence 1749

AGGTACATCTNTAGCTGATGATTCAAAAAANAAACCNTTTAANTTTANTTCNNTNNNCNA
NTTTTAANCCTAAAATGGTTTAACCTGTGAACCAAAATAATATGCATTCTNAAAGAAGAG
TATCTTCAGACTCCAGTGGGCCCGAGAATCTAGAGTTAAGCAATGGGAAAAATTAAGTCT
CGGGCTTCTGTTTCTGCCCACAGTTTTCAAATTAAGAACAATGTGTTTGCACTTAATGAA
ACAACCTCTACTGCTCTTCAAGAGGACTCAGGATACCGATTCTCGAGGCCCCTGGGCGGT
CCCCTGTAAGTACCTGCCCGG

Sequence 1750

TNCTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACAGCAGATAACTTATC CAAGGACAAATAGAAAGGGGACTGTGTCTAGAGGGTAATGCTAATGCCTGGCATGCTATA AAAATAAATGAAATCTGATTAACACTATTGGAGGGAAGAATAAGTCATCGTTTCTATGGA ATATTATTTTCCTGATTGGAACCATTTCCATTTTCGTCAGCTTAAAACATTGCATTAAAG

Table 1

Sequence 1752

ACCACTGCTTTCCCGGACTCTGCGTTGTTACCACTGCTTCCCGGGACTCTGCGTTGTTACCACTGCTTCCCGGGACTCTGCGTTGTTACCACTGCTTCCCGCGTCCT
Sequence 1753

CAATCTGTTCTGCTCACCAGCGAGTTGTTCGAGTTCATCGAAGACGGACACGGCGGCCAC CTGCTGAGAGTGGGGACCTCTAAATTTCCGGTCGGCACGCTGCGGTTCACCGCCCAT Sequence 1754

Sequence 1755

ACTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTGTTCGCTGCTTTT
CTTGAGTTCATTTGTCTTTCCAATGATCGTATATGATTGAATAGTAGAGAAGGCACCTGC
AAGTAGAAGCCAATGGCAAAAGATTGATAAGCATCTTTCCTGGACTCTGGTGCTTCGGGG
GTGCCAATAACTGCACTCTGAGTAATCCTGGGTCACTTTCATCAATTGAGAGAGTTTAAG
TCAGGGGACTTATGATTTCTTTCTCAACAAGACCAGGTGAACGTGTTTTTTGCAGTTCTAA
GTATTATTTGCAAATTAAATAGCCATATATCTCTAAAGCTTCCTGAGCAACAACCAGAGG
TACCTGCCCG

Sequence 1756

CTATCACTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACGC GGGTGAGATTCTGCTGGGTGAAGCCTAAGGGCATAGATGAAAAGTTAGGATTTGGAAGGG AGCCAGAAGCCAAAAGCAGTTCCCAGAGGCCAGGCAAAAACAGAAGCTGAGTGTGGGACT GAAGCCAAAAAGCGGAAGATGATGAATTCCACAGCGAACCGTGGGAGCCGTCCTGGAACA ATGCCTGAGATGCGCGCTGGCTTTCTGGGAGCAGTTAGGGCCCCTTTAGGTATGTGAACC

Table 1

CGCCTCACTAAATGGCCATGAGCAGAACTGAACTGCCTACCTGTTTCTCCACCTGTGCAA GACCAAGTTTTCTTAAGAANCCCAGACGAANGCTTCCTTTGAAAATNATACCGTTGCCAT TTGGCTTGGCCCCTTTGGCCTTAAAGCCTTAACAGGTTTANGGACTTTTGGGCCCCTGGG TTAAATTT

Sequence 1758

Seguence 1759

TGGGCCGCTTTTTCCGCTTTACTGACTTCGCTGCGGCGTTCCGGTTCNG GCTTGCNGGCGAGCGGGTATCAGCTTCACTCAAAAGGGCGGGTAATACCGGTTATCCACA GAATCAN

Sequence 1760

CTNCTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACAAGGATGAAATGAGT
GATTCTGTCCTTAACAAACTCCTAGTCTCGTGGGGTGGACAGCTGGGAACTCATTTAGAG
AGATTACAAGGATGAATACCCTTGGGCTCGATAGAGGTAGAAGCAAAGTGCTTAGTGTTA
GAGAGCGTTTCTTGAGGAGGGAAAATCAGAATCAGTCTGGGTTTTAGGAAGATAATTCTG
GAGGTTGAGTGAAAGATGAATGGAGAGGTGATAGACTAGCTTGGGCATTATGGAGATGGA
AGGAGAACGGAAGGGGCAGATAGGACAACTAATTGGAGGCCGGAGTGAGAGGAAGGGGCC
ATAGATGACTTCATGATTTCTGTCCTGGTTGCAATAAAGGGATCATGATCGTAAAGATCA
TTCCCATTTGACAAAGGGAAGA

Sequence 1761

Sequence 1762

CCGCGGTGGCGGCCGGGGCCATTGAGACTGCCATGGAAGACTTGAAAGGTCACGTAGCT GAGACTTCTGGAGAGACCATTCAAGGCTTCTGGCTCTTGACAAAGATAGACCACTGGAAC AATTGAGAAGGAGAATTCTACTGGTC

Sequence 1763

Sequence 1764

Table 1

Sequence 1766

Sequence 1767

AGGTACTTACAGTTTGACTTTGAGTCAGCTCAGCATTCTAAATCAAACGCAAACAGCAGA
ATCATATGGCATAGACACTTAGCAAATAGTTTGACTTTGAGTCAGCTCAGCATTCTAAAT
CAAACGCAAACAGCAGAATCATATGGCATAGACACTTAGCAAATAGGCAAGCGTCTCTGC
ATCCCAGAGCAAATCCTCTGAGATCCTCAGTCTCTCCTGCTGAAACTTCATCTTCCACTC
CTGCCTTTGGGTCATTTCCAAACGGCAGGGCACCAGACACGCTCTACCTTATGTGGAGCC
ATACTGTTCATTTATTAGTTTTCTGGCTTCGTGGAGAATTATCTGCCTTCTCTGAGTATT
GATTTCATTGTGCCCCCGCGTACCTGCCCG

Sequence 1768

Sequence 1769

Sequence 1770

CCGCGGTGGCGCCGAGGTACATGTGAATGGGAAACATTCATAAGTTCCTATTTGCCAAG GGCATGTAAATGTGATAAAGCGGATCCGAAGACACATGGGAGTGAGACTAGGAAAGTATT AAGAACATGGGCCTTGACCGGGCGCAGTGGCTTACGCCTGTAATCCTACCACTTTGGGAG

Table 1

Sequence 1771

Sequence 1772

TNNNCCNTCNGTCCTTTTNGGTTTGCNGCCGAGGCGGTNTTCAAGCTCACNTCAAAGGGCCGGGTTAATACCGGTTTATTCCACAAGAAATCAGGGGGATAACCGCAGGAAAGAACATTGT

Sequence 1773

AGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACAACTTGACAGTTTATAAAAAT
GCTAACCTATATCAACATTTTTCCCCACCAAAGTGTTCCCAAGGGCAAAGGTAAGTGAAT
ACATGTTTCCATGCTTGTGTCAGGGGCACACAGCAAGGGAAGGCAGAATGGGCATGACCT
ANATTNNANNCCNNAAAGCCTTCAAANTTCCTTTATTAAGAACTTGGGGACTGCATCTTT
AAAATAATATGGGTTTTNTTTTATTCTTTGATAATAAAAAGAATGGAACCAAATCCTGGG
TTGTCTGATTCTTTGCCCANTGCNTCTTTCTNATGTCTAACACTGCCTCGTCTTATGAAT
AACNTCTGNACATNTACAGAGGAAAGGACTTATTTGNNTT

Sequence 1774

Sequence 1775

CCGCGGTGGCGGCCGAGGTACTTACAGTTTGACTTTGAGTCAGCTCAGCATTCTAAATCA
AACGCAAACAGCAGAATCATATGGCATCGACACTTAGCAAATCCAATGCCTTCCAGGCAT
CTGTTTCCTGTTGATGAAATCCTCCCTATGGAGAGCAAACTGGTTCATATCTTCAGATAG
TGTCATCAACCCCTTGGCAGCTTTCTGGGCTACTAAATATCACACCGTCTGGTGGGACA
TTTCACCCAAGTTGTTCATTTATTAGTTTTCTGGCTTCGTGGAGAATTATCTGCCTTCTC
TGAGTATTGATTTCATTGTGCGCATGGTGAAGATATCGCCTGT

Sequence 1776

CGAGGTACGCACTTGTGTGCNTTTCTGTTGGGTATATAACAAGTATGATATTGCTGGGTC
TTAAAATATTTATATTAACTTCATTAAATGCTGCCTAAGAATTTTTCAAGTGGTTGCG
CTATTTTACCTTCACCAGCNCTAGNTGTTCCATATCCTTGCTGTNACTTGGCATNATCTG
TATTTTTTATTTTGACCAGACTGGTCTGTGTCATAGTATCCCATTGTCATTTTAAGTT
GCATGCCTTTGATGAAGACATTTTCTGATGCTTAATTGGCTCTTNGAATATATTCTGTAA
CTGATTTGTAGGAGTCCCNTTATATATTCTGGATATAAGNTTTTTTATTGGACATAAATA
TTGCANATATCCCTCTCCCACTTTAACTTGCCTTTT

Sequence 1777

Table 1

Sequence 1778

CTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCCCCGGGCAGGTACAAGGGAGA
CAGCATGCAGGGTGTTCAGAAGAGCTTGCTGAGGTGCTCGGCTCTTAGCATTAAAAAT
GTGATGTTGGTATATCATCCTGATAGAAAACACTGCTTTCCAAATCCTAGTCACTGGATG
GGAGGAAAGTAAGAACAGATTCTTTCCAACCCTACTGATTTGTTATAATTCTCCCCATTG
AAATTGGGACAAAATTTGTAACATGCTACTCTGAAATTGATCACATTCTCAGTTCTGTCA
ATAGCAGAGAATTTAGCCTCAACACCACCAATTCAAAATAGTTTAGGTCTTGCCCCTGCC
TGATTATGTAACAGAAAAGCATTAAAGTTTGCAGGGTGGAGCGGGAGGATTTTTCTAGGA
AACTTCCTTCTCTCCATTAACGTGTGAATGAGTA

Sequence 1779

CTACTTAGGGCGAATTGGAGCTCACCGCGGTGGCGGCCGGGTCCGGCGCATCCATGGCGA ACAGGCAGACGAACGCGCCTTGCTGCGCGCTGCTGGCGGCGCCCTGCGGCGCCAGCA CCGTGAATTGTGGCGCCGTCACCAGTTGCAGCAGCGGCTTGGCATCGGTGCGCAGCACGC GGCGCGGCTGGCGGCGCGGGCCCNGCGCCGCANCAATGGCGGGCCTGNAGTTCCAATNGG CAAGGGTGCGCGCGCGCNN

Sequence 1780

CCGGGCAGGTACAGCACCTTGTGTCCTGCCACCAGCCGGCTGTGAAACTGGTACGCGGGG
TAGATGGAAGGAAGAACTTGTGTGCTTAGACCTGACGCTGGGAGGAGATGCTGCCACCTA
GGTTACTTGTAGGACCCTATACGGCAACCTCCTTTGCCAGGAACTATTTATAAACATCCT
GCAGGAAAATGCAGTGAAGTAGAAGAGACAGGGATATCCCAGAAGGTTATGCAAAACATC
AAGAGAAGATGAGAGGTCAGAGATGGGAAGAACAAGAACTTTGACATGCTTGGTGTTCT
TGCCCAAGCTTTGAAGAAGTTTACAAAGTCTATATGTCAGAATACACATTTCCCACCTTG
CCCAA

Sequence 1781

Sequence 1782

Table 1

G

Sequence 1783

TTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACTTACAGGGGACC
GCCAGGGGCCTCGAGAATCGGTATCCTGAGTCCTCTTGAAGAGCAGTAGAGGTTGTTTCA
TTAAGTGCAAACACATTGTTCTTAATTTGAAAACTGTGGGCAGAAACAGAAGCCCGAGAC
TAATTTTCCATTGCTAACTCTAGATCTCGGCCACTGGAGTCTGAAGATACTCTCTTTGA
GAATGCATATTATTTTGCTCACAGCTAAAACATTTAAGTATCATAGCTGATCAGTGGAGT
GAGATTAAAAGGTTTCTTTTTTGAATCATCAGCTAGAAGATGTACCTCGGCCCGCTCTAG
AACTAGTG

Sequence 1784

NGCGGCCGAGGTACACTTATAGTTGAGAGCCAAGTCTNCCTTATCATTGGTTAATGAGAA TGAGCTACTGAAAACAAAAAGAGGGTCTTNTACTCAGCCTCTACCCCTAATATTTATATC AGAAGCAGAGATTAACTGTCCTTACTCATTCACACGTTAATGGAAGAAAGGAAGTTTCC TAGAAAAATCCTCCCGCTCCAC

Sequence 1785

Sequence 1786

Sequence 1787

GGTGGCGGCCGCCGGGCAGGTACAGATTGNGTCCACTGGAAAGGTAAATGATTGCTTTT
TTATNTTGCATCAAACTTGGAACATCAAGGCATCCAAAACACTAAGAATTCTATCATCAC
AAAAATAATTCNTCTTTCTAGGTTATGAANAGATAATTATTTGTCTGGTAAGCNTTTNTA
TAAACCCACTCATTTTATATTTAGAAAAATCCTAAATGTGTGGGTGACTGCTTTGTAGNG
AACTTTCATATACTATAAAACTAGTTGTGAGATANCCATTCTGGTAGCTCACTTAATAAA
AACAATTTCAGAATTAAAAGGAAATTTTCTATGCAAGGTTTACTTCTCANATGAACAGTAG
GACTTTGTACTTTTATTTCCACTAAGTGAAAAAAGAACTGTGTTTTTAAACTGTANGAGA
ATTTAATAAATCAGCANGGGTATTTTAGCTAATAGA

Sequence 1788

AACCTTTAGGGTTNTNCCCAAAGTCCCGGCCGNCCGGNTNGGGACTNGGGGGTTGAACAC
TTCGAAANTTTCANCTTNCGCACNACGAAANCAACACNNNGAGAAGGCAGATAATTCTCC
ACGAAGCCAGAAAACTAATAAATGAACAACTTGGGTGAAATGTCCCACCAGACGGNGNGA
TATTTAGTAGCCCAGAAAGCTGCCAAGGGGTTGAAAGACACCTATCTGAAGATATGAACC
AGTTTTGCTCTCCATAGGGGAGGATTTCATCAACAGGAAACAAGATGCC

Sequence 1789

Table 1

AAGGTAAATTCATGTGTTCCCCACTGCTGTGTCTAGAACCAAGATCACATTATATCATTG TTAAAATTGTGTTATCTAGAAAAGGTGCAATATAGGGGAAAACACTCTAAGAATCTTTTA AAAGCCTAGT

Sequence 1790

Sequence 1791

Sequence 1792

CCGCGGTGGCGCCGAGGTACATGCCAGGCACAAGCTGGAGTCACAGATGCCACACTGAC
TATCACATTGTCATCATCACAGAGAGAGAGAAAGGTGTATACACCCAGTATTTTCTTATGT
TTTCTCTATACTTCCATATCCCCACCCCCATTATCCCCCGAGACATTCCCAGTTGGAAGT
CAGTTGCTTATGGGAAACTGGCTGCAGGGGGATCAGTCCACCTGTAACACACGGAAAGGC
AGAGAAACAATGAGTCATGGATTTGAGTGCAAACAAGCCCAGTCCTGCTACAGAGAGTTA
CGGAAAAAATCTCACTGTTGAAGAGAGACATCTATAAGAGAGGTGAGGAAAATGACTGAT
AGATCCTTTTACAATATTCTAGGGTAGTCTGTCTGTGGGAGGGGGGGAGAGTCTATGGGA
ACTCT

Sequence 1793

Sequence 1795

CCGCGGTGGCGGCCGAGGTACTCTGCGTTGTTACCACTGCCTCCCGGGACTCTGCGTTGT

Table 1

TACCACTGCTTCCCGGGACTCTGCGTTGTTACCACTGCTTCCCGGGACTCTGCGTTGTTACCACTGCTTCCCGGGACTCTGCGTTGTTACCACTGCTTCCCGGGACTCTGCGTTGTTACCACTGCTTCCCGGGACTCTGCGTTGTTACCACTGCTTCCCGGGACTCTGCGTTGTTACCACTGCTTCCCGGGACTCTGCGTTGTACCACTGCTTCCCGGGACTCTGCGTTGTACCTGCCCGG

Sequence 1796

ACTATAGGGCGAATTGGAGCTCACCGCGGTGGCGGCCGAACATTTCGACATACGCCAGCA
TGTGATGGCCGAAGGTGATCGGCTGGGCCACCTGCATGTGGGTAAAGCCCGGCATGATGG
TGTCGGCATGCTGTTCGGCCAGGTCCGTCANCGCGCTGCGGAACGTCGCCAGCAGGGCGG
TGATGTCGTCGATGGCGGAACGCACGTTACAGGCGGGATGTCCGGTGGGCCACCTGGTCC
TTGCGCGAACGCCGGTGTGCAATCGCTTGCCCGCATCGCCTACCAGTTCGGTCAGGCGT
TTTTCGATATTAAGGTGGACATCTTCCAAGATCCAGCAGCCATTCTAAC
Sequence 1797

Sequence 1798

CGNATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTCAGATCTTACCACTGAGGAATTTT
AAGTTATCATTCCTGTAAACATTTCTCCAGTGGCTCCACGGAATTTAAAAATGCCTTCCA
AATTGCCTTCAGTTTTCACAGGCCATCTCTTACCCTGTGCTGTCTCTCCCCAGGATTTTC
TGAAGTTCCTTGTCTGCCTGAAGTNCAGACCTGCCTCCCACATCTGTGGTTTGGTGCG
GAGAGCATCTTNTGGGCACTGGAGGAACGGTACCTGCCCG

Sequence 1799

CTTAGGGCGAATTGGÁGCTCCCGCGGTGGCGGCCGCCCGGGCAGGTACTCACANGATCT GTTTCCAGAAACCACTACAAGTGTCATGAACCTTGGGTTGCTCTCTGATTGAATTCTGGG ATCCAAGCTGGGTAAGGAGAGAGAGATGAGTCCAGGCTGCTACAGAAGATTATTTTCCATAA TTTCAATATGAGCAGTTTTNAAACACANAAGGATTTNNTNGTCNATGTTAGCTAGGCCAG CCTTAACACTTCCTCTACCTCATTTCTTAGAAACCAACAAGGGCCTTTCCAGAGAGGGCC AAGGACGGTGGCATCCAGAAGGGATGAAAACACTTGAGTACCTCGGCCGCTCTAGAACTA

Sequence 1800

Sequence 1801

Table 1

TACAGAAGATTATTTTCCATAATTTCAATATGNGCAGTTTTAAAACACATAANGGATTTA
TAGGTCATGTTTAGCTAGGCTCAGCCTTAACACTTNCTCTACCTCATTTATTAGAAACCA
ACAAAGGGCCTTTTCCAGATGAGGGCCAAGGACGGTGGCATNCAGAAGGGATGAAAACAC
TGAGTACCTNGGCCGCTCTANAACTAGTGNGATCCNCCGGGCTGCAGGNAATTCGATATC
AAGCTTATCNGATACCNGTACGNCCTNTGAGGGGGGGGCCCG
Sequence 1802

Sequence 1803

TGGCCGCCCGGGCAGGTACGCGGGGATAATAAAAAATGTATTTACTGAGCCAGTTGTGGT GGCTCGCGCCTGTGGTCCCAGCGCCTTGGAAGGCCAATGAGAGTGGATCGGTTGAGGCCA GGAGTTTGAGACCAGCCTGGCCAACATGGTGGGATGCCGTCTCTACTGAGAATACAGAGA TGGGCCGGGCGCGGTGCCTGTAGTCCTCAGCCTCCCAAAGTGCTGGGATTACA GGCGTGAGCCACTGCACTTGGCCTGGACTCATCTTCATTGTCCACCTCCTAGGCTAAATT TATGTCTTTTATGTGCTTGTAATCTCTGCATACCACTTTAGTGACACTTGCCCTGGAGTG TGATTGGTAATCC

Sequence 1804

AGGTACTTCTGCCTGGGTTATGGGAGTAAAATCTTGTCCAGGGACATCCCAGGGAAGGTG
AACTTGCCCAGGCAGATGCGATAGACAGCGCTCAGAGGAATCCGCTGCAGCTACACACAA
CTCAGCATGATGAAGTCGTATTTGCAGATCAAGAGAGTCTTGTCTGTGACCAGTAGAATT
CTCTCCTTCTCATTGTTCCAGTGGTCTATCTTTGTCAAGAGCCAGAAGCCTTGAATGGTC
TCTCCAGAAGTCTCAGCTACGTGACCTTTCAAGTCTTCCATGGCAGTCTCAATGGCCCC
Sequence 1805

Sequence 1806

Sequence 1807

Table 1

CCTCAACCTAATAAAGGGCTTCTGTGAAAATCTCAAGGCTAATTTCGTATTAATGG Sequence 1808

CCGCGGTGGCGGCCGAGGTACTTCTGCCTGGGTTATGGGAGTAAAATCTTGTCCAGGGAC
ATCCCAGGGAAGGTGAACTTGCCCAGGCAGATGCGATAGACAGCGCTCAGAGGAATCCGC
TGCAGCTGCACACACTCAGCATGATGAAGTCGTATTTGCAGATCAAGAGAGTCTTGTCT
GTGACCAGTAGAATTCTCTCCTTCTCATTGTTCCAAGTGGTCTATCTTTGNCAAGAGCCA
GAAGCCTTGAATGGTCTCTCCAGAAGTCTCAAGCTACGTGACCTTTCAAGTCTTCCATGG
CAGTCTCAATGGCCCC

Sequence 1809

Sequence 1810

Sequence 1811

Sequence 1812

CCGCGGTGGCGGCGAGGTACGCGGGGGGGACAGGCCATCTCGCTATAGGAAAGGAAAGT GGAACAGCATTCATCCTCAACATTTTTACGAAGACAAAATGAAGACTGGAGTAGAAGACT GATCAGTGCAGGTGTAGCATAAAAGTGTAATCCTGGAAGATGTGGTGTGAGAAGGTAGCA CAAGTGAAANCAAGATACAGGAGATAGGGAANGGAAAGCTGGAAGCANAGGTCACTGGAG GGAGAAGGGAGATGGACACATTCAGGGCTACAAAGCAAGTTCTATGTGATTTGCTCACCT CTCAATTGTGGGACCCCTCAAAATGTGTACCTGCCCG

Sequence 1813

AGGTACTCTGCGTTGTTACCACTGCTTCCCGGGACTCTGCGTTGTTACCACTGCTTCCCGGGACTCTGCGTTGTTACCACTGCTTCCCGGG

Table 1

ACTCTGCGTTGTTACCACTGCTTCCCGGGACTCTGCGTTGTTACCACTGCTTCCGGGACTCTGCGTTGTTACCACTGCTTCCCGGGACTCTGCGTTGTTACCACTGCTTCCCGGGACTCTGCGTTGTACCACTGCCTCCCGGGACTCTGCGTTGTACCTGCCCG

Sequence 1815

CCGCCCGGCAGGTACAGTAGAATCCAGTCGTTGGTTTGGAGGCGAGGGCTCTCTGCGGT CCTCTCCTACTGTCAGGAGCTTCCCGTGCTCATTTTTCATTTACTGATGCACTAAAGGAG AGTTTGACTTTGAGTCAGCATTCTAAATCAAACGCAAACAGCAGAATCATATGGC ATAGACACTTAGCAAATCCAATGCCTTCCAGGCATCTGTTTCCTGTTGATGAAATCCTCC CTATGGAGAGCAAACTGGTTCATATCTTCAGATAGTGTCATTCAACCCCTTGGCAGCTTT CTGGGCTACTAAATATCACACCGTCTGGTGGGACATTTCACCCAAGTTGTTCATTTATTA AGTTTTCTGGCTTCGTGGAGAATTATCTGCCTTCTCTGAGTATTGATTTCATTGTGCGCA TGGTGAAGATATCGNCTGTTCTACAAGGGAGTAAGAATGAGTCCCCGCGTACCTCGGCCG CTCTAGAACTAAGTGGATC

Sequence 1817

Sequence 1818

CCGCGGTGGCGCCCGAGGTACTTACAGTTTGACTTTGAGTCAGCTCAGCATTCTAAATC

Table 1

Sequence 1820

TTGNCCTCCCTGGCTATAACTACTCTAATCTTCCACCTTTNTTTCTCCTTACCCTNACTG CTTTATCTCAAGAAGATCTTGTGTGGGTATATAGATGCGAGAAAGTTACCTGCATGATTCC GACAGGTGCCCTGCCATCACTCTAATGCTGTTCTCATTGCTNGGCCTTATGGCACATTCT CACTCACTCACTACCCCTGCCCGCGTACCTGCCCG

Sequence 1821

Sequence 1822

Sequence 1823

GCGGTGGCGGCCGAGGTACGCGGGCATGACAACTAATGGGAAAGACATGGCTCAGATGTG CAGCCTCAGAGAGCTTCTGAACATTTCTTCTCAGACTAAGCTCTTACACACAGTTGCAGT TGAAAGAAAGAATTGCTTGACATGG

Sequence 1824

CTCCTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGAGATGTGTT
ATTTATCATTTTATGATGCCAGAGATTTACACGAATTTGTGAAAGGTTTTTCTTACCAT
AGATTCAGAGGCGTGTTTGAGGCAAGGTTTTCATTGTGCAGTGAGGAAATTGGCACATAG
AAATCAATTGATGTGCAGGACTCTTGGACTGACTATTCTGGTTATGTTTCCTTATAACAC

Table 1

ATTAAGAAGAAATTTGAGATAAAGTTAGTAATTGTNAACTANTCTTTATTTTAATA ACAAATGTTGCAGTATAATTTT

Sequence 1825

Sequence 1826

Sequence 1827

GGAGCTCCCCGCGGTGGCGGCCGAGGTCGCGGGGGGGCTTANACCTGACGCTGGGAGGAGA TGCTGCCACCTAGGTTACTTGTAGGACCCTATACGGCAACCTCCTTTGCCAGGAACTATT TATAAACATCCTGCAGGAAAATGAGTNTATATGTCANAATACACATTTCCCACCTTGCCC AACAGTGGAAAANCATAAGAAGAGAAAAACNTTAAAAAATGACANGGAAGTTAATGGAAG TCAGCANTGTGATGGTGTTTGGAGGTGGAGCCTTCANAAGGTAATTAATGCCCTTGTAAN AANAGGCCANANAGCTTGCNCACCTTNTTCCTGCCATGT

Sequence 1828

CCGGGCAGGTACGCGGGGAGACCTGACGCGGGGGGAGATGCTGCCACCTAGGTTACTTGT AGGACCCTATACGGCAACCTCCTTTGCCAGGAACTATTTATAAACATCCTGCAGGAAAAT GCANTTGAAGTNGAANAGACANGGNATNTTTCCAAGAAAGGTTTATGCCANAAACATTNA TAGTAGAAAGTATTNNANNAAGGGAGGTNCTATATTGGTCAAGNAATAACCAACATTTTT TCCCCA

Sequence 1829

CTATAGGGCGAATTGGAGCTCCCCGCGGNGGCGGCCCGAGGTACTTACAACTTTTCATAT AGTATTGGTAGTGTTTTGAATAATTTAAAAAAATCATCTTANGTTTGTTATTTAACTTTAT TTATATAGTGCTTGTATTAATGATTTTTGTGAATGTTTTTTAAAGATGGATACCTTGATTT GGCTTGGCCTNCCAAAGTGCTGANATTACAGGCGTGAACCACCGCGCC Sequence 1830

Sequence 1831

CCCGCGGTGGCCGCCCGGGCAGGTACGCGGGAGTGACTAAATTTGTAGGAATGATAT
TTTCATGGGATTACTCAATCTCACCCACCATTAGTTGCAGGTGACAAGAAAGCTAAGTTG
GCAGATGTTTGTGCTAGAAGCTGTGGGTTTACGTCTCCTTTGTGCATGTGTTCCAGACAT
ACCAGTGGCTTGGTATTTAAACATCATGCTCAGGTGTGCAGGGTAGTTTTTGAGTTATAA
TAGGTATGCAGGCGCTGTGGGATTACTTGGTTGTTTATGTAAAAATTATTTTGCACTCAC

Table 1

TTCTGAAATGAGTGTTAGTAAGAATCATCTTTANAGGAGGTTCCAAGGCATTGAACTGAG ATACCTGCACTGTTTGCTGTAAATTTAAGCTTAAAATTGAAACCAGGTTATCAGCATTTC ATGCCAGGAGAGAGTGGGCATGAATGATTTNAGGAAATGAANAGCTAGATTTCACCTTGA ATTTGCTTCCACCCTTCTGTGGCAAATTAGTGTGGGCTCACTGAGCACTTTATCTGCCCG TGGTAATTTA

Sequence 1832

Sequence 1833

CTTAGGGCGAATTGGAGCTCNCCGCGGTGGCGGCCCCCGGGCAGGTACGCGGGGGTAGA
TGGAAGGAAGAACTTGTGTGCTTAGACCTGACGCTGGGAGGAGATGCTGCCACCTAGGTT
ACTTGTAGGACCCTATACGGCAACCTCCTTTGCCAGGAACTATTTATAAACATCCTGCAG
GAAATGCAGTGAAGTAGAAGAGACAGGGATATCCCAGAAGGTTATGCAAAACATCAAGA
GAAGATGAGAGGAGTCTATATTGTCAAGAATACACATTTCCCACCTTGCCCAACAGTNGA
ANAAAAAAAAACTANATTAAAAAAAAAAANGGTACCTNGGCCGNTCTAAAACTAGTG

CCGCGGTGGCGCCGAGGTACCAGGCTAGGCAGCTCTGGAGAAAGCAGAAGTGGATAAAT
AAGGTGTGGACTCACCAAAGACAGTTCCAAAGTCAATTTCACTCTGACACACTCTCTGTG
ATCTTCCACAGTCAGCACAATGCCTGCCCCCTGTGGGTGTTGTATAAATATTTGTTGAAT
GAATGAATCAATCATTCAACAGACCAAGGCCAAATCAGAACCCCAAACCCTAAGGTCTTT
ATACTCTCACTGTCCATCCATCGATCTTCCTGTCAGAAATCAGAATATACCTTTGCAATA
CCCTTTGCTAGCCTTTCAGTTATCTTTTGAATAGAGGCTCTGAGCCTTGAAAATATTGCC
TGGGAAATATTAACACCCCATTTGAGTATCTCCCAAACACCCTCAATTAACTATATGGTGCT
GTCTAGCCAGGACCTTATTTCAGTATAATGTGAACCTGA

Table 1

Sequence 1836

Sequence 1838

CATACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACACAATTG
TGCTGATTTTCTCTCATTTAAAACGGTTCCNCAAGTAGTTAGTCCAGGGCTGGTGTCAT
GGCTCCATGGTCACTGGGGCATTGTGTTCCTCCACGATTTCTGCTTCACCAGGCTTAGCC
TTTGCTTCCATCCTCTAGTTTGCCTCATGGCTCAAGATGGCTGCTAGAGCTCCAGCTGTC
TCTTATGCATTCCTGGCTGTAGAATGGAGGAAGGGAAAGGGTAACGGGACGCTTTACT
GGCTATTCTTGTTTAAAGGAGCATCCTTGATCATACTTAATGAGAATCTGGAGTAATTTT
CAGGAGATCTCAGAGAGGGTACCT

Sequence 1839

ACTNCTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACGCGGGT GTCCTTCTTCAACTGGACACCTCTAGATAAGAAGGCAAGAAATTCTTAAAACTTTTGCTA ACCTAATTGTGTATGTAATTAGAATAACCAAGTTCAGTTAATTGAAACAATGAGTATTGG AGTAAGAGTTTGGGATTTGATTCCTTAGGGATAAACTACTAAATCCAGGACAGTCATTTA ACTGCTGCAGATTTGAGTTCCCAGGGGAACCAAACAGAAGTCACACAATTTCTAGGATGA AAACATCTCAAAAAAAATCAGTCCTCCCAGCACTTCGGGAGGCTGAGGCANGGAGAGCAC TTGAAGTCAGGAGTTGAAGACCAGACCAGCCAACATGGTGAAATCCCCGTCTCTATAAAA AATACCGAAATTTAGTTGGGCCGTGGTGACCCCGTGAC

Sequence 1840

Table 1

Sequence 1842

Sequence 1843

Sequence 1844

Sequence 1845

Sequence 1846

CCGGGCAGGTACTTGCCAAGATCTCACTCCTCAGCAGCTTTTTATTTCTAAATTTAAGCT
TTTGGTTACTGAAAGTTTACAGCAGTTCTAGACTCCTATTCTTTAGCATTCCGTTACGTC
CAGACCATGTGACAACCTCCATTCTACAAATATGTAACCACAAAGAAGGTGAGTGGGGAG
GCAATAAGAACCCAGAACTAACAGAACATCAGAAAAGCTGGCATACGCACACATAAAGAAG
GGGGAGAATATAGGACTATATGGGAGGGAGGAAGGTCACAGAAAATGATTACGGTTTTGA
TGTTGTATTTGTGAAGGTGAGGAATACTAACTATATTTCTTTAGTCTTTGAAGATCACCA
TATTTAGCCATTATTCTATCAACTGTTAAGCCTTGG

Sequence 1847

CATTTTTGTTANCANNGAAGTGAGNGGCATCTATGTATTTTTTAAGGTATATAATGAAAT
TGTGCCTAGGGGAGTNATAATTTACTCTATGTATTTNTATATNTACTTAAATCAATACAT
TCTTACAGACTANCTTCTTTAGTGGTAACATACANGCCGATTTTCTCACTCCATGAATGA
TTACNGACATGTATCCANNANCGGAGGTCCCTCATCCACCATTTCACCCAGGTGTCTTGC
TCTTATCTTTCANAAGGGAAAATTGGCTAGCNGGTTTCTCCCACCATGTGCTGTTCTCC

Table 1

AGGGACTTTGGGTGAATCCAGGTGTGGGAAAGAAGGTAGCATCAGCTGTAAGATTCAAT Sequence 1848

Sequence 1849

CCCCGCGGTGCCGCCCCGGCCAGGTACATGCCAGGCACAAACTGGAGTCACAGATGC CACACTGACTATCACATTGTCATCATACTCAGAGAGAGAAAAGGTGTATACACCCAGTATT TTCTTATGTTTTCTCTATACTTCCATATCCCCACCCCCATTATCCCCCGAGACATTCCCA GTTGGAAGTCAGTTGCTTATGGGAAACTGGCTGCAGGGGGATCAGCCCACCTGTAACACA CGGAAAGGCAGAAACAATGAGTCATGGATTTGAGTGCAAACAAGCCCAGTCCTGCTAC AGAGAGTTACGGAAAAAATCTCACTGTTGAAGAGAGACATCTATAAGAGAGGTGAGGAAA ATGACTGATANATCCTTTTACAATATTCTAGGGGTAGTCTGTCT Sequence 1850

CTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGGGTTTCCTGCGT
TTGTAGATGGAAGAACTTGTGTGCTTAGACCTGACGCTGGGAGGAGATGCTGCCAC
CTAGGTTACTTGTAGGACCCTATACGGCAACCTCCTTTGCCAGGAACTATTTATAAACAT
CCTGCAGGAAAATGTCAGAGATGGGAAGAAACAAGAACTTTGACATGCTTGGTGTTCTTG
CCCAAGCTTTGAAGAAGTTTACAAAGTCTATATGTCAGAATACACATTTCCCACCTTGCC
CAACAGTAGAAAAACATAAGAAGAGAAAAACATTAAAAAATGACAAGGAAGTTAATGGAA
GTCAGCAATGTGATGGTGTTTGGGAGGGTGGGAGCCTTCAGNAAGGTAATTAAATGCCCT
TGTAAG

Sequence 1851

CTNCTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCCCCGGGCAGGTACGCGGGCAT
TGGTGAATGAGAATGAGCTACTGAAAACAAAAAGAGGGTCTTCTACTCAGCCTCTACCCC
TAATATTTATATCAGAAGCAGAGATTAACTGTCCTTACTCATTCACACGTTAATGGAAGA
GAAGGAAGTTTCCTAAAAAAAAATCCTCCCGCTCCACCCTGCAAACTTTATGTTTTTCTGT
TACATAATCAGGTAGGGGCAAGACCTAAACTATTTTGAATTGGTGGTGTTGAGGCTAAAT
TCTCTGCTATTGACAGAATTGAGAATGTGATCAATTTCAGAGTAGCATGTTACAAATTTT
GTCCCCAATTTCAATGGGGAGAATTATAACAAATCAGTAGGTGGNTGGCAGAATCTGTTCT
TACTTTCCTCCCATCCAGT

Sequence 1854

CCGCGGTGGCCGCCCGGGCAGGTACCTCCTCCCTATGCATCTGCTGTGGGAAGTGT GGGTAACTCACAGATGATGCCACAGGGCATGTATTCAGGCACCACAGGCAGCAGTGAATG

Table 1

AATGAAGTGAAATGGTATTTATCCATTTCCTGGAAAGGTCCAGGGTTTGGCTCTGCAGGG CCAAGAGAACAGCTTTAGTTGTGCCTTAACCCAGTCCTGGAGAAGCCAGCAGGCCGTAAT CACGGGGAGGAAACCCATCTTTTAAGGGCTCCTCGCTCAGGTGGTGACAAGGTGAGGTGG TCATCTATGCTGTCTTTATCAGTATCTGTCCTAAATACTGTGCTCTGACATTGATGCTAA TATTCCATATTATCAGGGCTTCTGTGGTGTTTAGGCCTCTAATTTTTCTCTTCAGTAAGG GGAAT

Sequence 1855

CAGGTACATGTCAAAGGAAAAACACGTGAAAGATGAATTCAGCCAAACCCACCAGTGTTC AACCTCAGCCTAATCAATCTCATACTCCTAGAGGCTTAAGTATCAGCAGGTAAGATCGTG ATGACCTGTCTNTGAGGCTCCAGACAATAATTTCTAACTGCCAACTGGAAATCCTTATAT GGTTAGGCTGCCAACATCCCANGGAACAGGACCAAAATAAAAAGCATCACTCATTATCCT ACTGCAATTTTCCTCTTCCCTTTGTCAAATGGGAATGATCTTTACNATCATGATCCTTNA TTGCANCCAGNACAGAAATCATGAATGTCATCTATGGCCCCTTNCTATCACTCCGGGCTC CAATTAGTTGTCCTAT

Sequence 1856

CGACTNCTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACAAGA
GCTCCCATTTCCCCACATCCTGGATGATACATGTTATTTAGACATTCTAATTTCTTTTCC
AATCCAGTAAGAACGACATGGCAACTCATTATATTCATTTGCATCCACTCTATTGCTATT
GAGATTAAGGGCTTTTACTGTTTTTCTTATATTTCTTGGCCACATGGCTTCATTTTCTGT
GAATTGCCTTTCTTATGGTCCTTTCATGGTTAAAACAGCCCTTTAGAAGACTCGGATTTT
AAGGTTGGATTAGGGGTTGGGATTTGAGAGTTTTACACCATGGCCATGCCTCGTTTCCCT
AAGTTATCATTAAAATGCTCAGCCTCCACAGCCCATATCCATGCATATCACCCAGGTTGT
CCCAGAACATTCAAGAACTTACTGCTCTTGCTTTTGAAT

Sequence 1857

Sequence 1858

Sequence 1859

Table 1

CTTTATTCACTTGGAGTAGAACTTCC

Sequence 1860

Sequence 1861

Sequence 1862

TATCACTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACACT GCACACCACAGGGTGGCTGCACTTTTTGGGTGGTGGGGTGGGGATGGGGGCAGGTATGAT CAATCATCCAAACCANGGCATTTTTAAGAGTAAAAGGAGGCTCTACTGATAACATGCTGC AACAACAGATTTNANNTAGGAAACTGGCCCGCTCTANNAACTANT Sequence 1863

Sequence 1864

ACTACTTAGGGCGAATTGGAGCTCCCGCGGTGGCGGCCGGGGGCCATTGAGACTGCCAT GGAAGACTTGAAAGGTCACGTAGCTGAGACTTCTGGAGAGACCATTCAAGGCTTCTGGCT CTTGACAAAGATAGACCACTGGAACAATGAGAAGGAGAGAATTCTACTGGTCACAGACAA GACTCTCTTGATCTGCAAATACGACTTCATCATGCTGAGTTGTGCAGCTGCAGCGGAT TCCTCTGAGCGCTGTCTATCGCATCTGCCTGGGCAAGTTCACCTTCCCTGGGATGTCCCT GGACAAGATTTTACTCCCATAACCCAGGCAGAAGTACCT Sequence 1865

Sequence 1866

GGAGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGGGTATTTAAAGGAGGAAAAGAGCGATGAATCTACATGGAAAATTAGGTGAAGGAGGAGAAAATTGCATCGGCCATATAAGTCCAACT

Table 1

Sequence 1867

ATCGACTCCTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACACTTATAGT
TGAGAGCCAAGTCTCCCTTATCATTGGTGAATGAGAATGAGCTACTGAAAACAAAAAGAG
GGTCTTCTACTCAGCCTCTACCCCTAATATTTATATCAGAAGCAGAGATTAACTGTCCTT
ACTCATTCACACGTTAATGGAAGAGAAGGAAGTTTCCTAGAAAAATCCTCCCGCTCCACC
CTGCAAACTTTATGCTTTTCTGTTACATAATCAGGCAGGGGCAAGACCTAAACTATTTTG
AATTGGTGGTGTTGAGGCTAAATTCTCTGCTATTGACAGAATTGAGAATTGTGATCAATTT
CAGAGTAGCATGTTACAAATTTTGTCCCAATTTCAATGGGGAGAATTATAACAAATCAGT
AGTGGTTGGCAGAATCTGTTCTTACTTTCCTCCCATCCAGTGACTAGGATTTGGAAAGCA
GTGTTTT

Sequence 1868

Sequence 1871

CCGGGCAGGTACTTGCCAAGATCTCACTCCTCAGCAGCTTTTTATTTCTAAATTTAAGCT
TTTGGTTACTGAAAGTTTACAGCAGTTCTAGACTCCTATTCTTTAGCATTCCGTTACGTC
CAGACCATGTGACAACCTCCATTCTACAAATATGTAACCACAAAGAAGGTGAGTGGGGAG
GCAATAAGAACCCAGACTAACAGAACATCAGAAAAGCTGGCATACGCACACATAAAGAAG
GGGGAGAATATAGGACTATATGGGAGGGAGGAAGGTCACAGAAAATGATTACGGTTTTGA
TGTTGTATTTGTGAAGGTGAGGAATACTAACTATATTTCTTTAGTCTTTG
Sequence 1872

AGGTACGCGGGGGTATTTAAAGGAGGAAAGGGCGATGAATCTACATGGAAAATTAGGTGA AGGAGTGGAAAATTGCATCGGCCATATAAGTCCAACTACATATGGATCTATTCCTCCATG

Table 1

AAAAACTGGAAATTTCACTTTAACATGGTATTTGCACAGTCAGCAGCAATTCTTAACAAT GTCTTTCTTGCTGCTGACATCATATTTTTTCACCCCAATAATAGAGGATAATTTGGACCC TTTCTGCTTTTCATTTAATTCTGTCTATTTCTGATTGCACTTCTCCTACTTCTCCCA CATGAGAGATGATTGTTTATTACTTGTGGAATATGATGAATCACTTC

AGGTACGCGGGGTCCAGTGGACGCCAGGGATCTGAAGGGCAAGGGCAAGGGCTGCTGGAGCCTGCATCATGTCGAGTCCGCAGAGGAGGAAGGCTATGCCCTGGGCACTGTCACTGCTTCTCATGGGCTTCCAGCTCCTGGTGACTTAT

Sequence 1874

Sequence 1873

Sequence 1875

CCGGGCAGGTACTTTCTTGGCCAGACATCATACATCTGCCTCTATAGAATCCCTCATTCA
GGGGGTCACTGATGAAGTGTAAGGCCCTAGGGTTGAGCTTCAGCTCCACTGTGGGGTAGG
TTTTACCTTCTCCAAAGCTTCATTTTCTCATTTGTAAAATGCAGATAATGTGTGTCTTG
CCAAACTCTAAGGGCTGTTGTAAGAGGGTTTAAATGGCATAAAATCTTAGCTTTTCT
ATTATCTCAACAAAGGTGATTTTCTTGTTAAGAAGGTTTAGTAGCCAGGCATTGGACAAC

Sequence 1877

CCGGGCAGGTACTTAGGACTATGGAGAAACAATGGAAGACATTAATTCTGCTTGTCTTGA TGGTAAGGGTGGGGATGAAAATACAGATCGAATTTGGGGGAGCATGTTAAGGTTAGGGGA ATAGAGATAGCTTATATTTAGAACAAGTTAGTAGAGACTGTATGATTTTCCAAATAGAGA AGGGTAAAAAGACATTCCATAGAGGAAGAAAATTACATGCAAAACCACAGAGACCTTAGT TTATAAAGAGTAACTGGGTATGGCCGGGTGCGGTGGCTCACGCCTGTAATCCCGGCACTT TGAGAGGCTGAGGAGGGTTGATCATGAGGTCAGGAGA Sequence 1878

AGGTACTTCTGCCTGGGTTATGGGAGTAAAATCTTGTCCAGGGACATCCCAGGGAAGGTG
AACTTGCCCAGGCAGATGCGATAGACAGCGCTCAGAGGAATCCGCTGCAGCTGCACACAA
CTCAGCATGATGAAGTCGTATTTGCAGATCAAGAGAGTCTTGTCTGTGACCAGTAGAATT
CTCTCCTTCTCATTGTTCCAGTGGTCTATCTTTGTCAAGAGCCAGAAGCCTTGAATGGTC
TCTCCAGAAGTCTCAGCTACGTGACCTTTCAAGTCTTCCATGGCAGTCTCAATGGCCCC
Sequence 1879

AGGTACCCAAGCCAGAAAGTGAGCCCACTCTGACTCTCATGAACTGGGTCCTGATTCCTT
TAAGGTTATTTTGCCTAAGTATATTTCCACTCTGGCCTCTCCTTTCCATGCCCACTGCAA
CCACCAAATGTGCCACATCCCACCCAGATAAGTACCTGCCCG
Sequence 1880

CCGGGCAGGTACGCGGGGAGACCTGACGCTGGGAGGAGATGCTGCCACCTAGGTTACTTG
TAGGACCCTATACGGCAACCTCCTTTGCCAGGAACTATTTATAAACATCCTGCAGGAAAA

Table 1

TGCAGTGAAGTAGAAGACAGGGATATCCCANAAGGTTATGCAAAACATCAAGAGAAGA TGAGAGGTCAGAGATGGGAAGAACAAGAACTTTGACATGCTTGGTGTTCTTGCCCAAGC TTTGAAGAAGTTTACAAAGTCTATATGTCAGAATACACATTTCCCACCTTGCCCAACAGT AGAAAAACATAAGAAGAGAAAAAACATTAAAAAATGACAAGGAAGTTAATGGAAGTCAGC Sequence 1881

Sequence 1882

Sequence 1883

Sequence 1884

ACTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCCCCGGGCAGGTACGCGGGGG
TAGAACAGGCGATATCTTCACCATGCGCACAATGAAATCAATACTCAGAGAAGGCAGATA
ATTCTCCACGAAGCCAGAAAACTAATAAATGAACAACTTGGGTGAAATGTCCCACCAGAC
GGTGTGATATTTAGTAGCCCAGAAAGCTGCCAAGGGGTTGAATGACACTATCTGAAGATA
TGAACCAGTTTGCTCTCCATAGGGAGGATTTCATCAACAGGAAACAGATGCCTGGAAGGC
ATTGGATTTGCTAAGTGTCTATGCCATATGATTCTGCTGTTTGCGTTTTGATTTAGAATGC
TGAGCTGACTCAAAGTCAAACTGTAAGTACCT

Sequence 1885

ANGGCGAATTGGAGCTCCCCGCGGTGGCCGAGCGGCCGCCCGGCCAGGTACTGTTACTAT
CCTTAAGATGAGGGAACTGAGGAACCAAGAGGTTAAGCAATTTGCCTTTGGTTCACATAG
CTAATGATGTGGAGATTTGAACTTAGGCTGTTTGTCTCCCAAGCCTATGTTCTTAAATTT
GGGGAAATAGTAAAGATAATTTCCACAATGTGAAGACAGTTAGCAGCCTTAAGGATGAAA
GGATGGTGCAAATACCATGCCCAGTGAGTGACAGAGTATCAAGGCTGGTAGAGCCTGATG
AAAGCACAAGTTTTCAGAAAAGAGGGAAACAACAATTCCTATAAAGTTAAGAAAATCAC
ATTGACACCAGACTTCTCATTGGTAGAGACCACAAAGCCCTTTTCAAAAGTGGGTCAAAC
TGGCAGGCTGAGCACATATCCTTCCCTCCCTTTCTG

Sequence 1886

CTCCTATAGGGCGTTTTGGAGCTCCCGCGGTGGCGGCCGCCCGGGCAGGTACCAAAAGA

Table 1

Sequence 1888

Sequence 1889

TNCTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCCGAGGTACTGTATTTCCAAAAG
TAAGTTTCTATTCCTAGAACTAAAACAGAAAAGAAGTGTTGTGAGATACATAAATGAAGC
CAATAAATTTAACCAAGGGCTTACCATTTTCCTGCAGGATGTTTATAAATAGTTCCTGGC
AAAGGAGGTTGCCGTATAGGGTCCTACAAGTAACCTAGGTGGCAGCATCTCCTCCCAGCG
TCAGGTCTAAGCACACAAGTTCTCCCGCGTACCTGCCCG

Sequence 1890

TTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACAAGCTTTAAATG
GGAATAAATCTTTTATAAGCCTTTCCATTTACTTTCCTGCTTATTAAAGGTGAATTGTAA
TGGAAAACCCTAAATGTCACAGAGTCTGGAAAATTGAAATAATAAGGGGCAGCATTCTCC
TTAAGTGGTATAACCTAGTAAAAAGTGGGCCTAATGGAAAGTCCACCGTGGAATCATCTG
TGTTTCTATGCAACAAAATTATTTTCCTTCTTTCTCTAACAAGGGAAGTAGTTCTGACCA
ACAAGGTTGGCTGTCTTAANCATTGNGGTGGAGAGCAATGGAAAGATGAGTGTGTAGTGG
GAG

Sequence 1891

Sequence 1892

ACTNCTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCCGNCCGGGCAGGTACAAGGG

Table 1

GAGACAGCATGCATGGTGTGNTCAGAAGAGCTTGCTGAGGTGCTCGGCTCTTANCGTTAA
AAATGTGATGTTGGTATATCATCCTGATAGAAANCACTGCTTCCCAAATNCTAGTCACTG
GATGGGAGGAAAGTNANNAACAGATTCTTCCGACTCACTACTGANTTGTTTATANTACTT
CCCCATTTGAAATTTGGGACAATTANTTTGNGGGCATNGCTACTCTG

GNCCGGCCAGGTACTGCCACAGGACTTTCAAAAAGGAGGGGGAAAATTAATGAAAGTGAC ATGCATCAAACAAATCAAGGGGCAGTGTTGAGGTCATCTCCACGGAGCTGTAAACTCAGA AGTGTTTCCTGGTCATATATGGTCAATTANGGTCAAGTCTGAAATAAATNTANAANAATG ACCTAATTTTCCAGCTTAACTCAGNAGCTAAAATCCATAACACTATCANACTTTCCTTTT AATTTATGAGATGGAGTCTTGCTCTTGTCGCCCAGGTTGGAGTACCTCGGCCGCTCTAGA ACTAGTG

Sequence 1894

Sequence 1893

Sequence 1895

Sequence 1896

CTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCTCGAGCGGCCGCCCGGGCAGGTACTC
TTTATGCACATCAGTGTGGGGCCTTAGTAACCACTGTGCAAGTTGAAACTGGGCAAAGTT
ATCTTAATAATTAATGGGAAAACATAAACTTCTTCCTGCAATCTTTAAAGACACTTGTCA
GTCAGGTGCGGTGGCTCACGCCGGTAATTCCAGCACTTTGAGAGGCCAAGGTGGGCGGAT
CACTTGAGCCCAGGGGTTTGAGAACAGTTTGGGCAGCATGACGGAACCCTGTCTCTACAA
AGACTACGAAGGGTTGGCCGGGAGTGGTGACATGTGCCTATAGTCCCG
Sequence 1897

TACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCCCCGGGCAGGTACATCTCTAGC
TGATGATTCAAAAAAGAAGCCTTTTAATCTCACTCCACTGATCAGCTATGATACTTAAAT
GTTTTAGCTGTGAGCAAAATAATATGCATTCTCAAAGAGAGTATCTTCAGACTCCAGTGG
CCGAGAATCTAGAGTTAGCAATGGAAAAAATTAGTCTCGGGGCNTTCTTGTTTCTGCCCA
CAAGTTTTCAAATTAAGAACAATGTGTTTGCACTTAATGAAACAACCTCTACTGCTCTTC
AAGAGGACTCAGGATACCGATTCTCGAGGCCCCTGGCGGTCCCCTGTAAGTACCT
Sequence 1898

CCGCGGTGCCGCCGAGGTACAGATAGAGTCTCACTATATTGCCTAGGCTGACAGAGTAT
TTTTTCCTTAATTATTCTTTATTCTCAAATGCAGTGAACAGTCACAGTAGCCCACCATA
GGGGGTTCATTTTCAGACATTACAGTAACTAGGGGAATTTTATTAAGGAACCAGCNGCTT
AACCCNTANTNGGTANTAATTCTTCTTTTTTTAAACCCAACCTCCAGAANTTNATTCAGAA
TTCATCAGTCCTTCCCNATCAGGTGGCTTGTCTTTTCTNGGTCCCATGGATCCAATGTAN
GGAATTCCACAATCACAAGTTAAGTNTTTTTAATCACTTCTTANGNNCCTNCTCCCCACT
TCTGGGGATGGGTTTCCCTCANNTAATCCTCTTTTGGTCTTTCCCAGGGGAACCCTGGAC

Table 1

CACCTTTTTNGAAAAGGAAGGTTANTTNGGGAACCAGGCCTTTTTTTT
Sequence 1899

CACTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACTATTAA
ATTTAATGAGAGGTAACCCATGCACCGGCAGAAAGTTCAAGGGGACAGAAGGGGCTTGCT
CCACTCTGGAGCCCTATCTCCTCTCACCTCCTTCCTTCTAGTTTGACATGCGATCTTGTC
TCTCTCTTTTATAAAGTGCTTCCAGGCCCNTTTTGATTAAGGATGCTGTCCTAAAATCCT
TCCTCCCGCGTACCTCGGGC

Sequence 1900

Sequence 1901

Sequence 1903

Table 1

Sequence 1905

CCGCGGTGCCGCCGAGGTACGCGGGAGACACGCATCTGAACCTTGCCGAGTAGGAATGT
TCCAGAAGTAAGAGACACTAGGGTTTCAAGAACAAGGACCAGCACCTATGAAGGCTC
TGAGGCACAGACCACTGTGACCTGTGGAGAAGTGACAGCAAAGTGAAAGGCACGTTTTGA
TTACTACCGACATTCACAGTCTGGACACGGGTGACAAATCTAAAAGATATTGCCCATTCG
TCCAACTGCCGCTGTCCTGCCAGTATATCGTCTGAGATTACCATCAGCTAAATATTTGCAT
TGTCTTTGGACAATTTTCCTACATTGTGACTCCTCACTACATTTTCAATGCTTTTCTAGT
CCCAGACAAGCTACAGACTGTTAATTTACACTTGCTTTTGCCTTGCCTGAGGAAATTGAA
AATAAATT

Sequence 1906

AGGTACAATATAGGCAGACAGTTTGCCTTCAGAAATTCAGAAATGCAGCTTTTGAGGGAG GTCAGCATCATTGGTCTCAGCTACCATTTTCCTGCAGGATGTTTATAAATAGTTCCTGGC AAAGGAGGTTGCCGCATAGGGTCCTACAAGTAACCTAGGTGGCAGCATCTCCTCCCAGCG TCCCCGCGTACCTGCCCG

Sequence 1909

Sequence 1910

Sequence 1911

TCAGCATTCTAAATCAAACGCAAACAGCAGAATCATATGGCATAGACACTTAGCANATCC
AATGCCTTCCAGGCATCTGTTTCCTGTTGATGAAATCCTCCCTATGGAGAGCAAACTGGN
TCATATCTTCAGATAGTGTCATTCAACCCCTTGGCAGCTTTCTGGGCTACTAAATATCAC
ACCGTCTGGNGGGACATTTNACCCAAGTAGGCAAATGCATGACAGAACTCACTGGATCAA
TATCTCAAAATGCTGGGAAGAAAAAAACGGTAACCAGAAATTCTACACAGAGTGAAACTA
C

Sequence 1912

Table 1

Sequence 1913

CGCGGTGGCCGCCCGGGCAGGTACTATTAAAATTTAATGAGAGGTAACCCATGCA CCGGCAGGAAGTTCAAGGGGACAGAAGGGGCTTGCTCCACTCTGGAGCCCTATCTCCTCT CACCTCCTTCCTTCTAGTTTGACATGCGATCTTGTCTCTCTTTTATAAAGTGCTTCCA GGCCCTTTTGATTAGGATGCTGTCCTAAATCCTTCCTCCCACGTACCT Sequence 1914

ATACGACTNCTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGGGGGCCATTGAGAC
TGCCATGGAAGACTTGAAAGGTCACGTAGCTGAGACTTCTGGAGAGACCATTCAAGGCTT
CTGGCTCTTGACAAAGATAGACCACTGGAACAATGAGAAGGAGAATTCTACTGGTCAC
AGACAAGACTCTCTTGATCTGCAAATACGACTTCATCATGCTGAGTTGTGTGCAGCTGCA
GCGGATTCCTCTGAGCGCTGTCTATCGCATCTGCCTGGGCAAGTTCACCTTCCCTGGGAT
GTCCCTGGACAAGATTTTACTCCCATAACCCAGGCAGAAGTACCT
Sequence 1916

Table 1

GCATGTTGAGACCTTAATGATAACTATTCAGAAACCATACTAAACATTTGATCTTGAAAT CTTCCATCGTTTTCCATCCTCTGCTTATGCCTCAGTTATTCCATTCGCATGATATGGGCA CTTAATTTAGCCAACTCACTGACCCATTTC

Sequence 1918

CCGGGCAGGTACTGTGATATCCACATATTTTTGAGAAAAATTCCCAAGCCAGGCGAATGT GGATTGGAATAAAGACATAGGCAGTGTATACCACCATAGCAATAATGGTTAGTAAGATGG TGTTAAACATAGATCGCTCCCAGGGCTCTAAAACAGCACAGCAGCTAATGATTTGGTATT GATAGTAGAGCCAGGAGAAATATTCCTTCACACGCCTCAAATCCATGGTTGGCTCCTTCA AGCTGCAGTAAGTTTGTCCTAAGAAAGTCCAGGTCTGGTTCTTCAGCCTTGCTCCTTCGC GAAATGATCCTGTGTGGGTTAAGTTCTCCTCTCTGGGTTGCTGTTTCCTCATCTCCCAGT TGGGGTGTATCTTCCCTGCGGCTTAGGTGAAGCGCCCGAGGCTT

Sequence 1919

Sequence 1920

Sequence 1921

Sequence 1922

Sequence 1923

Table 1

Sequence 1924

AGGTACAATGGGAACAAGGAGATAAGCAGTGAAAGGCCAAGGGAATGTCTGGAGTTAGGA CTTCAGGTGATTCACAACTTGGCTGCCACTCACCCGAGACTGCCCAAGCCCAGATTTCTT CCTTCTATAAGAATATTGATTCTTGCAAATAAGATGAACCTAAATGTGGTCCAGGAGTCA GCATCTTCTACATGGTACCTGCCCG

Sequence 1925

TCGACTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCAGGTTCAAAT
AGTCAGCAGCTCATCATAATCAATGAGCGAGGACATAAAGTAGGAAAAATGCATCACCAT
GGTGAGCAAGGAAAGCAAGTTATTGGAGGCACATGTTAACACATAAAATATAAAATTAAT
ATGATCACACTGGAAAGGCTTGCCTGAGCCCACAGTTTGAATGCCTACAATAAGATGAGA
TGCACAACAAAAAGCAAGAGAACCTGATCAAGTGGGTGACCTGGCCATGGTGCTCTCATC
AGTGGGGACCCAAATGCTTATGTGGACTCACCAGGTATCGAATTAGACATGAATAGGAGT
GTTTGTTGTGATCCAAGGAAACTATATAATCAAAATGAATACAATGAAACTTTAAAAATA
ATTGTAAGGATCTTTACACCAGCCCA

Sequence 1926

TCACTATAGGGCGAATNGGAGCTCCCCGCGGTGGCGGCCCGAGGTACAGGGAACTATTGG
AGCACCTAAGAGGAGCACCTACCTTGAATTTAGGGGTTAGCAGAGGCATCCTGAAAAAAG
TCAAAGCTAAGCCACAATCTATAAGCAGTTTAGGAATTAGCAGAACGTGCATGGTGAGGA
GATGCCAAAGGCAAGAAGAAGAAGAAGAAGAACATTTCCAAACAGGAGGAGTTCCAAAGAGAGAAGAAGAA
TATCCCAAACAACATTTGCACAAACCTGATGGGGAGAAATGTGGGGTGGGGÁTGGAT
GATGAGACTGAAGAAGAAGAANGCCAGGTCTAGATAATCA

Sequence 1929

AGGTACCATGATTAGTTAAATATAAGACTCCGTAATTTTTACAATTTTAACAATAATTTT

Table 1

Sequence 1930

Sequence 1931

AGGTACAATATAGGCAGACAGTTTGCCTTCAGAAATTCAGAAATGCAGCTTTTGAGGGAG GTCAGCATCATTGGTCTCAGCTACCATTTTCCTGCAGGATGTTTATAAATAGTTCCTGGC AAAGGAGGTTGCCGTATAGGGTCCTACAAGTAACCTAGGTGGCAGCATCTCCTCCCAGCG TCAGGACTAAGCACACAAGTTCTTCCTTCCATCTACCCCCGCGTACCTGCCCG

Table 1

Sequence 1934

CCGGGCAGGTACCTTCACAGCTGCACCACACCAGTTCTGGGCACATGGACAACAGATCAA GCTCCCCCATCATCACATAAGTTAGGCACCAAAGAGTTAGCAAGGGTATTCAGTTCCCAC TTAATTGATTTGCATATCATGCAGGCTCTGATTTCAGTACCT

Sequence 1935

GANATGCTGCCACCTAGGTTACTNGTAGGACCCTATACGGCAACCTCNTTTGCCAGGAAC
TATNTATAAACATCCTGCANGAAAATGCAGNGAAGTNGAANAGACAGGGATATCCCATAA
GGTTATGCANGAACATCAAGAGAAGATGAGAGGTCANAGATGGGAAGAAACAAGAACTTT
GACATGCTTGGTGTTCTTGCCCAAGCTTTGAAGAAGTTTACAAAGTCTATATGTNAGAAT
ACANATTTNCCACCTTGCCCAACAGTAGAAAAACATAANAAGANAAAAACATTAAAAAAT
GACAAGGAAGTTAAT

Sequence 1936

Sequence 1938

Sequence 1939

CCGCGGTGGCGCCGAGGTACGCGGGGACAATGAAATCAATACTCAGAGAAGGCAGATAA
TTCTCCACGAAGCCAGAAAACTAATAAATGAACAACTTGGGCGAAATGTCCCACCAGACG
GTGTGATATTTAGTAGCCCAGAAAGCTGCCAAGGGGTTGAATGACACTATCTGAAGATAT
GAACCAGTTTGCTCTCCATAGGGAGGATTTCATCAACAGGAAACAGATGCCTGGAAGGCA
TTGGATTTGCTAAGTGTCTATGCCATATGATTCTGCTGTTTTGCGTTTTGATTTAGAATGCT
GAGCTGACTCAAAGTCAAACTGTAAGTACCTGCCCG

Sequence 1940

Table 1

TTGTATGGCATCTCTCACAATGTGTTTGCACAACTCAGCAGAGCCAAGGCTAAGCAGTGC ANAGGACAGGGTGA

Sequence 1941

Sequence 1942

Sequence 1943

AGGTACAACTTGACAGTTTATAAAAATGCTAACCTATATCAACATTTTTCCCCACCAAAG
TGTTCNNAAGGGCAANGGTAAGNGAATACATGTTTNCNTGCTTGTGTCAGGGGCACACAG
CAAGGGAAGGCANAAATGGGCATGACCTAGTATTNAGAATCCCCAANAAGCCCTTTCATA
ATTCCCTTAATAAANGAACTTTGNGNGACCTTGCATTNNTTTAAANANATNAAATTAATT
TGGGTTCATNTTTTCTTTAATNTCTNTGCGAATTAAACTATATAAAGTAAATTGGGGAAA
ACCNCANAAATTGCNCATGNGNCTTTGGTTACTTTGNAATCTTCCTTTTTTGGACACCCC
AAGNTNTGGCCTTCCTTTTCTNCCTNTTAANTTGATNCCNTTAAAACCAATCCTTGGNCC
CCTTNCNGGTTTCTTTTAAATTGGNAAAATTTATAATCNTTCNATGGNNACCAATTTTAA
CCAATNTATGNAANATAGGNAACCTNAATTTTGGGTTNTTTGGTNTTNCAAGTNTTTTCA
AAAACNATCTTTTCCAAAATTTTCCCCAATT

Sequence 1944

Sequence 1946

Table 1

Sequence 1947

TACTATAGGGCGAATTNNAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACAAGGGAGA CAGCATGCAGGTGTTCAGAAGAGGCTTGCTGAGGTGCTCGGCTCTTAGCATTAAAAAT GTGATGTTGGTATACATCCTGATAGAAAACACTGCTTTCCAAATCCTAGTCACTGGATG GGAGGAAAGTAAGAACAGATTCTGCCAACCACTACTGATTTGTTATAATTCTCCCCATTG AAATTGGGACAAAATTTGTAACATGCTACTCTGAAATTGATCACATTCTCAATTCTGTCA ATAGCAGAGAATTTAGCCTCAACACCACCAATTCAAAATAGTTTAGGTCTTGCCCCTGCC TGATTATGTAACAGAAAAGCATAAAGTTTGCAGGGTGGAGCGGGAGGATTTTTCTAGGAA ACTTCCTTCTCTCCATTAACGTGTG

Sequence 1948

Sequence 1949

Sequence 1950

Sequence 1951

AGGTACGCAACATGACATTGGCTGGTGTAAAGATCTTACAATTATTTTTAAAGTTTCATT GTATTCATTTGATTATATAGTTTCTTGCCATCACAACAACACCTCCTATTCATGTCTAAT TCGATACCTGGTGAGTCCACATAAGCATTTGGGTCCCCACTGATGAAGAGCACCATGGCC

Table 1

AGGTCACCCACTTGATCAGGTTCTCTTGCTTTTTGTTGTGCATCTCATCTTATTGTAGGC
ATTCAAACTGTGGGCTCAGGCAAGCCTTTCCAGTGTGATCATATTATATTTTAT
GTGTTAACATGTGCCTCCAATAACTTGCTTTCCTTGCTCACCATGGTGATGCATTTTTCC
TACTTTATGTCCTCGCTCATTGATTATGATGAGCTGCTGACTATTTGAACCTGGTA
Sequence 1953

Sequence 1954

CCGGGCAGGTACTTGGTTTTNTTTTTTTTTTTTCCTTTTGGCTTTGACTTTGAGTCAGC
TCAGCATTCTAAATCAAACGCAAACAGCAGAATCATATGGCATAGACACTTAGCAAATCC
AATGCCTTCCAGGCATCTGTTTCCTGTTGATGAAATCCTCCCTATGGAGAGCAAACTGGT
TCATATCTTCAGATAGTGTCATTCAACCCCTTGGCAGCTTTCTGGGCTACTAAATATCAC
ACCGTCTGGTGGGACATTTCACCCAAGTTGTTCATTTATTAGTTTTCTGGCTTCGNGGAG
AATTATCTGCCTTCTCTGAGTATTGATTTCATTGNGCCCCGCGTACCTNGGCCGCGACCA

Sequence 1955

CGCGGTGGCGCCCATACACGCGGGCGATGACTTCGTCGCCCGGTTCTGGTCGATGGC GCGCGTGACGATGGGCTGCGTCCGGGCGGCAGCTCGTCGATCACCGACACTTCCAGGTC GGCGTAATACGTCATGGCCAGGGTGCGCGGGATCGGCGTGGCCGACATCATCAGCTGGTG CGGCACGGC

Sequence 1956

GAGCTCCCCGCGGTGCCGCCGCCGGGCAGGTACTGATCTAACCAAGATATTTTGTTTTT
CTCATCCACCAGTCACTTTCTCAGTCCTTTCTGTATCCCTTGCAATTTGAACAAAGCTTG
GTGAATAGTGTGCACCACAAAAAGCACACTAGGTGAAAGACAGATACATAAAAAGGGTAAA
GTCAGGATATTTTAACAAACCTATCAAGCTCTAAATATAAGCCTCCTTGGTAGTTTTCTC
TTTAACCCTCTCTCCACTGTTGGATGAAATTTGCTGCATTCAATTCCAGTTCCCACCCCA
ACTTCCTTCTTAACACAAGGTCAGGGTTAAGCCTTCGGTGCTTTAATCCAGAGGAAAATT
ACTTATTTTAAAAAGCAGTGAAAAACACCGCATTCCTTTGGC

Sequence 1957

CCCCGCGGTGGCGCCGAGGTACGCGGGGGCCCTCAACTTCTGAGAGCTTAAGGTATTTG
TTCATGTTAGGCAGGTAATGTCTATAAACCAAAAGCTGCCACATACTATCTCTCTGCTCA
ACACTITACTGGATACTGGAGGATTTAAGGGAAGGAAAAAGTGACCTTTTTTGCCTTTT
TAAGAGCTTGTAATCGGTAAAGGAGATAAAACTCACACAAAGGTCAGGGTATATTTTGTG
CTAAGCATATGACCGTAGACATTTAAAGTGCTGCCCGTAATGCAGAAAAGAAGAAGAAGAAGT
GGTGTGATCTAAAAGTAACATAGGTTTTGGTTTTGGTTTTGNTTTTTTCTTTTT
TCTTTTTCTTTTTCT

Sequence 1958

CCCGCGTGGCGGCCGAGGTACGCGGGGGTAGATGGAAGAACTTGTGTGCTTAGAC CTGACGCTGGGAGGAGATGCTGCCACCTAGGTTACTTGTAGGACCCTATACGGCAACCTC CTTTGCCAGGAACTATTTATAAACATCCTGCAGGAAAATGCAGTGAAGTAGAAGAGACAG GGATATCCCAGAAGGTTATGCAAAACATCAAGAGAAGATGAGAGGGTCAGAGATGGGAAGA AACAAGAACTTTGACATGCTTGGTGTTCTTGCCCAAGCTTTGAAGAAGTTTACAAAGTCT ATATGTCAGAATACACATTTCCCACCTTGCCCAACAGTAGAAAAACATAAGAAGAGAAAA

Table 1

ACATTAAAAAATGACAAGGAAGTTAATGGAAGTCAACAATGTGATGGTGTTTTGGANGTGG AGCCTTCAAAAAGGTATTAATGCCCTTGTAAGAAGAAGGCCAGAAAAGCTTGCGCCCCTT CTTTCTGCCCTGTGGANGGAGCCCAAGANNCCGGCTGGTCTTGCNACCTTGCAAGAAGGA CCCCTCACTTAGAAGCTAGGCCNTACTTGGGCTTNCTTAATCTTGGGCTTTTCCNACCTT NCAGAACTTGTGANNAAGTTNTNTTGTTTGGGGGTTAATCCAATGGGCTATNGGAAATTT TTTTATNACCNNNCCCNNGCCAAGANAGGGCCCTTATTTACTTCCTTCCCTT Sequence 1959

GGCGAATGGAGCTCCCGCGGTGGCGGCCGGGGGCCATTGAGACTGCCATGGAAGACTTG
AAAGGTCACGTAGCTGAGACTTCTGGAGAGACCATTCAAGGCTTCTGGCTCTTGACAAAG
ATAGACCACTGGAACAATGAGAAGGAGAGAATTCTCTGGTCACAGACAAGACTCTCTTGA
TCTGCAAATACGACTTCATCATGCTGAGTTGTGTGCAGCTGCAGCGGATTCCTCTGAGCG
CTGTCTATCGCATCTGCCTGGGCAAGTTCACCTTCCCTGGGATGTCCCTGGACAAGAGAC
AAGGAGAAGGCCTTAGGATCTACTGGGGGAGTCCNGAGGAGCAGTCTCTTCTGTCCCGCT
GGAACCCATGGTCCACTGAAGTTCCTTATGCTACTTTCACTGAGCATCCTATGAAATACA
CCNAGTGAGAAAATTCCTTGAAATTTGCAAGTNGTCTGGGTTCATTGTCTAAAGCTTGGT
TCCAACTTTTCCAGAATGCCCCCCAAAGAATTCACTNGGATCTTGGAAAAAAGA
CCTGATGGNGGTTAACTGAANCCATTTTGGTTGGNACCCTANCCAGGGCTNGATGTCATT
TATTTGGGAAACCCNNACAAACTTGGCTTTTTCCTTTGCCCCNGGGANGNNTTGGGTTTT
GAGAAGCTTTTTTGGNNCCTCGGCCCCTTTTANAACTTAGNGGATNCCCCCCGGCCTNNG
GGAATTCNAATNCAANCTTTTNGATNCCCGNNACCCTTGNGGGGGGGGGC
Sequence 1960

TATAGGGCAAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGGGTAGATGGAAGG
AAGAACTTGTGTGCTTAGACCTGACGCTGGGAGGAGATGCTGCCACCTAGGTTACTTGTA
GGACCCTATACGGCAACCTCCTTTGCCAGGAACTATTTATAAACATCCTGCAGGAAAATG
GTAAAGCCCTTGGTTAAATTTATTGGCTTCATTTATGTATCTCACAACACTTCTTTTCTG
TTTTAATTCTAGGAATAGAAACTTACTTTTGGAAATACAGNACCTGCCGGCGGCCGTCTA
GAACTAGTGGATCCCCCGG

Sequence 1961

Sequence 1963

Table 1

Seguence 1965

Sequence 1966

CGCTTTCTCATAGCTCACGCCTGTAGGTATCTCAAGTTTCGGTGTAAGGTCCGTTTCGCT CCAAAGCTGGGCCTGTGTTGCACAGAACCCCCGGTTTCAAGCCCCGGACCCGGCTT Sequence 1967

CCGGGCAGGTACGCCTACTCAACCCGGCTGTTCACCATTGATGGCATCAGCATCCCATAC ACATGGAACCACACCGTTTTCTATGATCAGGCACAGGGAAGAATGCCTTTCTTGGTTGAA ACACTTCATGCATCCTCTGTGGAATCTGACTATAACCAGATAGAAAGAGACACTGGGTTT TAAAATTCATGCTTCAATATCCAAAGGAGATCGCAGTAATCAGTGCCCCTCCGGGTTTAC CTTAGACTCAGTTGGACCTTTTTGTGCTGATGAGGATGAATGTGCAGCAGGGAATCCCTG CTCCCATAGCTGCCACAATGCCATGGGGACTTACTACTGCTCCTGCCCTAAAGGCCTCAC CATAGCTGCAGATGGGAAGAACTTGTCAAGGATATTGATGGAGTGTGCTTTG Sequence 1968

GGGGCCATTGAGACTGCCATGGAAGACTTGAAAGGTCACGTAGCTGAGACTTCTGGAGAG
ACCATTCAAGGCTTCTGGCTCTTGACAAAGATAGACCACTGGAACAATGAGAAGGAGAGA
ATTCTACTGGTCACAGACAAGACTCTCTTGATCTGCAAATACGACTTCATCATGCTGAGT
TGTGTGCAGCTGCAGCGGATTCCTCTGAGCGCTGTCTATCGCATCTGCCTGGGCAAGTTC
ACCTTCCCTGGGATGTCCCTGGACAAGAGACAAGGAGAAGGCCTTAGGATCTACTGGGGG
AGTCCGGAGGAGCAGTCTCTTCTGTCCCGCTGGAACCCATGGTCCACTGAAGTTCCTTTA
TGCTACTTTCACTGAGCATCCTATTGAAATACACCAAGTTGAGAAATTCCTTGA
Sequence 1969

Sequence 1970

CCGCGGTGGCGCCCCGGGCAGGTACGCGGGGAGACCTGACGCTGGGAGGAGATGCTG CCACCTAGGTTACTTGTAGGACCCTATACGGCAACCTCCTTTGCCAGGAACTATTTATAA ACATCCTGCAGGAAAATGCAGTGAAGTAGAAGAAGAACAGGATATCCCAGAAGGTTATGCA AAACATCAAGAGAAGATGAGAGGAGGAGGAAGAAACAAGAACTTTGACATGCTTGGTGT

Table 1

Sequence 1972

Sequence 1973

CTTAGGGCGAATTGGAGCTCCCCGCGGTGGCCGAGCGGCCGCCCGGGCAGGTACCTTAGC
AAATAGATAGTTTATTCACCAACTATAATCACCTTAACAATAAAAGCTCTCTTTTCGAGA
ACACTGCGTGTCAGGCACTTCATGAAAATTATACTAAACACTTTATGAAAATTATCTCTA
GCTGCAAATTCCCGCGGATGCTATGCAAATTAGGTATAGCTACACTTTGCTGATGGGGAA
AGTATAGCTTAGAGAAGGTAGACGAACTGCCCAAGGCCAGAGCTATGTGGCAGAGATGGA
ATTCAAATGCAAGTATAAATAATAGAATAATTTTCAGTTGGAAATTTCAAAAAGCTGTTC
TAGTTACATTGATGTTAAAATCTGTTATTCATTTAAGATGAAGATGGCAAGGGGAAGTAA
AATTACAGGGAAGTGGTGAGGATAGAGCTGAGGAAAACTTGGAATGAGATTTTAAAA
AGAAATCTGGAAA

Sequence 1973

CTTAGGGCGAATTGGAGCTCCCCGCGGTGGCCGAGCGGCCGCCCGGGCAGGTACCTTAGC
AAATAGATAGTTTATTCACCAACTATAATCACCTTAACAATAAAAGCTCTCTTTTCGAGA
ACACTGCGTGTCAGGCACTTCATGAAAATTATACTAAACACTTTATGAAAATTATCTCTA
GCTGCAAATTCCCGCGGATGCTATGCAAATTAGGTATAGCTACACTTTGCTGATGGGGAA
AGTATAGCTTAGAGAAGGTAGACGAACTGCCCAAGGCCAGAGCTATGTGGCAGAGATGGA
ATTCAAATGCAAGTATAAATAATAGAATAATTTTCAGTTGGAAATTTCAAAAAGCTGTTC
TAGTTACATTGATGTTAAAATCTGTTATTCATTTAAGATGAAGATGGCAAGGGGAAGATAA
AATTACAGGGAAGTGGTGAGGATAGAGCTGAGGAAAACTTGGAATGAGATTTTAAAA
AGAAATCTGGAAA

Sequence 1975

GGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACAAGGAGACAGCATGC
AGGGTGTGTTCAGAAGAGACTTGCTGAGGTGCTCGGCTCTTAGCATTAAAAATGTGATGTT
GGTATATCATCCTGATAGAAAACACTGCTTTCCAAATCCTAGTCACTGGATGGGAGGAAA
GTAAGAACAGATTCTTCCAACCACTACTGATTTGTTATAATTCTCCCCATTGAAATTGGG
ACAAAATTTGTAACATGCTACTCCGAAATTGATCACATTCTCAATTCTGCAATTAT
GTAACAGAAAAGCATAAAGTTTGCAGGGTGGAGCGGGAGGATTTTTCTAGGAAACTTCCT
TCTCTTCCATTAACCGTGTTGAATGAGTAAGGACAGTTAAT

Table 1

Sequence 1975

GGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACAAGGGAGACAGCATGC
AGGGTGTGTTCAGAAGAGCTTGCTGAGGTGCTCGGCTCTTAGCATTAAAAATGTGATGTT
GGTATATCATCCTGATAGAAAACACTGCTTTCCAAATCCTAGTCACTGGATGGGAGGAAA
GTAAGAACAGATTCTTCCAACCACTACTGATTTGTTATAATTCTCCCCATTGAAATTGGG
ACAAAATTTGTAACATGCTACTCCGAAATTGATCACATTCTCAATTCTGCAATAGCAGA
GAATTTAGCCTCAACACCACCAATTCAAAATAAGTTTAGGTCTTGCCCCTGCTGATTAT
GTAACAGAAAAGCATAAAGTTTGCAGGGTGGAGCGGGAGGATTTTTCTAGGAAACTTCCT
TCTCTTCCATTAACCGTGTTGAATGAGTAAGGACAGTTAAT

Sequence 1977

Sequence 1977

CCGGGCAGGTACGCGGGAAAGAGAAGAGAGAATATACAGTCTTTGTATTGACCTGTATGCT
TCTCATTTTTGTTCTTTTTGTTCCTTTCTATAATTCTGGATTTCCATCTTGTTTAATAGC
CCTCAGCCTGAGGGATATCAGCATTTCTTGTGCTATGGATCTTCTAGCAACATATAATTT
CATCTTTTATGCATATCCAGAAATTGTTGCTTTGGTTTGATTTTTGTTTTTGTAGTTTCAC
TCTGTGTAGAATTTCTGGTTACCGTTTTTTTCTTCCCAGCATTTTGAGATATTGATCCAG
TGAGTTCTGTCATGCATTTGCCTACTTGGGTGAAATGTCCCACCAGACGGTGTGATATTT
AGTAGCCCAGAAAGCTGCCAAGGGGTTGAATGACCACTATCTGAAGATATGAACCAGTTTG
CTCTCCATAGGGAGGATTTCATCAACAGGAAACAGATGCCTGGAAGGCATTGGATTTGCT
AAGTGTCTATGCCATATGATTCTGCTGTTTGCGTTTTGATTTAGAATGCTGAGCTGACTCA
AAGTCAAACTGNAAGTACCT

Sequence 1980

Table 1

Sequence 1981

Sequence 1982

Sequence 1985

Sequence 1986

CCGCGGTGGCGGCCGAGGTACACTTGGTGCAATAAAGTGCATCTTTAAAGTGTTTTGAGT

Table 1

ATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCCGAGGTACACTTATAGTTGAGAGCCA
AGTCTCCCTTATCATTGGTGAATGAGAATGAGCTACTGAAAACAAAAGAGGGTCTTCTA
CTCAGCCTCTACCCCTAATATTTATATCAGAAGCAGAGATTAACTGTCCTTACTCATTCA
CACGTTAATGGAAGAAGGAAGTTTCCTAGAAAAATCCTCCCGCTCCACCCTGCAAACT
TTATGCCTTTCTGTTACATAATCAGGCAGGGGCAAGACCTAAACTATTTTGAATTGGTGG
TGTTGAGGCTAAATTCTCTGCTATTGACAGAATTGAGAATGTGATCAATTTCAGAGTAGC
ATGTTACAAATTTTGTCCCAATTTCAATGGGGAGAATTATAACAAATCAGTAGTGGTTGG
CAGAATCTGTTCTTACTTTCCTCCCATCCAGTGACTAGGATTTGGAAAGCAGTGTTTTCT
ATCAGGATGATATACCAACATCACATTTTTA

Sequence 1988

CGGCCCTCGTGGTGGCCAGGCGCGATGCGCGCGGCGTGGCAGAACTGCTGCGTCCGTAC
ACCAAAGAGGCGCTGGCGCCCGGCGAATTCCTGCTCGAACTGACGCCGAAGGATGGCAAT
TGGGTGCTGGTCAGCGATGCCTGGTTCTTCAAGGAAGGCGAGGCGACGCGCTGGGAAAAG
GCCCGCTATGGCGAGTTCCGCGTGCTGCCCGATGGCCGCGCCTTGCTGGTGGGCATGCGC
GGGGAAGATTTACAGGCACTGTAACCGCTTGATTGAACAAACCCAATG
Sequence 1992

CGGGCAGGTACTTTGGCACATGCTGGTAGCCAGGAGTCTGGGCCTGAAATTTGGTCCTGA

Table 1

CTCCACCTCATCTCTGCATGACTTCTCTGGGAGATACAGCCTCTCCATTTTACACTG AGAGAACTAAATGAGCTCTAAAGCTGCCCTGACAGCTGACAGCTCAAGGTTAGCATATTTC TGTGTGGCTCTGGCAAAAGTACCT

Sequence 1993

CCGCGGTGGCGGCCGAGGTACACTTATAGTTGAGAGCCAAGTCTCCCTTATCATTGGTGA
ATGAGAATGAGCTACTGAAAACAAAAAGAGGGTCTTCTACTCAGCCTCTACCCCTAATAT
TTATATCAGAAGCAGAGATTAACTGTCCTTACTCATTCACACGTTAATGGAAGAGAAGGA
AGTTTCCTAGAAAAATCCTCCCGCTCCACCCTGCAAACTTTATGCTTTTCTGTTACATAA
TCAGGCAGGGGCAAGACCTAAACTATTTTGAATTGGTGGTGTTGAGGCTAAATTCTCTGC
TATTGACAGAATTGAGAATGTGATCAATTTCAGAGTAGCATGTTACAAATTTTGTCCCAA
TTTCAATGGGGAGAATTATAACAAATCAGTAGTGGTTGGCAGAATCTGTTCTTACTTTCC
TCCCATCCAGTGACTAGGATTTGGAAAGCAGTGTTTTCTATCAGGATGATATACCAACAT
CGCATTTT

Sequence 1994

CGGTGCCGCCGAGGTACCGGTTGATGTAAGCACAGGGATGGTGGGGACAGGGTGACCAA
AGTGAACTGGCACGAGATGAGTAGCTGGTATATAGTGACTTTGGAAGGCAAGGTGCTTGA
AATTTCCTGGAAAATCTCTGCAAGTGCACAGTAGAAACTATTATCATTGGTTACGTGCTT
CAAGAGGACTGGGCAGATGGGGGGGCAGGAATAAGAGAGCCACTATTCACTTGACAAATT
CTTGGACATTTTGATTTCTGAGCCATATGGATGTGTCCTATCAAAAAGAATAAGTGAA
AATGTTCAATAGTAAGAGAACACTTTGTAAATCTCTGGCTGCTGCTCTTTGTGATTAGCC
TCTCAGCACTCTTATTTGGAATAATCAGAAAAATAAGTATCAAATTTTGGGAGGAGA
GTATACTTGTGGAGATTTGGGAAGAAAAATAAGTATGGAAAGTTTCCCCCAATAATA
AAATGAAATTCATTGGAAAGCCATTTCAAACATTTAGAAAGTTAACCCAGAAAAATAGAA
AGG

Sequence 1995

GGCGGCCGCCGGGCAGGTACTCGNNAAGCAGTGGTAACAACCCAGAGTACTCGGGAAGC AGTGGTAACAACGCAGAGTCCCGGGAAGCAGTGGTAACAACGCAGAGTCCCGGGAAGCAG TGGTAACAACGCAGAGTCCCGGGAAGCAGTGGTAACAACGCAGAGTCCCGGGAAGCAGTG GTACCT

Sequence 1996

Sequence 1997

Sequence 1998

ACTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACATTCTAATCCCAGT TTACATTTAAAACACTTCAAATGGAGCCACTAGGACTCAAAGTTGCTAAATACACCCATG

Table 1

CCCTCTTATCGCCTTCCACTGGGGGTGGTTCTTCGGTATTTTAAGTCTTGGAAGTTAATT
TTTGAGGAAAAAAAAGTAATAGACATGTGACAAAAACAGGAAGAAGGGACACAGTTCAAC
TGGGTTGTAGCTCTAATCTCACTTTATCAGCTGCTTGAAAGAGGGAAATGAAGGACAGAG
CGGTAGGAAGTCTGCACACCCCAACCTCATGGAGACCAGCTCAGCCCCCAATGCAGTCAA
GCTACCTAACCTCCTGGAAACATAAAGATCGGCGTGTTACTTG

Sequence 1999

Sequence 2000

Sequence 2001
AGGTACATTCTAATCCCAGTTTACATTTAAAACACTTCAAATGGAGCCACTAGGACTCAA
AGTTGCTAAATACACCCATGCCCTCTTATCGCCTTCCACTGGGGGTGGTTCTTCGGTATT
TTAAGTCTTGGAAGTTAATTTTTGAGGAAAAAAAAGTAATAGACATGTGACAAAAACAGG
AAGAAGGGACACAGTTCAACTGGGTTGTAGCTCTAATCTCACTTTATCAGCTGCTTGAAA
GAGGGAAATGAAGGACAGAGCGGTAGGAAGTCTGCACACCACCTCATGGAGACCAGC

TCAGCCCCAATGCAGTCAAGCTACCTAACCTCCTGGAA

Sequence 2002

Sequence 2003

ATTGGAGCTCCCCGCGGTGGCGCCCGAGGTACAGGTCCCCTCACACCTTCTGTTGATGCC
TTATTACCACCAGGCAGATTAGAAGTTCTGGTTTCTCTAAATTTCAGTTGACTCTGTAAA
CTTATAATACTTATCTTTATAATTCTGTTGAGAATATAAAAATGAAATGATGCATGTAATAT
ATCAAGCCACTGTCTGATGTAGAATAATATTACTAACATTTATGATTTTGAAAATTAATA
ACAAAGTTGGAGGAAATACACCACCAACTTCAAATGCTAATATGAAGTTACAACGATCAA
GATAGTGTGGCATTGGTGTAAAAACAGACATGCTTATCAATGGCGCAGAATTAAAAGAAT
AGAAATTAACTTCTGCTTTG

Sequence 2004

Table 1

Sequence 2005

CCGCGGTGCCGCCCCGGCCAGGTACTTGGAATGCTGTGTGGAGTCCTTTTTCTACTT
TTGTTCCTGAGAAAGAGAGATTCACAAACTTCCCACATTCTTCCAGTGGCATCTAAGGAT
CCCTTCCTAAATGGCCTTTCTCCCAGCCAATAGACTGAAGCAAACCATGTCCCTGATGCT
TCCTGCCCACCACCATCCATTCTTTCAACCAACAGCTTCTCCGGGCTTTCACGTGCCATG
CACTTTGCTAAGAGCTTGAGGGAAATACAGCAATGAAGAAGAAGATGATTTCTGTTTGGAC
CCAGTGCTCAGGGATTCCTCCTATTAGGAAATCAAAGGAGGCTTCCAAAAGCCCTACAAT
TTTTTCCCTGNTAACTAAAGA

Sequence 2006

AGGTACGCGGAGGAAAACACAACATGAACAGGCAGAGTGCACACGCCGTGGCCTCGGGA AGCCACAATCATGTGGCTGACATGGTTCCAGAGTGTGGCATTAGGGAGACCAACTTCTGA GCTGCAGATTCACAGCATGGCCATGCAAGCAGGGAAGATGTGCTCTACTCCAGGATCAAG GAGCAAGCCCATATTTCCTCTTGATTCTGGGACTCCCTCTTGAGACTGATTTGCTCTAAT GTTAGCTCTTGAGAGAACTGGGGTCCCTGCCTTCTTGGGGAGCCTGAAAAGAAGTTTTGC T

Sequence 2007

TCACAAAAATCGACGCCTCAAGTTCANNAGGTGGCNGAAACCNCGTACAGGAACTTATT AANAGCATACNCANGGCGGTTTTCCNNCCCTGGNAAAGCTTCCCCTNCGTGGCGCCTCTTCCCTGTTATCACGACNCCTGGCCCGCNTTTACNCGGNATACCTTGTNCCGGCNCTTTTCCTCCCCTTTCCGGGGNAAAGNCCGGT

Sequence 2010

CTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACAACGATGCAC
ACAGATGGGAGGAGCTGCCTTGAGCGAGAGGACACTGTCCTGGAGGTGACAGAGAGCAAC
ACCACATCAGTGGTGGATGGGGATAAACGGGTGAAACGGCGGCTGCTCATGGAAACGTGT
GCTGTCAACAATGGAGGCTGTGACCGCACCTGTAAGGATACTTCGACAGGTGTCCACTGC
AGTTGTCCTGTTGGATTCACTCTCCAGTTGGATGGGAAGACATGTAAAGATATTGATGAG
TGCCAGACCCGCAATGGAGGTTGTGATCATTTCTGCAAAAACATCTGTGGGCANGTTTTT
GACTGCGGCTTGCAAAGAAAGGGATTTT

Sequence 2011

CTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCCCCAGCACTTTAGCCC
TGTGTGGCCAGCGCCCCATGCGCAAGCGTCTTTCTGCCCCAGAGTTGCGGCTGAGTCTGA
CTAAGGGGCCTGGAAATGATGGAGCTTCACCCACCCAGTCTGCACCTTCCTCTCTGATG
GCAGTTCTGACCTGGAGATAGACGAATTGGAGACACCTTCAGACTCGGAGCAGCTGGACA
GTGGACATGAATTTGAATGGGAAGATGAACTACCCCGGGCAGAGGGTCTGGGCACCAGTG
AGACAGCTGAAAGGCTGGGCCGAGGTTGTATGTGGGGATGTGACTGGAGAAGATGGACAT

Table 1

CACTGGGAGGGGGTGTTCCGAATGGGGACCC

Sequence 2012

GGGGACCGCCAGGGGCCTCGAGAATCGGTATCCTGAGTCCTCTTGAAGAGCAGTAGAGGT TGTTTCATTAAGTGCAAACACATTGTTCTTAATTTGAAAACTGTGGGCAGAAACAGAAGC CCGAGACTAATTTTTCCATTGCTAACTCTAGATTCTCGGCCACTGGAGTCTGAAGATACT CTCTTTGAGAATGCATATTATTTTGCTCACAGCTAAAACATTTAAGTATCATAGCTGATC AGTGGAGTGAGATTAAAAGGTTTCTTTTTTGAATCATCAGCTAGAGAT Sequence 2013

CCGGGCAGGTACGCGGGATGATTAATCTTCCCTTATCCACAAACTTAACTGTGGAGAAAC
AGGAGAAAGTGTGTGCCTAGAAGCTGGATTCAGGGACCCATGGTTACCCACTTCTACTTA
TGATTCCGTCATTACTGTTTTTTAGGAAAATAAACAGATCTTGATTCTTTCATAAAAGT
CGATTCTTCAACAAGCAAATGGGAAAATCGGCAGGCCCAGATATGTGTGTATAGCAGCTA
CTGGTTGGAAATTTGGACACAAAAGTCTTTATCTACCCAGCCTGTGAGCCACAAATCTGG
ACTGAGTATAAAAAAAGAATAAAACTAAATACCACCATGGTTCTCACTTATTAAGTGGGGA
ACTAAA

Sequence 2014

CCGGGCAGGTACCCTGGATCGTTTCAGAGATCTAACGTGTTGCCACACCATANCTCTAAG
AAGCTGTGGGGCACAGTTCAAATTCTTANTGGAGTGTATGATTGCACAANGAAATACTTT
AAATATGTTTACTTTTTAATTTCTAATNGACTAAGAAAATCAGCNAGCATAAAAACTAAC
TTTTTTTANAAGGACTCCCCAAAAATTTTGCATGTTTTTTTCCAGGTNTTTTTATTTTTA
ATTTANNTNTGNTANGGGGCATTAAATTAAATNTNGTTGGCCANAATTTTAAAACNTTAN
TTGNNTTACCCNTTCGNGCCCCGCCTTTCTTATGNAAAACCTTNGATTNGGGAAATTCAC
CCCCCCNGGGGGGNNTTGGGCAANGGGGTAAAAATTTTCCNGAATTTATTTNCAAAAGG
ACCCTTTTAAATTCCGGTNAATNAACCACNGGTTCNNNAATCCCCTTTCTATGAAANGNG
NGGGGGGNGGGGGNCCNCCCCNGGTGTTAACCCCCCAAAAACC

Sequence 2015

CCGCGGTGGCGCCGCTTTCTCTTACTGATAGTAGGATATTTCTGCTTTAGTTATTGTCA
CCTTAAATATTTTCAATGTTGAAATCCTCACAGCATGTTTGATGAAATCTAGTTTTCA
AATTTCTTAGGTATATTTCTGTCACGTTGGCATGATAACAAATGCAATAACCCAAAAGA
CCCCAAAAGCTAGTGTAATCCCTTTTGCAATCCAAGCATGAGGATTCATCTTCATGTTGA
CAGTGCGTGAATGTTCGGTAGGCTTTGTCAAGCTTGCATACAATAAATTATATTATGTCC
CTTTTTCTTTTAGGGGGTCTCCTGTTTAAAGGATGGGTCTTCTGGAAGGGCTAACCTGCGG
GAATGGAAAAGTTT

Sequence 2016

Sequence 2018

Table 1

CCGCGGTGGCGCCCCGGGCAGGTACCAGGCTAGGCAGCTCTGGAGAAAGCAGAAGTG
GATAAATAAGGTGTGGACTCACCAAAGACAGTTCCAAAGTCAATTTCACTCTGACACACT
CTCTGTGATCTTCCACAGTCAGCACAATGCCTGCCCCCTGTGGGTGTTGTATAAATATTT
GTTGAATGAATGAATCAATCATTCAACAGACCAAGGCCAAATCAGAACCCCAAACCCTAA
GGTCTTTATACTCTCACTGTCCATCCATCGATCTTCCTGTCAGAAATCAGAATATACCTT
TGCAATACCCTTTGCTAGCCTTTCAGTTATCTTTTGAATAGAGGCTCTGAGCCTTGAAAA
TATTGCCTGGGAAAATATTTAACACCCATT

Sequence 2019

GGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACATGCATACTCAATGTTTAGTTCC
CACTTATAAGTGAGAACATGTGGTATTTAGTTTTATTCTTTTTTATACTCAGTCCAGATT
TGTGGCTCACAGGCTGGGTAGATAAAGACTTTTGTGTCCAAATTTCCAACCAGTAGCTGC
TATACACACATATCTGGGCCTGCCGATTTTCCCATTTGCTTGTTGAAGAATCGACTTTTA
TGAAAGAATCAAGATCTGTTTATTTTCCTAAAACAACAGTAATGACGGAATCATAAGTAG
AAGTGGGTAACCATGGGTCCCTGAATCCAGCTTCTAGGCACACACTTTCTCCTGTTTCTC
CACAGTTAAAGNTTTGTGGGATAAGGGG

Sequence 2020

NTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCTGGTAGTCCCAGCTACTC
AGGGGGCTGAGGTGGGAGGATTGCTTGAGTCTGGCAGGTCGTAGCTCAGTGAGCCCAGA
TGGCACCACTTCATTCCACCCTGNGTAACANGAGTGAGACCCTGTCTCAAAAAAAAAGAAA
AAAACATACACACAGACATATATGCATACATACAAGGAGCAGCCACTACCCTTAGGGCTA
AGACAGTGTGTCCAAGAATGAGTCCCCCATTTCCCTACCACCACCCCCAGGGCTTGATNAT
TCATACCCTGGTTTAGNAAAGGGGCCTCAGTTGTGGGCTCACTGGAATGGCCAGAGNTAA
TTGCNTGNATGTGCCTTCTCTGGGGGAAAGCGTTG

Sequence 2021

Sequence 2022

CACTNCTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGNCNGGCCNNGTNCTTCTN
TTTTNCATGCTTGATTTGTGAGGCTTATTAGAAAACAATGGCATTTGACGTTTCATTTCT
GACTCCTTGATTTCCATTGTTTTCAGGAAGTTTTCATCTGCTGAAGGCAACTAATCCACA
ATGAGCAAATTATCCTGCCCTGNAGGGTAAGCTATAATATCGGCCCCATGCTTCAGGAAG
AGAAAATCATGTGTTCAGGGGTGACTTTGAGTCAGCTCAGCATTCTAAATCAAACCGCAA
ACAGTANCAATCATTATTGGCATAGAACACCTTAAGCAAAATTGGGTCATTTTACNTAAN
GTTTTCTGGCTTTCGTGGGAGAATTAATTCTGCCC

Sequence 2023

Sequence 2024

CCGCGGTGGCGGCCGAGGTACCCTGCTGAAAGATTATTTCTAACAGGCTTGTAGAGAAAC

Table 1

GTCGGTTCATGTAAATTAGAAATTATGGGGCCACTTTGCCATTCTTCACACCTGCAATGA ACAGGTGTTTATCTGCAGTTCTGACTTATCTCTTGAACTCCATTTGCATGTTATAGTGGG ATGCAGCTGATGCCCTGTCCAGATCTTCTTCAGGCCACTACATCTATATATGCATTCATA TTCCAGTGGCTGTGAGTGTTGGCTGTTGGTTGACAGAGGAGGTGCATCCTCCTGGGAGGG AAACTGGAACTCAGCCTGGATGAAAAGCCACCCTGGTCCTGGGAGGTGAAAGNCATCTTC CAAATGACAGC

Sequence 2025

Sequence 2026

GAGCTCCCGCGGTGGCCGCCCCGGGCAGGTACAGATGTAACTGGAAGATACCTGAA TGTGCAGTCAGTGCCAAGTGGAGGCCTAGGTAGGTTATTTGGTTATTGGGAAAAGGAGT GGCACCAGAAAATTGGAGGACTAGAGGACAGTTGGGTGAGAGCAGTTTAGTTTCTTTGAT TCTGTGCTAACTTTTTTGGATATTTGCTGGAAAATGCAATTTATAGAGGATATTTGCTCT TGGCTATGGAATGCATTTGCTGTTTCTTCTCTTTTATACGTAAGATACATCTGTGAGACC CTCTACAGGAGATGAATTCCTGGTGTAAAAGAGTCATGTGAATATTGTGGAGTAATTATT CTGAGCCAGGGGAGCAGGCTAATTAGCCTTCTGGGGAATG Sequence 2028

Sequence 2029

CCNCNGCGGTGGCGGCGCNGNCNCGGGGATCTCACTCAATCTTACTCCCTTGTAGAACA
GGCGATATCTTCACCATGCGCACAATGAAATCAATACTCANAGAAGGCAGATNATTCTCC
ACGAANCCNGANAACTAATAAATGAACAACTTGGGTGAAATGTCCCACCAGACGGTGTGA
TATTTAGTAGCCCAGAAAGCTGCCAAGGGGTTGAATGACCATTTGCTCTCCATAGGAGGATTTCATCAACAGGAAACAGATGCCTGGAAGGCATTGGAT
TTGCTAAGTGTCTATGCCATATGATTCTGCTGTTTGCGTTTTGATTTAGAATGCTGAGCTG
ACTCAAAGTC

Sequence 2030

Table 1

ACTGGTCAGGATTTTACGGTGTTGTCTAGGAGAGAGCAACCATGATGGGCATGCAATGCT CAAGTTCACAGAAAAACATGAATAGCAAGACTCAAATCTGGCTGCCAGATTTCTGCAAGG TATTTTTCTCTCCAAACGAGGTAATGTGTTTCTTATAACAGTCTTTATAATAAGGAGATG TGTGTGGAAAAAAATCAAGTGTTAAACGGAGTCATGCAAATTAGCCATCTGGATAAAAC Sequence 2031

Sequence 2032

Sequence 2033

Sequence 2034

Sequence 2035

Table 1

GAAATGAGATATTGGAAACTGAGAACATTGGCTTTATGTTTAAGGAAGTGTGTTTTTGGTAAAATTGCCATTCCACAAAAATTT

Sequence 2037

Sequence 2038

Sequence 2039

Sequence 2040

CTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGGGGGCCNTNGAGACTGNCNTGGN
AGACTGGNNAGGTCACGTNTCTNAGACTTCTGGNGAGACCATNCANGGCTTTTGGCTCTT
GACANAGATNGACCACTGGAACACTGACNAANGAGAGAATTCTACTGGTCACANACAAGA
CTCTCTTGATCTGCAAATACCACTTCATCATGCTGAGTTGTGTGCAGCTGCTGCGGATTC
CTCTGAGCGCTGTCTATCGCATCTGCCTGGGCAAGTTCACCTTCCCTGGGATGTCCCTGG
ACAAGAGACAAGGAGAAGGCCTTAGGATCTACTGGGGGGAGTCCGGAGGAGCAGTCTCTTC
TGTCCCGCTGGAACCCATGGTCCACTTGAAGTTCCTTATGCTACTTTCACTGAGCATCCT
ATGAAA

Sequence 2041

GGGGCCATTGAGACTGCCATGGAAGACTTGAAAGGTCACGTAGCTGAGACTTCTGGAGAG ACCATTCAAGGCTTCTGGCTCTTGACAAAGATAGACCACTGGAACAATGAGAAGGAGAGA ATTCTACTGGTCACAGACAAGACTCTCTTGATCTGCAAATACGACTTCATCATGCTGAGT TGTGTGCAGCTGCTGCGGATTCCTCTGAGCGCTGTCTATCGCATCTGCCTGGGCAAGTTC ACCTTCCCTGGGGATGTCCCTGGACAAGAGACAAGGAGAAGGCCTTAGGATCTACTGGGG GGAGTCCGGAGGAGCAGTCTCTTCTGTCCCGCTGGAACCCATGGTCCCTGAAGTTCCTTA

Sequence 2042

Table 1

Sequence 2043

Sequence 2044

Sequence 2045

Sequence 2046

Sequence 2048

CCGCGGTGGCGGCCCGGGCAGGTACGCGGGGAGACCTGACGCTGGGAGGAGATGCTGCCACCTAGGTTACTTGTAGGACCCTATACGGCAACCTCCTTTGCCAGGAACTATTTATAA

Table 1

ACATCCTGCAGGAAAATGCAGTGAAGTAGAAGAGACAGGGATATCCCAGAAGGTTATGCA AAACATCAAGAGAAGATGAGAGGTCAGAGATGGGAAGAACAAGAACTTTGACATGCTTG GTGTTCTTGCCCAAGCTTTGAAGAAGTTTACAAAGTCTATATGTCAGAATACACATTTCC CACCTTGCCCAACAGTAGAAAAACATAAGAAGAGAAAAACATTAAAAAATGACAAGGGAA GTTTAATGGGAA

Sequence 2049

Sequence 2050

AGGTGGCACGGTGTATGAAGGCCTGTGTTTGAAGACTTAGGTCAGACCTTTTGCCCGCCT TTCCCCTATGCAGCTCTATGCAACTGTCTGTGCAAGGTCCTGTAATTTGCGTAGGACGCC TTGACACAGTCTCTGCTTATGGACGCTTTACAAAACTATCTTGCAAAGAAATAAGTACCT GCCCG

Sequence 2052

Sequence 2053

Sequence 2054

Table 1 ~

Sequence 2055

CCGCGGTGGCGCCGAGGTACTTCTGTGACATGTATCACCAACTCACACAGTGATTCTTA CGTTCTTAGGTCACTGCTTGGATTATGCAGCAAGAACAAGGCCATGTAAGGGGTAGGGGT GGGGCCAGGATTAGACCTGATCATTGAGAAATGGCAGATGGTAAGGGAAGGTCAGTCGCA GATACCTACACTGGTAGGAAATAAAAAGCATATGAGACAGAACANAGTATTACAAATGAA GTGTAACAGACCACAGGTCCTGGGGTGTACCTGCCCGGGC

Sequence 2057

CCGCGGTGGCGGCCGAGGTACTTACATGGGGACCGCCAGGGGCCTCGAGAATCGGTATCC TGAGTCCTCTTGAAGAGCAGTAGAGGTTGTTTCATTAAGTGCAAACACATTGTTCTTAAT TTGAAAACTGTGGGCAGAAACAGAAGCCCGAGACTAATTTTTCCATTGCTAACTCTAGAT TCT

Sequence 2058

ATAGGCCAATNGGAGCTCCCCGCGGTGGCGGCCCGCCGGGCAGGTACAATCTCTGGCCC
TACATTTTCTAAACGTTATGCCACCCTGACCAAGGGGCAACTCCTACAAAGCCAGGCAAA
ATAATAAAATCATATTTGTCTCTAGTGGAATGGATAACTATGCCTAAAACTGCCCCTTTG
AAAAGCAACTAGAGAGATAATTTCTGAAGTGTTTGTCCCTACCTGAATGTGTGGCAAAAT
TCTAAACTCCCTGAAGTGTGAAAGTGGTTTNCAAGCCACATGCACATCCAGTTGTGGTAA
AGGGTGAAAATCTAACTGGCTAAGAGGGCTTCATAGCAACAATTAACCAAAAAGTGGTTAT
GTAGACTTTGCCTGCTTCATAATTCCCTAGGGCATTCTATGCTATTCTGTACCTTNGGCC
GCTCTAGAACTAGTG

Sequence 2059

TCTCCGGCTTCTATTTTGCCCACCCGGAGTCGAAATACTTCGTCGTCGGCAAGATCGGCA TGGACCAGGTGGAAGACATGGCCAAGCGCCGCGCGCGCAGCATCGAGGACGTGGAACGCT GGCT

Sequence 2060

TCTCCGGCTTCTATTTTGCCCACCCGGAGTCGAAATACTTCGTCGTCGGCAAGATCGGCA
TGGACCAGGTGGAAGACATGGCCAAGCGCCGCGCGCGCACATCGAGGACGTGGAACGCT
GGCTGGCACCGAATCTGTCGTAGTGCCATAATATAAGCACAAGGCGCGCGGAACTTATCG
CGCGCCGNAGCGCACTAACGCAGTATGCCGGTCGGNATGCTGNATGCCCGNTCCGGCCCG
TTCCCTGACTGGCTAAGGAGGATATATGGCAAGCAATTTCAAACTGAAACGCTGGCAAGA
TCAAGTGATCCTGTTGCTGGGCCTGTGG

Sequence 2061

Table 1

Sequence 2062

CGAGGTACAGCACTGGGCTTACAGCGGCGCTCAACAGATTTTTTTCTTTTTAAGAAAATG AATTCACTGAGGTTTAGAGATGTTAAAATACTTGCCCAAGTTCCTGCTTGCCCAGATGTG CCTTTGGGAATGCATCTTCTTTCTCAAGCCTCCTTACAGGGGTTGTAGTGAAGATTGGAA NGGGATAANGCAGGTG

Sequence 2063

GAATTGGAGCTCCCGCGGTGGCGGCCCGCCCGGGCAGGTACGCGGGGAGATGCTGCCA CCTAGGTTACTTGTAGGACCCTATACGGCAACCTCCTTTGCCAGGAACTATTTATAAACA TCCTGCAGGAAAATGTGAAGTAGAAGAGACAGGGATATCCCAGAAGGTTATGCNAAACAT CAAGAGAAGATGAGAGGAGTCTATATGTCAANAATACACATTTCCCACCTTGCCCAACAG TNGAAAAACATAAGAAGAGAAAAACATTAAAAAATGACAAGGAAGTTAATGGAAGTCAGC AATGTGATGGTGTTTGGA

Sequence 2064

CGAATTGGAGCTCCACCCGCGGTGGCGGCCGAGGTACCTCTCCTGGGAAGCTCTTCTTCA
AACATTGGTGACTCAGGGATTTGGGCTGCTTTCATCTTTATAGCTCTGTCATCTCTATCAT
GGAGCTTTCAAGGCCTTGTTTGCGCCAATATCCTCTCCTGGATGCTTGGGAAACACATCG
ATGCATCCCGTCAGTCAGCAGCTGTTTACGGAACACCAGCTGCAGGCCAGGCACCGTGCT
GCAAGGCGTAGATATGTTGCTGAACACGACTCCCTTCCAGATGTTCAGGATTTAACAGGC
AAGTAAACAGAGGGTCCAGAAGAAGGCACTCAGCACTGCCTCATGACATCAGGGAGGATTG
CTCAAAGGAAGTGATGCCTAAACCCAGCTGGATCGNAGTGTAATGGATAGAGGGGTAAAC
AAGAGCTGATTTCCTAGCGGTCCTGAGTCTCGACAGGTTGCCACCGTCAGGAGTATTGAT
CTTTTTCTCCCCGC

Sequence 2065

Sequence 2066

Sequence 2067

GTACCCGGGACGCTGGGAGGAGATGCTACCACCTAGGTTACTTGTAGGACCCTATACGGC AACCTNCTTTGCCAGGAACTATTTATAAACATCCTGCAGGAAAATGTGAAGTNGAAGAGA CAGGGATATCCCAGAAGGTTATGCAAAACATCAAGAGAAGATGAGAGGAGTCTATATGTC

Table 1

AGAATACACATTTCCCACCTTGCCCAACAGTAGAAAAACATAANAAGAGAAAAACATTAA AAAATGACAAGGAAGTTAATGGAAGTCAGCAATGTGATGGTGTTTGGAGGTGGAGCCTTC ATANGGTAATTAATGC

Sequence 2068

Sequence 2069

AGGTACGCGGGGGTTTCCTGCGTTTGTAGATGGAAGAAGAACTTGTGTGCTTAGACCTG
ACGCTGGAGGAGATGCTGCCACCTAGGTTACTTGTAGGACCCTATACGGCAACCTNCTT
TGCCAGGAACTATTTATAAACATCCTGCAGGAAAATGTCAGAGATGGGAAGAAACAAGAA
CTTTGACATGCTTGGTGTTCTTGCCCAAGCTTTGAAGAAGTTTACAAAGTCTATATGTCA
GAATACACATTTCCCACCTTGCCCAACANTTNAAAAACATAAGAAGAGAAAAACATTAAA
AAATGACANGGAAGTTAATGGGAAGTCAGCAATGTGATGGTGTTTTGGAGGTGAGCCTTN
ACAAGGTAATTAATGCCCTTGT

Sequence 2070

Sequence 2071

CCGCGGTGGCGCCCCGGGCAGGTACGCGGGGACTCAATCTTACTCCCTTGTAGAACA GGCGATATCTTCACCATGCGCACAATGAAATCAATACTCAGAGAAGGCAGATAATTCTCC ACGAAGCCAGAAAACTAATAAATGAACAGATGGCTCCACATAAGGTAGAGCGTGTCTGGT GCCCTGCCGTTTGGAAATGACCCAAAGGCAGGAGTGGAAGATGAAGTTTCAGCAGGAGAG ACTGAGGATCTCAGAGGATTTGCTCTGGGATGCAGAGACGCTTGCCTATTTGCTAAGTGT CTATGCCATATGATTCTGCTGTTTGCGTTTTGATTTAGAATGCTGAGCTGACTCAAAGTCA AACTGTAAGTACCT

Sequence 2073

Table 1

Sequence 2074

Sequence 2075

CCGCGGTGCCGCCGAGGTACAACCAGGGCTGTTACTCCTCAACAAGGAGGAATAACGC CTCTTAGAAGCATGGCAAGCAGGTGCCATAAAACATGTCTACTACTACTTCTCACTGCCT GGAATAATTGGAAAAGTTTCATAAATGCTCTGGCTTTCAGGTTCTTCACTTTTGCAATAA AGCTGCTAAGTCTGGTTGCAAAGCTTTTATGATGATTAGAAATAATATATGTAAAATGCC TGATGCACAAGAGTCACTCAATAAGTGACAGCAGTGTGATTAATCTATGACATANTAAAA AGTTCTAACTTGAAACACGAGAGAAAAAAATAACTTCCAGTGCGNAAAGAGATAATTTCA TGATCTCAGGGACACTAA

Sequence 2078

CGAGGTACTCAAATCTCTGCCTCAGGAAAACATCCAACTTTCAAAGTTTCTGGTAAGGGT
TGTAAAGGAAGCAATTAGTGTCATTAGAAAGAACTATCGATGTCACTATGCCAAGGGAGA
AAAGGGGTAGCAAAAATGAGAAAGAAGGCATGAGGCACAGACATTGAAAACTAACCTGTA
TTTAAGCTTAGTGTATTTTCGCTTTGCCTCTACTCCAAGTGGGGAAGTTTTCATTGCAGGC
ACTACAAACCCCAGGTATGACAATGACATAAGAATCAGGGAAGTGGCTGGAAAGGGAAAG
CTATATAGTTAGACTGGCCTGCCTTTGAGTCCTGCCCTGCCATTTGTACCTGCCCG
Sequence 2079

CCGCGGTGGCGGCCGAGGTACTGCAGGAAACCATGTTGCCAGCACTCTCCTAGCCCAAA AAAATTACATCTAGGAAGCAGGGGCCATTAACCTACTGGAATCATTGACTATGTCATAGA

Table 1

GGAGCTCCCCGCGGTGGCCGCCCCGGGCAGGTACGCGGGGGTTTGTAGATGGAAGGA
AGAACTTGTGTGCTTAGACCTGACGCTGGGAGGAGATGCTGCCACCTAGGTTACTTGTAG
GACCCTATACGGCNNCCTCCTTTGCCAGGAACTTTTATAAACATCCTGCAGGAAAATGCA
GTGAAGTAGAAGACAGGGATATCCCAGAAGGTTATGCAAAACATCAAGAGAAGATGAG
AGGTCAGAGATGGGAAGAAACAAGAACTTTGACATGCTTGGTGTTCTTGCCCAAGCTTTG
AAGAAGTTTACAAAGTCTATATGTCAGAATACACATTTCCCACCTTGCCCAACAGTAGAA
AAACATAAGAAGAGAAAAACATTAAAAAATGACAAGGAAGTTAATGGAAGTCAGCAATGT
GATGGTGTTTGGAGGTGGAGCCTTCAGAAGGTAATTNATGCCCTTGTAAGAAGAGGCCAN
AGAGCTTGCGCACCTTTTTCCTTGCCATGTGANGAGCCANGAAGCCGGCTGGCTGCAACC
TGCA

Sequence 2081

GGAGCTCCCCGCGGTGGCGGCCGAGGTACACTTGCCAATTGAGATAATATGAAATTGTA
TTCCATTTTAGTTTTAATTACATTTCCATGATTACTGCTGAGGTTTAGCATCTTTTTGAG
TATTACGGAATTTAGTTTACTCCTACGTGCATTACATTTTCATAATTTTGCCCAGTTTTT
CCTTGGGTTGTTTTTATTTTCTTACTGATTCCAAAGGTATCTGTAAATTATTGAAATGAA
TTATTTTAGTATTGTGCTTTTCAGCTTTTCACTTTAATTGTGCATTACATCATAT
AAAAGTTTTCATTTTAATGTAATCTTAGTTGNAAATATTTTTAAATTTGGTTTTGC
CTGNTATTTTTTA

Sequence 2082

CCGGGCAGGTACAGGAGAGTTCCCATAGACTNCTGCCCCCTNCCACAGACAGACTACCCT
AGAATATTGTAAAAGGATCTATCACTCATTTTCCTCACCTCTCTTATAGATGTCTCTCTT
CAACAGTGAGATTNTTCCGTAACTCTCTGTNNCAGGACTGGGCTTGTTTGCACTCAAATC
CATGACTCATTGTTTCTCTGCCTTTCCGTGTGTTACAGGTGGGCTGATCCCCCTGCAGCC
AGTTTCCCATAAGCAACTGACTTCCAACTGGGAATGTCTCGGGGGATAATGGGGGTGGG
Sequence 2083

Sequence 2085

CCGCGGTGGCGGCCCGAGGTACTCCACTTGTAACTGCTTCTCCCCTGATGCCACCACTGA

Table 1

CCTCTGTAGCCATGGTTCTGCAAGTTCTCTAATTTTCTGAGCCTCTGAGTCACTGACGAA GTCATGGTAGAGAGCAATGTAGGGCTCCAGGTGGATGACCTCCTTCCGGATGGGCTGGAG CAGCAGGTAGGCGTTGGAATTGGTCTCATAGGAACAGTAGAGGCTAGGGATCTGGTAGAG AGTGGGCTGGGAACCCAGGGTCTGACATAGCCCCTCGTAGGTGTCTCTGGTCTGCAGGTG GGGTATATTGGGCCTCTGGATGACGGCCTCAGCTACCACGTGGTTGGGGCTCTCTGCCAA GAGCCTTTCATATTTCAAGACATTCCTGGCCATCCTCTTATTATCTGGGCTGTAGAGAAG AAACTCCCGCCGCGTACCTGCCCG

Sequence 2086

GCGAATTGGAGCTCCCCGCGGTGGCGGCCCGAGGTACTTACAGTTTGACTTTGAGTCAGC
TCAGCATTCTAAATCAAACGCAAACAGCAGAATCATATGGCATAGACACTTAGCAAATCC
AATGCCTTCCAGGCATCTGTTTCCTGTTGATGAAATCCTCCCTATGGAGAGCAAACTGGT
TCATATCTTCAGATAGTGTCATTCAACCCCTTGGCAGCTTTCTGGGCTACTAAATATCAC
ACCGTCTGGTGGGACATTTCACCCAAGTTGTTCATTTATTAGTTTTCTGGCTTCGTGGAG
AATTATCTGCCTTCTCTGAGTATTGATTTCATTGTGCGCATGGTGAAGATATCGCCTGTT
CTACCCCCGCGTACCTGCCCGGGCGGCCGCTCTAGAACTA

Sequence 2087

Sequence 2088

GATCAGCTTGGATATACACTTAGGTCATAATACTAAATATGAATATTCGTTTTTTNCCAT
AACCATAGGGTGTAATCATATGCCTATGANTCTGATCCTCTACTTTATCCATCTGAATGC
TTCTCGATCCACTCATGCAAGATGTGTAAAGCTCATCATGGAAATAATCTATACTAAGCT
TTCAATATTGACATATTTATATAAAAAATTTATNGTAATANGATTGAATAAACANTAAGTA
ACTTTTTTATATTGATAAGNCACCACAATNTTTATCTTAAAAAGCAATCTTATTATTCA
AGTATAAATTCAGTATTTTTTCAGATCCTACAATTCGCCTGGTTNGGTGTATCATTAGNC
TATAATAAATNNNNGTGGAATGGCAATTTTACCAAAACAACACACCTTGCTTAAACATAAA
GCCAATGTTCTCAGTTTCCAATATATCTCATTTCAATAGCTAACATCAACAAAAATATATA
TAT

Sequence 2090

Table 1

AAACTAGAAGGAAGGAGGTGAGAGGAGATAGGGCTCCAGAGTGGAGCAAGCCCCTTCTGT CCCCGTGAACTTCCTGCCGGTGCATGGGTTACCTCTCATTAAATTTAATAGTACCTGCCC G

Sequence 2092

AGGTACTGTATATAAATACTGAAACAAACAATGGAAAAAGCAAATAGGAAATAGAGTGA
GAATCAGGGGAACTGAGGGGAAGCACCAAGTTTATCTTCTTTAGATAGTTCTTATTTTGG
AGACAGGATATTTATTTCTTGCGAGCTCTAAGGACTGTGCATTTAGCAAGGACCGTTCAT
TTTTCATCTTCCTCACTAATGTCTTAAGGGAGGGAAAGATAAATCTGAGTGTCATCAGGA
TACATATGGAGCTGAGGGCCACAGTTGCTAATTAAGTCCTCTTCAAAGACCCATTTGGAT
GCCTCAGCATACGTGATAAAAAAAGATTACCCCCAATGATGTCATGTTTTTCCAGGCATCA
AAAGAACCCCAAATTACCTTGTGTTAACAAGAGTGGTTGGAGAAAGCTAAGATTCCTGATA
ATTACTACTTTTAAGGAGATGGTTGTTGCAGTGTCACTGAGGAAACGGGATTCCAA
TCATAACAGCCCCGAACAATTTTAAGTGCTGCAAACCCGACCCAAATANAATCACTTGAA
CCTTGNCNGAAATTGGAATNTACTTTCTTGAACCTCAAGGGGAGAAAAAGTAATTTGG
GAACAAACAGTTCCCTTGCCCGGC

Sequence 2093

Sequence 2094

Sequence 2095

Sequence 2096

CGACTACTATAGGGGCGAAATTGGAGCTCACCGCGGTGGCGGCCCGTCACGGTGATGTTG
TTGTCGCGCCGGGGCACGCCAGCGAGCGCACGCCGGCGTGACATTCACG
CTGGTGCGCGCACTGGCTGCCAGTTCCAGCCCACGTTGGCGCCGATCTGGCGCGTGCGG
TCTTCGCTGCCGAACTCCATGCCGGGCAGCAGGGCGCTGTCGATGCCGCTGGCCGTTTGC
GCCGTACGGTCGA

Sequence 2097

CCGCGGTGGCGCCCGAGGTACGCGGGTCCCTGAGTTCAGAACATAGGAATTAGATTGAT AGACATCAACATACCCGCTTTATTGCTGACTCATGACAACTAATGGGAAGACATGGCTCA GATGTGCAGCCACAGTGAGCTTCTGAACATTTCTTCTCAGACTAAGCTCTTACACACAGT

Table 1

Sequence 2098

CCGCGGTGGCGGCCGAGGTACATCTCTAGCTGATGATTCAAAAAAGAAACCTTTTAATCT CACTCCACTGATCAGCTATGATACTTAAATGTTTTAGCTGTGAGCAAAATAATATGCATT CTCAAAGAGAGTATCTTCAGACTCCAGTGGCCGAGAATCTAGAGTTAGCAATGGAAAAAT TAGTCTCGGGCTTCTGTTTCTGCCCACANTTTTCAAATTAAGAACAATGTGTTTGCACTT AATGAAACAA

Sequence 2099

CCGGGCAGGTACATGTCAAAGGAAAAACACGTGAAAGATGAATTCAGCCAAACCCACCAG
TGTTCAACCTCAGTCTAATCAATCTCATACTCCTAGAGGCTTAAGTATCAGCAGGTAAGA
TCGTGATGACCTGCTCTCTGAGGCTCCAGACAATAATTTCTAACTGCCAACTGGAAATCCT
TATATGGTTAGGCTGCCAACATCCCAGGGAACAGGACCAAAATAAAAAGCATCACTCATT
ATCCTACTGCAATTTTCCTCTTCCCTTTGTCAAATGGGAATGATCTTTACGATCATGATC
CTTTATTGCAACCAGGACAGAAATCATGAAGTCATCTATGGCCCCTTCCTCTCACTCCGC
CTCCAATTAGTTGTCCTATCTGCCCCTTCCGTTCTCCTTCCATCTCCATAATGCCCAAGC
TAGTCTATCACCTCCCATTCATCTTTCACTCAACCTCCAGAATTATCTTCCTAAAACCC
AGACTGATTCTGATTTTTCCTCCTCAAGAAACGCTCTCTAACACTAAAGCACTTTGCTTC
TACCTCTATCGAGCCCAANGGTATTCATCCTTGNAATCTCTTCAAATGAGTTCCCAGCTG
NCCACCCCACGAGACTAGGAGTTTGGTAAGGACAGAATCACTCATTTCATCCTTGNACCT

Sequence 2100

CACTATAGGGGCGAATTGGAGCTCCCCGCGGTGGCGGCAGGTACTGTGTGGTTTAAAGA
TAAGCAGCCTGTGCTGTCTTTTATTTTCAGAAATAACAAAAAAACAACAATTACTGAA
CGCAATGTGCAATCTCTATCTTCTGTGTTTCGGGGTCAATTGTCTAACAGGAGCCACAGG
AAGAGCTTCAGAGGCACCCAGATGCCAAGCCTCAATTCCCACTGTGACTCTACTCTGGCA
GAGGTGAGACTTCACCTTCCAGAAACTATGCTGGGGGCCTCTGTGTCTGTGGCATATTGT
TTATATTGTGTGTTTATAGGCAATTTTAACAATCACTGTTTCTAGATTGCAACCCTCCTG
AGGCACTGCGCTGACACAGCAAAGTTATTCCCCTTACTGAAGAGAAAAATTAGAGGCCTA
AACACCACAGAAGCCCTGATAATATGGAATATTAGCATCAATGTCAGAGCACAGTATTTA
GGACAGATACTGATAAAGACAGCATAGATGACCACCTCACCTTGTCACCACCTGAGCGAG
GAGCCCTTAAAAGATGGGTTTCC

Sequence 2101

CTCCTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCAGGTTCAAATAGT CAGCAGCTCATCATAATCAATGAGCGAGGACATAAAGTAGGAAAAATGCATCACCATGGT GAGCAAGGAAAGCAAGTTATTGGAGGCACATGTTAACACATAAAATATAAAATTATATGA TCACACTGGAAAGGCTTGCCTGAGCCCACAGTTTGAATGCCTACAATAAGATGAGATGCA CAACAAAAAGCAAGAGAACCTGATCAAGTGGGTGACCTGGCCATGGTGCTCTCATCAGTG GGGACCCAAATGCTTATGTGGACTCACCAGGTATCGAATTAGACATGAATAGGAGTGTTT GTTGTGATCCAAGAAACTATATAATCAAATGAATACAATGAAACTTTAAAA Sequence 2102

Table 1

CTGAATCTTGTGCTCTAGCTCTACAGCCCAGTGAAGAAGCAATATATCTTTAATTCAGGG CTTGCCTCTTGCTTTCCAACTCTAACCTGAGAGCAGTGCTACTTTTGTAATTGCAGGTCT AAATAACTTAAGCGTATATACAGAAGCCAATCACTGATCACTTCCATTGCAATGAGGCAT CTGTTGTCAAAGAAGGAAACCATTTGTCAAGTCCCTTATAGATATTGAATCTTCAAACCC AAATCTGGGGATGTTTACATTTCT

Sequence 2103

Sequence 2104

TACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGGTAGATGGAAG
GAAGAACTTGTGTGCTTAGACCTGACGCTGGGAGGAGATGCTGCCACCTAGGTTACTTGT
AGGACCCTATACGGCAACCTCCTTTGCCAGGAACTATTTATAAACATCCTGCAGGAAAAT
GGTAAGCCCTTGGTTAAATTTATTGACTTCATTTATGTATCTCACAACACTTCTTTTCTG
TTTTAGTTCTAGGAATAGAAACTTACTTTTGGAAATACAGTACCTGCCCG
Sequence 2105

Sequence 2106

Sequence 2107

Sequence 2108

CCGCGGTGGCGCCCGGGCAGGTACATGCCAGGCACAAACTGGAGTCACAGATGCC

Table 1

Sequence 2109

TTTTTTTTTTTTTTTTTTTGGGGAACAAGGTGAGGTTCTCTGAGGTAACATTCCCTAA GACAGGAACCCCAGGACTTTCCAACTCTAAGGATTTCCCACATTCAGGATCCAGAAGTTT TCAAAATTACCTCTTAAGTTTTCCTACTAAGTTTATGGCCCCAGAGGCTTCTACTCCAGG TAAGCAGTTCTCTGCAACTCTGAATTTGCTTGTATTTCTAGATTTTAAGGTGACAGTTTG CCCTGTAATATCAGTTCTCTGACGGGTCCAAGACAAGCCATCAATTTTAAGGTTCTTTAA CTATTTCTTATTGNAAGGGATGGGAATTGGAAATGCTAAAGCTCTTTAAAGATTTGGGC Sequence 2110

CTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACNCGGGGGTTTGTAGATG
GAAGGAAGAACTTGTGTGCTTAGACCTGACGCTGGGAGGAGATGCTGCCACCTAGGTTAC
TTGTAGGACCCTATACGGCAACCTCCTTTGCCAGGAACTATTTATAAACATCCTGCAGGA
AAATGGTAAGCTGAGACCAATGATGCTGACCTCCCTCAAAAGCTGCATTTCT
GAAGGCAAACTGTCTGCCTATATTGTACCTTGCCCNNATCAAATTTT
Sequence 2112

GGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGGTGAAGGGCTCTCTGTAT
ACTGCTGAAGATTCTATAGTTTCTCCTGAAATCCATGAGGGAGCCCCCTGAAGGATTTTG
GCCAGGAAAGTGTCATGAATCAAATTTCTATTTTAAGAATAGTATCGAGGCAGCAATGTC
AAAGTTTGTTTAGAAAATAGGATGGTTCCTGTAATCCCAGAACTTTTGGAGACCAAGGCG
GGAGGATTGCTTGAGTCCAGGAATTTGAGTCCAGCCTGGGCAACATGGGAGAGGACCTCA
TCTNTNCTAAAATTTNANTNNTTNTAATAAAAGGTTCCCT
Sequence 2113

GGCTAGGCAGCTCTGGAGAAAGCAGAAGTGGATAAATAAGGTGTGGACTCACCAAAGACA GTTCCAAAGTCAATTTCACTCTGACACACTCTCTGTGATCTTCCACAGTCAGCACAATGC CTGCCCCCTGCTAGGCCTGATGGATGATCTGATAGAAAACTGGCTTCAGCAAGGAGCTTC CACAGGTAACCTTGGTTCTGCAGTGATAACAGCTCCTATGAAGGAGACCCCATCAGACTA ACAGTGGATTTCTCAGCAGAAATCATAAAGGCCAGAAAACAGTGGAATGGCATTTTCAAA ATGCTCTTTCCATTGCTTTTCCATACCACTGCTTT

Sequence 2115

TAGGGCGAATTGGAGCTCCCCGCGGTGGCAGCGCCCCCCGGGCAGGTACCAAAAGAAT GTTCATAGCAGCATTATTTGTCATAGTCAAGAGCTGGAAGCAACCCAGTTGTGCATCAAT GGTAGAATGGATGACTAAATTGTAGTGCATTCTTACAATAAAATACTATAGAGCAATGAA

Table 1

Sequence 2116

CCGGGCAGGTACGCGGGGGTAGAACAGGCGATATCTTCACCATGCGCACAATGAAATCAA TACTCAGAGAAGGCAGATAATTCTCCACGAAGCCAGAAAACTAATAAATGAACAACTTGG GTGAAATGTCCCACCAGACGGTGTGATATTTAGTAGTCCAGAAAGCTGCCAAGGGGTTGA ATGACACTATCTGAAGATATGAACCAGTTTGCTCTCCATAGGGAGGATTTCATCAACAGG AAACAGATGCCTGGAAGGCATTGGATTTGCTAAGTGTCTATGCCATATGATTCTGCTGTT TGCGTTTGATTTAAAAT

Sequence 2117

CCGCGGTGCCGCCCGGGCAGGTACAAATTTGGGCATAGTCAGAAACTCTGCTGACT
CTCTCTTCCCATTTAACCTAATCTTACCATAGCACTCCTCACCCTATGACTTGCCCATTG
CAGTAAACCAGAAAGCAAAAAAAGGTCAAGCACGTGTGTTTGAGATCCAACTCTAGTGTT
TGTAGCAGCTCTGCAGAACCACAGTTTGCACATCTGTAAATTGAGCAATAACAACTGCCC
TGCCTGTTTCACAGGGTTGCTTAAAGAGTTATATGAGCTATTGCATGTGAAAGTGTTCCA
TAAGCTGCCATTTGCTCTGAAGCTCACGGGTATAATTATTCTAGTCTAACCTACTTATGT
TTGCCCTCTTTTCTGCAGTTGCATCTTTGTGCATAAAGAATCTTCTCTGACC
TTCAACTCTAAACTAGAGTAATTTACTAACTGGTATTTATCAAATTCTTCATTA
GGTCTTGAATCATAGAATATTGGTTACCCATTG

Sequence 2118

Sequence 2119

0

Table 1

GGCCCGAATGCTTAACAATTGGTATTGTTAGGTTATGGGATCCCGGGGGGGTGGTTGTCCT

Sequence 2120

AGGGCGAATTGGAGCTCCACCGCNGTGGCGGCCGGGGGCCATTGAGACTGCCATGGAAG
ACTTGAAAGGTCACGTAGCTGATACTTCTGGAGAGACCATTCAAGGCTTCTGGCTCTTGA
CAAAGATAGACCACTGGAACAATGAGAAGGAGAGAATTCTACTGGTCACAGACAAGACTC
TCTTGATCTGCAAATACGACTTCATCATGCTGAGTTGTGTGCAGCTGCAGCGGATTCCTC
TGAGCGCTGTCTATCGCATCTGCCTGGGCAAGTTCACCTTCCCTGGGATGTCCCTGGACA
AGATTTTACTCCCATAACCCAGGCAGAAGTACCT

Sequence 2121

CGAGGTACTTCATACTACTTTAAGTTACCTCCTATTGGGGGCATTATAAATGGGTAAGCA GAGAACATCATGGAAAGACATGGAGCTTAGTATATGCAAATGTTGAGTTACTCAGTGTAA TGTGTGAAAAAGGAGTTTCATAAGTTTCGGTCAGGGAAGAAGGCAGGGTCAAAATTTCTG CTTGAGAGTTTGGGAGCTTGGGGAGACTTTAAACAGGGAGCAACACAGCGCCTCTGTACC TGCCCG

Sequence 2122

Sequence 2123

ATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACACCTGTCCATGTGATGAAT
TAGAACATGCTTTTCCACCTATAAACTACAACTTAATTTGCATAACTTAATATAAGTAGT
ATTAATGTAAGTGTTATACATATTTCAGGTTATAATTTTGCATAACTTTAAACATTAAACATAA
ATACAATTGGTTTAGTTATAAAATTACACTACTTACTTGCTACTTTATAACTGCTCACTA
CCTCCTTAGTGGAACCCAGATTTTCTCTATGATTTGAGAAAAATTACTCCACATGTTGCC
TAGTTATCAAACTATATTGGGAAGCAGAAAAAGCTATGAAAGGCTTCAAAGCTTCTGAGA
ACCTTAGCACGAAAAACTCTTCCAAAAAGCTTTTTCCATGCTTGATTTTGTGAGGCTTATT
GAAAACAATGGCATTGACCGTTCATTCTGACTCCTTTTCC

Sequence 2125

Sequence 2124

AGGCCAATTGGAGTTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACGCGGGAATGAGAGCCCTACAGTTGAAAGCACACTTGGATGAGGCTCGGACCCTGCTTCATGGCACCAGAGGAACCCACCAGCACCAGGTTGAGCTTATTGAGCGAGATGAGGTTAGTCTTCATAAGAAGCTGAGGACTGAAGTAATTCAGCTAGAAGATACATTGGCCCAGGTCCGCAAGGAGTATGAAATGCTGAGGATAGAATTTGAGCAGACCCTTGCTGCCAATGAACAAGCAGGCCCTATAAACAGGGAGATGCGCCACCTCATCAGTAGCCTCCAGAATCACAATCACCAGCTGAAA

Sequence 2126

CCGGGCAGGTACGCGGGAATGAGAGCCTACAGTTGAAAGCACACTTGGATGAGGCTCGGA

Table 1

CCCTGCTTCATGGCACCAGAGGAACCCACCAGCACCAGGTTGAGCTTATTGAGCGAGATG
AGGTTAGTCTTCATAAGAAGCTGAGGACTGAAGTAATTCAGCTAGAAGATACATTGGCCC
AGGTNCGCAAGGAGTATGAAATGCTGAGGATAGAATTTGAGCAGACCCTTGCTGCCAATG
AACAAGCAGGCCCTATAAACAGGGAGATGCGCCACCTCATCAGTAGCCTNCAGAATCACA
ATCACCANCTGAAAGGGGAGGTCCTGAGATATAAGCGGAAATTGAGAGAAGCCCANTCTG
ACCTGAACAAGNACACGCCTGCGTTANT

Sequence 2127

GCCCGCGTGACGAGCGGACTTGCGTCCGGCGTATCGGCGATTTCGCGGTTCTCGTTCAG CAGGGAAAACAGGCGTTCCATGTCGGCCAGGCTTTGCTTGATTTCGCGGTAAATGACGCC CAGGAAATTGAGAGGGATGTACAGCTGGATCATGAAGGCGTTCACCAGCACCAGGTCGCC CAGGGTCATGCTGCCGTTGATCACGCCCACGGTGGCGCGCCACAGGATCAA Sequence 2128

GGGGCCATTGAGACTGCCATGGAAGACTTGAAAGGTCACGTAGCTGAGACTTCTGGAGAG ACCATTCAAGGCTTCTGGCTCTTGACAAAGATAGACCACTGGAACAATGAGAAGGAGAGA ATTCTACTGGTCACAGACAAGACTCTCTTGATCTGCAAATACGACTTCATCATGCTGAGT TGTGTGCAGCTGCAGCGGATTCCTCTGAGCGCTGTCTATCGCATCTGCCTGGGCAAGTTC ACCTTCCCTGGGATGTCCCTGGACAAGAGACAAGGAGAAGGCCTTAGGATCTACTGGGGG AGTCCGGAGGAGCAGTCTCTTCTGTCCCGCTGGAACCCATGGTC Sequence 2129

CCGGGCAGGTACGAGATGCCACGGCACGAAGTCTACGTTCTCCTGATCCGAAACATCTTT
TTGAAAATATCAATCATTGGCATTCTTTGTTACTATTGGCTCAACACCGTGGCCCTGTCT
GGTGAAGAGTGTTGGGAAACCCTCATTGGCCAGGACATCTACCGGCTCCTTCTGATGGAT
TTTGTGTTCTCTTTAGTCAATTCCTTCCTGGGGGAGTTTTTTGAGGAGAATCATTGGGATG
CAACTGATCACAAGTCTTGGCCTTCAGGAGTTTGACATTGCCAGGAACGTTCTAGAACTG
ATTTATGCACAAACTCTGGTGTNGGATTGGCATCTTCTTCTGCC

Sequence 2130

ACACTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCGTTCCTCCAGT GCCCAGAGATGCTCTCCGCACCAAGCCACAGATGTGGAGGAGGCAGGTAGGGGGTCAAAG AGGGTGGTATCGGTTATTNAGGACTTTTTTTTTTCTTAAATATCCTGTGCTTCTTTCA ATCATTTGAAGGTAAAAACCAGCNTCCCTGTGAGTGGTAANCTGATTTTTAGGTTNTTAT GAAGGTATTATTTTCTGNGTAGATAGTNGTTAACTTGGTGCCCTTGCANGGTAAGACGAT CAGCGAAGCTTTCTGTTCCACCATCTTGCTCCTCTCATTTTANACCTAATA

Sequence 2133

TAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCCTCGGTTGCAAGCACAAGCAAATGTGCCAGGGTGGTTGATGCAGCTGTGGTCACAGGTCCTATCCAAAGAGCACTCATCCACATCTTGGCAAGACTTCTCATCTGTTAATAATTTAAATCCTTTCTTGCAGCCCGCAGTCAAAACTGCCCACCGATGTTTTTGCAGAAATGATCACAACCTCCATTGCGGGTCCCCGCG

Table 1

TACCTGCCCG

Sequence 2134

GGTACGCGGGACCCGCAATGGAGGTTGTGATCATTTCTGCAAAAACATCGTGGGCAGTT TTGACTGCGGCTGCAAGAAAGGATTTAAATTATTAACAGATGAGAAGTCTTGCCAAGATG TGGATGAGTGCTCTTTGGATAGGACCTGTGACCACAGCTGCATCAACCACCCTGGCACAT TTGCTTGTGCTTGCAACCGAGGGTACCT

Sequence 2135

Sequence 2136

CCGCGGTGGCGGCGGGGCCATTGAGACTGCCATGGAAGACTTGAAAGGTCACGTAGCT
GAGACTTCTGGAGAGACCATTCAAGGCTTCTGGCTCTTTGACAAAGATAGACCACTGGAAC
AATGAGAAGGAGAGATTCTACTGGTCACAGACAAGACTCTCTTGATCTGCAAATACGAC
TTCATCATGCTGAGTTGTGCAGCTGCAGCGGATTCCTCTGAGCGCTGTCTATCGCATC
TGCCTGGGCAAGTTCACCTTCCCTGGGATGTCCCTGGACAAGAGACAAGGAGAAGGCCTT
AGGATCTACTGGGGGAGTCCCGGAGGAGCAGTCTCTTCTGTCCCGCTGGAACCCATGGTCC
ACTGAAGTTCCTTATGCTACTTTCAC

Sequence 2137

Sequence 2138

CCGCGGTGCCGCCGAGGTACAACAGGCTTGTAGTTCTTTGTGAAGGATGCAGGCAAGAG
GGATGTCCAGTTTAGACGGCCCCTGACAGCAGCAGCAGCCTCTTCCACATCAAGTGAAGTGTG
ATTGTTAACGATCATTGCCTGCACAAAGTATAGTTGCCTTTGAAGTAGTCCACCCAATAC
TTCACCATGACATAGCGGGGCAGGATTGGGGTGTTCACATTTTGCTGATAAGATGGTGTG
TTAAAATCTAAAGCTTGAAGAACTGGATAAATTAAAGCTTGTAGTTTGAGCTTATTTTTT
AGGCTGGCATCTTGAGTAAACTGTTGTCCAAGGGCAGCAGCCAGATTTCCACCAGCACTG
TCACCAGAAATGCAAATTCTGCCTGGATCAACCATATACTTCTGTAAGACTTCTGGCTTC
AGGAAATACTTTGTGGCCCGTC

Sequence 2139

Sequence 2140

GTAATTTAATCTTCACATCACTTTTACTTAGACCTTGATGAATGCTCCCAGTCCCCGAAA CCATGCAACTACATCTGCAAGAACACTGAGGGGGAGTTATCAGTGTTCATGTCCGAGGGGG TATGTCCTGCAAGAGGATGAAAGACATGCAAAGGTGAGAGAGTCTCTGACAATCGT

Table 1

GACCCTAGTCTGTATCTTTCAAATTTAAATATTAGATTATCAGGAATTATGCCAT GTGCATCACCTTCATTAAAAGGTCCCATCCTAGTGGCCATGTTATTGCTCATAAGAAAAA CTCTACCAATATGCTCATTGCAGGAAGCAGAGGAGTTAAAAC Sequence 2141

Sequence 2142

Sequence 2146

AGGTACGCGGGAAGCACATATTTGGTAGCCTTTGCATACAAGAATGTGAAATTTGTTCTC
AAGCACAAAGTAGCACAGAAGAGGGGAGGATGCTGTTTCCAAAGAAGTGACTCGAAAACTT
TCTGAAGCTGATAATAGAAAGGATGTCCTCGGTAAGGGGAGAAAGATTGAAAAGNAATCC

Table 1

TTGTTGTNAAGAAAGAAATGAAAGTTGCTTGATTATNGAAGCTACAAACATTTTTCCATC
TTTNCTATAAACAANCACTCTTGTTTCCCTGGGTCCGATGGGCTCATNTGATTGCTTTCC
TTCTTTCATTANTTGNAAGGAACCTTTNAACTCCCACAAGTTNNAAACCTAACANNATTT
GGTTCCATTAAAGGTNGNCTTTTCAATTCCAGGGGAACCTTCAATNCGGNCCCCTTCCCT
NGATNCTAACNTTGGGGCCTTCCCCAAAAANTTAGGTAACTCAATTGGTTCAAGANCTTT
TCNACCCCCCCCTNGNGCCTNTTTTGATTGGTCCTTAATTGGGG
Sequence 2147

Sequence 2148

Sequence 2149

Sequence 2151

Sequence 2152

Table 1

TACAGATGAGGAAACAGGCCTGAGAAGATGGAGGGAGTTACCCACAATCTGAAGGGGCTC
TACCATGACTAGACCCAGGTCACCTGCCTCCCAGGCCTGGCTCTTTCCACTCCGAGGTGC
TGGCTCACCACAGACTTATTCTTTAATGGAATTTTGGAAAGGCCTCACTCCAGTGGACTC
TTTGGGATCT

Sequence 2153

Sequence 2156

Sequence 2158

Table 1

ATGAACTCATGCCTACCTTCTCTTGTTTTATAAGCTTCATGAGGCAGGTACCTCGGNCCG CTCTAGAACTAAGTGGGATCCCCCGGGCTGCAGGNAATTCNATATTNAAGCNTATTGAAT NCCCNCNAACCTTAAGGGGGGGG

Sequence 2159

Sequence 2160

Sequence 2161

CCGCGGTGGCGCCGAGGTACGCGGGGGAAAATGTCAGAGATGGGAAGAACAAGAACTT TGACATGCTTGGTGTTCTTGCCCAAGCTTTGAAGAAGTTTACAAAGTCTATATGTCAGAA TACACATTTCCCACCTTGCCCAACAGTAGAAAAACATAAGAAGAGAAAAACATTAAAAAA TGACAAGGAAGTTAATGGAAGTCAGCAATGTGATGGTGTTTTGGAGGTGGAGCCTTCAGAA GGTAATTAATGCCCTTGTAAGAAGAGGCCAGAGAGCTTGCGCACCTTCTTCCTGCCATGT GAGGAGCCAAGAAGCCGGCTGTCTGCAACCTGCAAGAGGACCCTCACTAGAAGCTAGCCA TACTGGCATCCTCATCTTGGCTTTCCAACTTTCCAGAACTGTGAAGAAGTATATGTTT Sequence 2162

Sequence 2163

CCGCGGTGGCGCCCCCGGGCAGGTACGCGGGGGCAGTGGGAAGCTCGCAGCAGCTGGG GAGGAGCCAAAGCCTCGGCGCTCACCTAAGCCGCAGGAGATACACCCAACTGGGAGATG AGGAAACAGCAACCCAGAGAGGAGAAACTAACCCACACAGGATCATTTCGCGAAGGAGCAA GGCTGAAGAACCAGACCTGGACTTTCTTAGGACAAACTTACTGCAGCTTGAAGGAGCCAA C

Sequence 2164

Table 1

Sequence 2165

Sequence 2166

AGGTACGCGGAAGGAGATGTTGCCACCTAGGTTACTTGTAGGACCCTATACGGCAACCT
CCTTTGCCAGGAACTATTTATAAACATCCTGCAGGAAAATGCAGTGAAGTAGAAGAGACA
GGGATATCCCAGAAGGTTATGCAAAACATCAAGAGAAGATGAGAGGAGTCTATATGTCAG
AATACACATTTCCCACCTTGCCCAACAGTAGAAAAACATAAGAAGAGAAAAAACATTAAAA
AATGACAAGGGAAGTTAATGGAAGTCAGCAATGTGATGGTGTTTTGGGAGGTGGAGCCTTC
AGNAAGGGTAATTAATGCCCTTGTAAGGAAGAGGCCAGAGAGCCTTGTGGCACCCTTCT
Sequence 2167

Sequence 2168

GACTNCTATAGGGCGAATTGGAGCTCCCCGCGGTGGCCGGCCGCCCGGGCAGGTACCCTG
CTGAAAGATTATTTCTAACAGGCTTGTAGAGAAACGTCGGTTCATGTAAATTAGAAATTA
TGGGGCCACTTTGCCATTCTCACACCTGCAATGAACAGGTGTTTATCTGCAGTTCTGAC
TTATCTCTTGAACTCCATTTGCATGTTATAGTGGGATGCAGCTGATGCCCTGTCCAGATC
TTCTTCAGGCCACTACATCTATATATGCATTCATATTCCAGTGGCTGTGAGTGTTGGCTG
TTGGTTGACAGAGAGGAGCTGCATCCTTCTGGAGGAAACTGAACTCAGCTGATGAAAGCCAC
CTGGTCCTGGAGGTGAAGC

Sequence 2169

Sequence 2170

Table 1

Sequence 2171

AGCAAGTCAAAAAGCCCAATCNTCTTTCCGGNCGGGTTGGCCGCCAANGGGCCGGGGGCC ATTTCGGCCGCCACCTTCTTAATGGGGCAATTTGGCTTGGGTTTCTTACCCAAACCGTTG GAACCAGGGGTNGAATCCAAAGGTTTTAAAAGAAAAAGCCTTGGGAACCGTTCNCTTCTT NCCAAACCGAACCCCTTGGGNTTTAATTGAAACCANTGTTTAAAAAAGGTTCAATTCCCT TTTTTGCCCCACCCGTTGGTTGCTTCCTCCGTTGGTTCCAAGGAAAAGGAAAAGGAATA CCCCCTTTTGGAATTGGGGGGAATTCCTTTTTCCCAAAACCAATTTCCGGGAATTTTGG GGGGGCCAATTTCCTTNAATTAAGGGAAAAAAAANGGNAAAAAAATTTCCCAAAANCCTTG GGAATTGGGAAGGNCCCCCTTTTTTCCTTTGGNAAAGAAAAANGGGGAAATTGGGCCTT TCCCCGGCCAAAAAACCCCCAAGGGGGNCCCCGGGGG

Sequence 2172

ATCCTGANCTGTGCCACACTTTCTTGGTTGGGATTATTTCTCGGTTTCTACTTNCCTNGT TCTGANAGTATGTTGGCCANNGTGTAGTAGTTGANACATAGTCNTGNATGCTCCACNCAC TCTAGGCAATCAACNAGCACCNCAGTAATCTTCAAACGTAATTTTTCCCATTGGGGTACN CACCAAGNCATTCTTCCAATTCTTNTTGGNGACTTGGAATNCTCACGNAANATAGAAACC GGGGCCTTCCTTGGCCTTTTTTGGAACCACTTGNANAGGNTTAATTTTTT

AGGTACTTTATTTTTTTTTTTTTTTTTGGCAGTGGGAGAGTTTTTATTCAATTTG TGAAGGACAGTTTTAAGAACAAAATGTTANTANACACCTCTTAGAAACCACTGGGTTNGT AAAAAAGGTTAAAAAAATTTNCATTTCCCAAATTAATTTTTTGGCAANGGAGGTTATTAA NACCCCACNTTAAGTTNTNGCCCNTTAAGNAACCAAAAAAAAGGCCTTAAAATTTTTTNC TTAACCAAAAAAATTTCCANAAAAAANACCTTTTAAAANTNGGCCAAGGTTTTTTTTA AATTITAAAAGAAAAGGAAGGTTCCANAAAAAATTTTTCCTTCCTTCCAAGNTTTTAAAA CCTTGGGGAATTTATTAACCAATTAAGGGTGGGGGNTAATTANTTAATTCCTTTTAAAAA AGGCCANGGAAAAAAACCCCCCCCAANAAAAAANAAANCCAAAAANNAACCCAGANGG GGGAAAAAAANAAAAGGGGAAAAAAAATTTACCCATTTGGTTTNCAAAACCNAGGNTCC CAAGGNTTATAAAAAAATTAATTTTTTTGGAA

Sequence 2174

AGGTACGCGGGGACGCTGGGAGGAGATGCTGCCACCTAGGTTACTTGTAGGACCCTATAC GGCAACCTCCTTTGCCAGGAACTATTTATAAACATCCTGCAGGAAAATGAGTCTATATGT CAGAATACACATTTCCCACCTTGCCCAACAGTAGAAAACATAAGAAGAGAAAAACATTA AAAAATGACAAGGAAGTTAATGGAAGTCAGCAATGTGATGGTGTTTGGAGGTGGAGCCTT CAGAAGGTAATTAATGCCCTTGTAAGAAGAGGCCAGAGAGCTTGCGCACCTTCTTCCTGC CATGTGAGGAGCCAAGAAGCC

Sequence 2175

TTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACGTGGCGTAGCATTCCATGT TCAGCTTTGACATTTATTTTCTCATATCAACCCTTTTTACACGTGAAACACAATCCCGCT CTTGAATTCTTAACTGCATGATCTGTGAAACCTGTATTTATATTTTCTTCAGTGGTATTC TTTGTCGGTGTGTGTCCTAAACAAACCAAAAGAAAACTTTCCAAATCTAAAGTATTCA CTTGTCATATTTACTTATGATTGATAAATAAATCTATTTTGCTTTTTAGAGCCTCCCGAGA

Table 1

AGCCATCTGCCTTCGAGCCTGCCATTGAAATGCAAAAGTCTG Sequence 2176

CGAATNGGAGCTCCCCGCNGTGGCGGCCGACGTACNGTGATCATTACTCCCCAGCGCAGC
TCAATCCACTTNCAGACTGNTCTAATTGTNGGAATAATTNTCCTTATGTAATTCAATNTC
CCATCTATTAATTNATGAGATATTTATTTAAAACTGACCGTATTCCAGGAACTGGGCTAA
ACGAAGAAGAGTAGTGAATTAATACAGAAATCACCCTNGATTTGGCAGAATATTNTCCCT
GGTAGTGTAGGTCACCCCTATTGTGGTGATAATCCCCCANATCATACAGCANAAGAAACA
ACACACAGACAAAAACCAAGTCATNCTTCTAGGATGTTTTCATCCAAGGATTTGAAAAGA
TTTAGGTGATCTTCCATTNTTCATCCTATGCAATCTGGGCTATGCTACTGTTCTAGGT
GCAGTTCAATTAAAATCACTGAACTTTCAATAGTCACCAATGATCACTGTTCTAGTT
GCAGTTCAATTAGGTGTTCAAGGAAACACTTATAACTTAAATTTAATGTCTAAATCTTAC
ACCTTTAATTGGAAAAATAATGTAATAAGTGAGCAATTAGGTTATCCAGCACTTTTGGGANGCA
GAGGCAAAANGGATTGGTTTAAGTCANGAGTTCCNAAAACAACCTGGGCAAAACCGGCAA
GAACTNCATCTNTTNAAAAANNANNNNAANNNNNANGGTCCTTGCCGGGCGGGCCNTTT
ANAACTTGTNGGATCCCCCGGCTNGAAGAATTCCANTTTAANCNTATNGATACCGNGNAC
CTGANGGGGGGCCCN

Sequence 2180

CCGCGGTGGCGCCCCCGGGCAGGTACCTGTGAACTGAGGAATTATAGATAAACCTTAG GTCAAATCATTTCACAATTGCATTGGTGGTATTGAAAAATGATGAGAATTTCTCTGACAGA GAGCTTTGTCCTAGTTTTTGTCTTCATAGGTCAAAACTGGCAATATTCTCTTGTCTGCAA GATAAAGTGTTTGTGCTTCTATCACCATATGCATGAACATGTAAGAATCAGATACAATTT

Table 1

Sequence 2181

Sequence 2182

Sequence 2184

CCGCGGTGGCGCCCGGGCAGGTACGCGGGGGAGATGCTGCCACCTAGGTTACTTG
TAGGACCCTATACGGCAACCTCCTTTGCCAGGAACTATTTATAAACATCCTGCAGGAAAA
TGAGTCTATATGTCAGAATACACATTTCCACCTTGCCCAACAGTAGAAAACATAAGAAG
AGAAAAACATTAAAAAATGACAAGGAAGTTAATGGAAGCAATGTGATGGTGTTTGGAGGT
GGAGCCTTCAGAAGGTAATTAATGCCCTTGTAAGAAGAGGCCAGAGAGCTTGCGCACCTT
CTTCCTGCCATGTGAGGAGCCAAGAAGCCGGCTGTCTGCAACCTGCAAGAGGACCCTCAC
TAGAAGCTAGCCATACTGGCATCCTCATCTTGGCTTTCCAACTTCAGAACCGTGAGAAGT
ATATGTTTGTGGTTTAAGTCAATGGTCTATGGTAATTTTTTTATAGCAAGTCCCAGCCCA
AGACAGTGCCTCATTTACTACATACCATTTATTATTATTATTATATAGGCTNCTTTCAGAAACC
CATGTTCAAAATAAGAGATAAGATCCTGGAAA

Sequence 2185

TAGGGCGAATTGGAGCTCCCCGCGGTGGCTTGGAAAGCCAAGATGAGGATGCCAGTATGGCTAGCTTCTAGTGAGGGTCCTCTTGCAGGTTGCAGACAGCCGGCTTCTTGGCTCCTCACA

Table 1

Sequence 2186

CGAGGACGCGGAGACCTGACGCTGGGAGGAGATGCTGCCACCTAGGTTACTTGTAGGAC
CCTATACGGCAACCTCCTTTGCCAGGAACTATTTATAAACATCCTGCGGGAAAATGCAGT
GAAGTAGAAGAGACAGGGATATCCANAAGGTTATGCAAAACATCAAGAGAAGATGAGAG
AGTCTATATGTCAGAATACACATTTCCCACCTTGCCCAGCAGTAGAAAAACATAAGAAGA
GAAAAACATTAAAAAATGACAAGGAAGTTAATGGAAGCAATGTGATGGTGTTTGGAGGTG
GAGCCTTCAGAAGGTAATTAATGCCCTTGTAAGAAGAGGCCAGAGAGCTTGCGCACCTTC
TTCCTGCCATGTGAGGAGCCAAGAAGCCGGCTGTCTGCAACCTGCAAGAGGACCCTCACT
AGAAGCTAGCCATACTGGCATCCTCATCTTGGCTTTCCAACTTCCAGAACTGTGAGAAGT
ATATGTTTGTGGTTTAAGTCAATGGGTCTATGGTAATTTTTTTATAGCAGTCCCAGCCA
AAGACAGTGCCTCATTTACTACATACCATTTATATTTATATAGGGCTCCTTTCAGAAA
CCCATGTTCAAATAAGAGATAGATACTGAAACACATTACACCCTTCACTAGTTTTTTAGT
ATACAAATATTGAGAAAAAT

Sequence 2187

Sequence 2188

Sequence 2189

Sequence 2190

CGCCCGGGCAGGTACGCCTACTCAACCCGGCTGTTCACCATTGGTGGCATCAGCATCCCA
TACACATGGAACCACACCGTTTTCTATGATCAGGCACAGGGAAGAATGCCTTTCTTGGTT
GAAACACTTCATGCATCCTCTGTGAATCTGACTATAACCAGATAGAAGAGACACTGGGTT
TTAAAATTCATGCTTCAATATCCAAAGGAGATCGCAGTAATCAGTGCCCCTCCGGGTTTA

Table 1

CCTTAGACTCAGTTGGACCTTTTTGTGCTGATGAGGATGAATGTGCAGCAGGGAATCCCT GCTCCCATAGCTGCCACAATGCCATGGGGACTTACTACTGCTCCTGCCCTAAAGGCCTCA CCATAGCTGCAGATGGAAGAACTTGTCAAGATATTGATGAGTGTGCTTTGGGTAGGCATA CCTGCCACGCTGGTCAGGACTGTGACAATACGATTGGATCTTATCGCTGTGTGCTCCGTT GTGGAAAGTG

Sequence 2191

Sequence 2192

Sequence 2193

Sequence 2194

Sequence 2196

Table 1

ATTGGANCCACTAGGAATCCTGAGAAAGAGGAGTGGACATACTCAGAGGAGTATAGGCCA TTTGACTCGGCATTGGGAAACCTGGAGCCACACCTGGTCATTTTCTGTGAGATCGATGAT GGCACTCCCTGAAGCCTGATCCAGGTAGCCTTTGGTGTATTCATCATANGTGTACCT Sequence 2197

Sequence 2198

Sequence 2199

ACTTAGGGCGAATTGGAGCTCNCCGCGGTGGCGGCCGAGGTACAGAGGTGATAGATCCCT TCTTGGTAGTGGTAATTCTTTCCTGCATAGTACGCGGGGGGCTGTAGTGGCTTCGTCTTCG GTTTTTCTCTTCCTTCGCTAACGCCTCCCGGCTCTCGTCAGCCTCCCGC Sequence 2201

Sequence 2203

Table 1

NTTCCANTTAAAGGGCNTTGGTCNTTNTNCCCCTTGGNTGGGTTNGNANAAAATTTTGG GTTTTAATTCCCCGGCCTTTCAACCAAAA

Sequence 2204

Sequence 2205

CTCCCGCGGTGGCGCCGCCCGGGCAGGACGCGGGGTTTGTAGATGGAAGAAGAACTT
GTGTGCTTAGACCTGACGCTGGGAGGAGATGCTGCCACCTAGGTTACTTGTAGGACCCTA
TACGGCAACCTCCTTTGCCAGGAACTATTTATAAACATCCTGCAGGAAAATGAAGTCTAT
ATGTCAGAATACACATTTCCCACCTTGCCCAACAGTTNGAAAAACATAAGAAGAGAAAAA
CATTAAAAAAATGACAAGGAAGTTAATGGAAGTCACCAATGTGATGGTGTTTGGAGGTGGA
GCCTTCANAAGGTAATTAATGCCCTTGTAAGAAGAGGCCAGAGAGCTTGCGCACCTTCTT
CCTGCCATGTGAGGAGCCAAGAAGCCGGCTTGTCTGCAACCTGCAAGAGGACCCTC
Sequence 2206

Sequence 2207

CCGCGGTGGCGCCGAGGTACTTTATAAATACGCCAGAGATTGAGTCGAGGCTCTGAAG
AAAGTCCACCATGTGAAATTCTTTCCGGTGACATTATCCAGTTTGGAGTAGACGTGACAG
AGAATACACGGAAAGTTACCCATGGGTGTATTGTTTCCACAATAAAACTTTTTCTACCCA
GATNGGTATNGGAAGCCCGGCTCCGCTCAGATGTCATCCATGCACCATTACCAAGTCCTG
TTGACAAAGTTGCTGCTAACACTCCAAGTATGTACCTG

Sequence 2208

Sequence 2209

TATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGGGGGCCATTGAGACTGCCATGGAAGACTTGAAAGGTCACGTAGCTGAGACTTCTGGAGAGACCATTCAAGGCTTCTGGCTCTTGACAAAGATAGACCACTGGAACAATGAGAAGGAGAGAATTCTACTGGTCACAGACAAGACTCTCTTGATCTGCAAATACGACTTCATCATGCTGAAGTTGGTGTGCAAGCTTGCAGCGGATTCCTCTGAGCCGCTGTCTATCGCATCTGCCTGGGGCAAGTTCACCTTCCCTGGGATGTCC

Table 1

CTGGACAAGAGACAAGGAGAAGGCCTTAGGATCTACTGGGGGAGTCCGGAGGAGCAGTCT CTTCTGTCCCGCTGGAACCCATGGTCCACTGAAGTTCCTTATGCTACTTTCACTGAGCAT CCTATGAAATACACCAGTGAGAAATTCCTTGAAATTTGCAA

Sequence 2210

GGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACAAAACAAGCAAAGTCT CCCATAACTGAAACAGGATTCTGTTTTAGAAAAAGGCCCAGCTGAGCTTANGAGCAGA GAAGGAAAAGAAGAAAATAGAGAGCTTTGTGCATCTTCTACGATGCCTGCAATTTCAGAG CTTGCATCATTGCTTATGGGAAGGAATCTTCAGATTGAAGAAATTAAACCTTTCTCTCCC AAGATCATCAGCCTAGAGTCGAAAGAACCACCTGCCTCTGTAGCTGAAGGAGGCAACCCA GCAAGAATTTCAGCCATTTACTTTTTCTTTAAAAGGATTATCANAGGAGGTTAGCCATCC AGCCCGACTTTAAAAAGGAGAAATCAAGAAATAGGCCCATTACCACCAACTGGAAATT TGAAGGCACAAGTCATGGGAGATATTTTTANAATAAGCTAAGTG

CCGCGGTGGCGCCGAGGTACGCGGGGACAGCGATGTGAGCTGAGGTGCAGGCACCAGAC
CTAGGAATTCCTAGAAAAATAGTCAGGAAGCATTTAGACACATCAAATGTTAAACGAGTC
CTGATTATGATGATAATGATGATGATTTTGGTGGTTGCAATAGCAAAGCCTTAAGTATGA
AGGAGACGTGCCAGCTGGAAATACAGGTAGACAATGAACAACTGAATTTAGAGGACGAAG
ACATTGAAAGCATTGATGCCACCAAATTGAGCCGTTTCATTGAGATCAACAGCCTCCACA
TGGTGACAGAGTACCTGCCCG

Sequence 2213

CACTNCTATAGGGCGAATTGGAGCTCNCCGCGGTGGCGGCCGAGGGACCCGGGGGCTTGN CCCCTNATGCCTCCGTGCTTGCGCGTGTGCCATTTCCTCCCAGAGGACCTTTCCTGC CTAGGACTCATCATTGTCCCCTCCCTGGCATTTTTTTACACCTGGAGCAGTCAGAGGACGC ATGCATGGCTCTTCGGAAGCCTTCTCCTGCCACGGCATGCACCCACACATGCGAGCCTCC CGGGTACCTGCCG

Sequence 2214

Sequence 2215

CCGCGGTGGCGGCGGGGCCATTGAGACTGCCATGGAAGACTTGAAAGGTCACGTAGCT
GAGACTTCTGGAGAGACCATTCAAGGCTTCTGGCTCTTGACAAAGATAGACCACTGGAAC
AATGAGAAGGAGAGATTCTACTGGTCACAGACAAGACTCTCTTGATCTGCAAATACGAC
TTCATCATGCTGAGTTGTGTGCAGCTGCAGCGGATTCCTCTGAGCGCTGTCTATCGCATC
TGCCTGGGCAAGTTCACCTTCCCTGGGATGTCCCTGGACAAGAGACAAGGAGAGGGCCTT
AGGATCTACTGGGGGGAGTCCCGGAGGGAGCAGTCTCTTCTGTCCCGCTGGAACCCATGG
TCCCTGGAAGTTCCTTATGCTACTTTCACTGAGCATCCTATGAAATACACCAGTGAGAAA
TTCCTTGAAATTTGCAAGTTGTCTGGGTTCATGTC

Table 1

Sequence 2216

GGAGCTCCCCGCGGTGCCGCCCCCGGGCAGGTACGCGGGATTGACATCCCACACTACC
TGATTTGATACACTAAGAAGGGCTTATCATTTCTGTGGTACTCTTGGCCAACAATGCACG
TGTAACATTTATTCATTGAAACACATTAGGCAGAATTGCAGGACATTCTTCAAAATAGCT
GTCCCAATACTCTTCAAAAGTGTCAGGTCCTGGAAGACAAAGAGATACTGAGGAACCATC
ACAGAGTGGGAGAGACATAGAGTGATAAAAACTAACTGTGATGTGGAATCCTACATTGG
ATCATGGACCAGAAAGACAGCACTGATGGGAAGACTGATGAAATCTGAATAAGTCTGTAG
NTTTGGTTTAAAGAAGAAGAAGAATAATAACAATAATGGTTTAGCTGCTGGCTCCTTAATAAA
ATTCCCCTAGTTACTGTAATGTCTGAAAATGAACCCC

Sequence 2217

Sequence 2219

Sequence 2220

Sequence 2221

Table 1

GGGGAATTGGAAAATTACTAATTCATGAAAATGAAAATGTGGGCTTCTTTTAAGGAAAAA TTCCTTTGAACATTGACAGAAGTGGGCCGTAGGGAAGGGGAAGAATTTGCCTGGATTCTT CACTTAACTCTTGTCACCACTGGAGCATNCTGACTCCCTAGACACAAAGTGATGGAAGTT ATTTGTTTCCACTCTTAAACACTGTCTCAAGGGGGACATTGATGGGATGGGNGG Sequence 2222

TATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACAGCAACAGAATGAGAAGC TACAAACAAGAATTGGAGAACCTGGAAACAGAATTTTAAAAGGTCACGGATCGCCTACAGT GACGAAGTACGGAATGAGGCTCCTGGGGGATGATGGGAATTCCTCAGAGAACCAGAGGGCA CATCTGCTCGATAACACAGAGAGGCTGGAAAGGTCATCTCGGAGACTAGAGGCTGGATAC CAAATAGCAGTGGAAACCGGTAAGAATTCTGAGAGTGAGCAAATTGTCTTGCTTATGCAC AGCAGTCTTCACAACACACTGACATTTCAGGGAAACTTCAAAGGAGTAGCANAGACAGCAN CCCGAGATGTGGTTTACATATTGGGGAGACAATTGGGGAGCFTATTTGCGCTTATCTTTTT TCAAGGT

Sequence 2223

AGGTACACAAAGACAAACCTGAACTTAATTTCAAGGAAAACTTAAACCCATGCACAAA TAATTGGTGAGCCTTCATTTCCCTGACTTCAAGTTTCCATGTGAGGACTCATGCTCTCTC CACTTTCTTCTTGGGAGGAGGGAAGATTTACCTAATGGGTAAATTTGGGCAAAGCACATT GAGTGTGCTTGTTTGGCTCTGAGTCTCTTTGCAAACATGTCTCTGCCCACAGTAACATGA GTTTGCGTTGACTGTCATGCAGGAAGCTGCCTGCTCCTGTGGCCATGTCAAGCAAT TCTTTCTTTCAACTGCAACTGTGTGGTAAGAGCTTAGTCTGAGAAGAAATGTTCAGAAGC TCACTGTGGCTGTACCTGCCCGGGCGGC

Sequence 2224

Sequence 2225

Sequence 2227

TCTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACGCGGGGGCAG

Table 1

Sequence 2228

Sequence 2229

Sequence 2230

Sequence 2231

TACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGGGGGCCATTGAGACTGCCATGG
AAGACTTGAAAGGTCACGTAGCTGAGACTTCTGGAGAGACCATTCAAGGCTTCTGGCTCT
TGACAAAGATAGACCACTGGAACAATGAGAAGGAGAGAATTCTACTGGTCACAGACAAGA
CTCTCTTGATCTGCAAAATCCACTTTCATCATACTGAGTTGTGTGCAGCTGCAGCGGATT
CCTCTGAGCGCTGTCTATCGCATCTGCCTGGGCAAGTTCACCTTCCCTGGGATGTCCCTG
GACAAGAGACAAGGAGAAGGCCTTAGGATCTACTGGGGGAGTCCGGAGGAGCAGTCTCTT
CTGTCCCGCTGGAACCCATGGTCCACTGAAGTTCCTTATGCTACTTTCACTGAGCATCCT
ATGAAATACACCAGTGAGAAATTCCTTGAAA

Sequence 2232

TCGACTCCTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCTGTGTCAGGA GTCCCCAAGCCCACTCCCAAAATAGAAAATTCACTAAAAGGAGTCAAAGGATTCAGCATA CAGTAATATTAACAACTAAGATTTATTCCAGCAGGATACAAAGCAAAATAAGAAAGGAAA AGTCGCATGGGGCAAAATCAGGTGAAAGCTTTCCAAGAGTCCTCTCCCAATGGAGTTACA

Table 1

Sequence 2233

NCCGGCCGCCGGGCAGGTACNTTATGACCCAACATTTACCTCAAAAGCTNTNAATGACC
TTTGCGGGGAACTGTCCCCAAGACAACCTNAAAGAGACAGCACAACATTTGCAGCTGTTT
CTCTTTCAGCCCAAGGTCGCAAAGGATATAAGAAGCCAATGCAGCTTGGANGGAGAAAGG
GATTCCTGTAAATCACTCACTATGATTTCCCACAGCAGGCAAGTGGATCCCCTAAAGAAA
GAAGGCTTATAGAGTTCCCTCAAAAGAGCTCAGAACTTCAACAATGATTCTATTCACATA
GGCATTTCTGTCTTCCAAATTTTAGCTTTAAGAGTCTGAGGAAGTACCTCGAGCGGCCGC
CCGGGCAGGTACTGGAAAACCTCCATCTTGGCTCCCAGAGCTCTAGGAACTCTTCATCAC
AACTAGGATT

Sequence 2234

Sequence 2235

CTNCTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTGACCTCTTAGGGA
TCTAAGGAAAAGATTCTGGACCAGAATGGGCCTAGGCTTGAAGTGGATCTCTTCCAAAAG
AATAGTGAATAGTTTTATCTTTTCTAAAAGATGGATTGAATGGAATTCTTCCATTTGTA
AGTAAGTTCTTGTAAGTTTAATTAATTTTGTAACATCTTTTGAGAATTTACCACATGCCA
CTCCTTGAGCTGGGTGCTTACTATGTGTTTATTATTTTAACCCTCACAACAACCTCAACA
CCCTCATGAAGTAGGTCCTATTAGGATCCCTGTTTTGAAGATGAACTGAGGCTCATGTTT
AGCCCAAGTTCACTGAGCTAGTAACTGGCAAAGTTAGAATCTGAAATGAAATCTGCCTGA
TGTCAGAATGATGTTGTTCATTCATAGGCTGATATTCTT

Sequence 2236

Sequence 2237

Table 1

AAACCTTAGGGGAAAAAAAGAATTGGCCAAGGTTTCNGGAAAAAGAATTTCTTANGGAA AAAAGGCCGNTGGGGGTTAAAAANGGGAAGGCCCCGTTCCCATTGGAACCGGTTTTTAAA AAGAACCGGTTTCCCTTTTGACCTTTCAAGTTANCCCTTGGCCCCNGGG Sequence 2238

Sequence 2239

Sequence 2240

Sequence 2241

GGCCGCCGGGCAGGTCCTCGGGAGATCAGGACTCTTACAGCCAGTCATTGAAGTCTCCT
TTAAATGAGATGTCTGATGATGATGACNATGATGATGATGACAGTGACTAAGGACACATTTGG
GAGTATTTAATCAGGTGTGGCTATCCGAGAAATCAACTTTGGGGGAAATGTAANATTCTG
AGCTCTCTGTTTNGTTCTAGCCATGAATTTGCCTGACAAACTTGTAACCTATGTGCCTCA
ATATATTCCATAGAAAGTAGGTCCCCCTGCCTTCTCCCACTCCTCACACTCTTCTACAGG
GATAGGCTTTTGCAAATATATCAGATAAATTTTTTTGTTTCTTTTATTTTTAGGTTATT
TTCTTGGAAGGTTGGGAAAAGATGTTTGTTTTAACAGATCATGTACCTC
Sequence 2242

Sequence 2243

GGCGAATTGTTTTCCNCCGNGGTNGCGGCCGCCCGGGCAGGTACNNTGATTAGTTAAATN TAAGACTCCGTANTTTTTACAATTTTAACAATAATTTTATTTCTTCAAGCTTGTTAGTTT GGGATTGTATTAAAACTACAGTGTGACCTTAGAAAATGATAATGCTGCTTTATGGAAAA

Table 1

Sequence 2245

Sequence 2246

Sequence 2248

Sequence 2247

Sequence 2249

GTCCCGGCCGCCCGGGCAGGTACNTATTGTGTCCACTGTAAAGGTAAATGATTTNTTTTT
TATATTGCATCAAACTTGGAACATCAAGGCATCCAAAACACTAAGAATTCTATCATCACA

Table 1

AAAATAATTCGTCTTTCTAGGTTATGAAGAGATAATTATTTGTCTGGTAAGCATTTTAT
AAACCCACTCATTTTATATTTAGAAAAATCCTAAATGTGTGGTGACTGCTTTGTAGTGAA
CTTTCATATACTATAAACTAGTTGTGAGATAACATTCTGGTAGCTCAGTTAATAAAACAA
TTTCAGAATTAAAGAAATTTTCTATGCAAGGTTTACTTCTCAGATGAACAGTAGGACTTT
GTAGTTTTATTTCCACTAAGTGAAAAAAGAACTGTGTTTTTAAACTGTAGGAGAATTTAA
TAAATCAGCAAGGGTATTTTAGCTAATAGAATAAA

Sequence 2250

CTACTTAGGGCGAATTGGAGCTCNCCGCGGTGGCGGCCGAGGTACGCGGGGACCTCAGAG CTGAGCTGGGCATGAGTAGATGCTCAGTAAGTGGTGCACAGGGTTGGTCCCTATGGTGGA GGCCCCCTAACACCGCCCAACCCCCCTCCATGTTCTCACAGCTCCACGCACTGAGCACGG GCATGAAGGCCATGATGTCAGAATTCTGGCACCCAGGGAGCTGAGATGTGCCGCAGGGCC TGTGGCGGACATGGCTACTCAAAGCTGAGTGGCCTGCCATCACTGGTCACCAAATTGTĆG GCCTCCTGTACCTGCCCG

Sequence 2251

Sequence 2252

TNGGGCGAATTGTTNCTCCACCGCGGTGGCCCGCCCGGGCAGGTACACAAAGACAAAC CTGAACTTAATTTCANGGAAAACTTAAACCCATGCACAAATAATTGGTGAGCCTTCATTT CCCTGACTTCAAGTTTCCATGTGAGGACTCATGCTCTCCCACTTTCTTCTTGGGAGGAG GGAAGATTTACCTAATGGGTAAATTTGGGCAAAGCACATTGAGTGTGCTTGTTTGGCTCT GAGTCTCTTTGCAAACATGTGTCTGCCCACAGTGACATGAGTTTGCGTTGACTGTCATGT CTGCAGGAAGCTGCCTGCTCCTGTGGCCATCCCGCGTACCTN Sequence 2253

GGAGGCTATGCAGATATATTCTTTTCTCTTTAAAGTTTTGCCCACCAGTTTTAGAATTCA
TCAGTAAATCTTGTCTACAGTAATTATTACTATTTGCTATTCTAATGGGAATTTTGTATA
TCTCCATCCCTTCTAATATATTTAACAACTGAATTCTATAAACAAGATTTGTTTCTC
CACATTATTTATTATCAATACAGACACATACTTTGGGGGGTTATAATCCAATACTATTG
TTATTTATTATGTNGTTCATATTGTTCTAGCTTTGGCTACTGGGATCTTTTATAAGTGTN
TTCTGTGNCCTTTTGACATGCCCCATTTTTTTCTTTTTAAGCACATCTTTACTTTCTGAG
ACTACAAGATTGTCCAGGTTCTCATCTTGTGTTTTCCCTTCCCTAGCCTTGGAATGAGCT
GNTTTTCCAATGATCTCTAGTTCCTTTATTAGAAAAATGGTGGCCAACATGGTGAAACCCC
ATCTACAAAAATACCAAAA

Sequence 2254

CTATAGGGCGAATNGGAGCTCCCCGCGGTGGCGGCGGGGGTACATTTCTTCTAATTGATC
ATATCTGCTTATTTTCCTCTGGATTAAGGATCAAGGAGATAGTATATTAGATGATTTTGAT
AAATTTCCAATGCTTTGCAAAGTAGTTGAACAACTTTTTCTTTGTGATGCTAGGTGGCAC
TACTAGTCAAGACTTGGTATTTCATAGCTGGCTTTCTTATTCTGAAGGTTGTAAAAAGAC
ATATGAAGTAATATTTAACATTGAAAACATGATAATCAATTTGATTATCTATGAATTGTC
CTAAACGTTCAGAGTAAAGTTTCCTTTAAAGTTAAAATCTTTCAAGTGAAGGAAATTATA
AAGTCACATGTAAACACCAAAATAAGAGGAATAGAGCAATAGGATATTTTTTGGCTTTATA
ATTCAATTTAAAAATTAAGGTGCATTTATTTTTTTTTGGCAGCTGGCCATAAAGCTTCAATG
TCCAGTAAGCAGTTGCTATCTATGATTCATGAGATCATGGGGTT

Sequence 2255

Table 1

GAACAGCATTCATCCTCAACATTTTTACGAAGACAAAATGAAGACTGGAGTAGAAGACTG ATCAGTGCAGGTGTAGCATAAAAGTGTAATCCTGGAAGATGTGGTGTGAGAAAGCATTAT CANCAATNATGCNTNTTNCCAATCCCAAACCATGGGGGGGTTTCTCACAGCTTTACACCAA AGGGCATCACTATCCCTCAAAGAGAGAAACCTGGACACATGTACCTTGCCCG Sequence 2256

CCGCGGTGGCGGCCGAGGTACACACTTGTGTGCATTTCTGTTGGGTATATAACAAGTATG
AAATTGCTGGGTCTTAAAATATTTATATTTAACTTCATTAAATGCTGCCTAAGAATTTT
TCAAGCGGTTGTGCTATTTTACCTTCACCAGTTCTAGTTGTTCCATATCCTTGCTGTCAC
TTGGCATTAATCTGAATTTTTTATTTTGACCAGACTGGTCTGTGTCATAGTATCCCAT
TGTCATTTTAAGTTGCATGCCTTTGATGAAGACATTTTCTGATGCTTAATTGGCTCTTTG
AATATATCCTGTAACTGATTTGTAGGGAGNTTTTATATATATCTTGGATATAANTNTTTT
TATNTGGACATAAATATTTCGCAGATTATCTNCTCCCACTTTTAACTTCCCTTTTTTC
Sequence 2257

Sequence 2258

Sequence 2259

Sequence 2260

Table 1

CCGCGGTGGCGGCCGAGGTACGCTTTGACGACACTCTCAGACATGCTGTGCAACTTAACG
TCACTGCCACCCGGCAGCTCTTGCTTATGGCTAGTCAGATGCCAAAGCTGGAAGCCTTTA
TACATATCTCTACTGCCTATCCAAATTGTAACCTGAAGCACATCGATGAAGTTATCTATT
CCNGCCCTGGNGGACCCAAAAAAAATCATNGATTCCCTTGAGTGGTTAGACGATGCTATT
ATTGACGAGATTACACCCAAGCTGATCAGAGATTGGCCCAATATTTATACCTACACCAAG
GCCTTGGGAGAAATGGTGGTGCAGCAAGAGAGCAGGAACCTGAACATTGCCATCATAAGG
CCCTCCATTGTGGGAGCAACTTGGCAGGAGCCTTTCCCAGGTTGGGTTGATAATATAAAT
GGACCTAATGGAATCATTATTGCGACTGGGAAAGGGTTTCTTCGGGCCATAAAAAGCTAC
TCCAATG

Sequence 2262

CGAGGTACGCGGGGGAGATGCTGCCACCTAGGTTACTTGTAGGACCCTATACGGCAACCT
CCTTTGCCAGGAACTATTTATAAACATCCTGCAGGAAAATGAGTCTATATGTCAGAATAC
ACATTTCCCACCTTGCCCAACAGTAGAAAAACATAAGAAGAGAAAAACATTAAAAAATGA
CAAGGAAGTTAATGGAAGTCAGCAATGTGATGGTGTTTTGGAGGTGGAGCCTTCAGAAGGT
AATTAATGCCCTTGTAAGAAGAGGCCAGAGAGCTTGCGCACCTTCTTCCTGCCATGTGAG
GAGCCAAGAAGCCGGCTGTCTGCAACCTGCAAGAGGACCCTCACTAGAAGCTAGCCATAC
TGGCATCCTCATCTTGGCTTTCCAACTTCCAGAACTGTGAGAAGTATATGTTTGTGGTTT
AGTCAATGGTCTATGGTAATTTTTTTATAGCAGTCCCAGCCAAGACAGTGCCTCATTTAC
TACATACCATTTATATTATTATATAGGCTCCTTTCAGAAACCCATGTTCAAATATTGAGAAATAGT
TTGGTATTAACTATCTCATNCAAGAAATGCAGATTCATGTTGGTTCTAATTTTATTATA
TAAATGACAAAATGNAGAAACTTAACACCATCCTAGATTTTAGCTGCCCCNG
Sequence 2263

Sequence 2264

Sequence 2265

Sequence 2266

Table 1

Sequence 2267

Sequence 2268

Sequence 2269

Sequence 2270

ACTNCTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCGGGGGTACGCGGGATGATTTT
TTATTTTAAAATAATCTGGAAGTAATGGGAACTTAGTTTTTCCTGAACTCCAACCAGAAT
CCAAATTGGTTAGATGAGGCCGGGCGCGCGGTGCTCACGCCTGTAATCCCGGCACTTTGGG

Table 1

Sequence 2272

Sequence 2273

Sequence 2274

Sequence 2276

Sequence 2277

ACTNCTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACTGTTGC AGTGAGCTCAAGTGTTGGGTGTATCAGCTCAAAACACCATGTGATGCCAATCATCTCCAC AGGAGCAATTTGTTTACCTTTTTTTTCTGATGCTTTACTAACTTCATCTTTTAGATTTAA

Table 1

Sequence 2278

Sequence 2279

Sequence 2280

Sequence 2281

Sequence 2282

Sequence 2283

GGGCGAATTGGAGCTCCCCGCGGTGGCGGCNCGCCCGGGCAGGTACCAGGCAGGATGGAG CAGGATGGTGTGAGATTTCATCACACTACTCAGGATAGTGCACAATCTAACACTTATGAA TTGTTTATTTCTAAAGTTTTCCATTTAATATATTTTGAAATGAAGTAGACCCTGTGTGTAG

Table 1

TATAGGGCGAATTGGAGCCTCCACCGCGGTGGCGGCCGCCCGGGCAGGTACTTAAACAGT
TATAGTCACCATCACCTGCTTCAGAATGGTCTTTTAGATTTGTGTTTTGTTTAAAGT
TGTTGGCACCAGGATGCAGAGAATCAGACTGGCCTGAGGTGAAGGAGCACACAGCCCTGA
GGGCTTGGAACCCTGGGTCCAGTTCCTCTTCACACCCCCTTCCACTCTGAGTAGCACATC
TCCCCAGGTGCCCATGGAACACCTGCTTTCATCCCAAATATCCGTCCACCTAGGCGGGGT
GGTATGTTCTTACGTCTCTGACTTTGATGCCACTCATTCTATAGTTTAGCTGGTTTTC
GTTCAAGATATTCTTGGTAGTAACTGACAAGTATGTTGCACAGGATTTTGATGGTGGGAA
TATCCTAAGTGGTAGCCTTCCAAAGTAGCAGTTGACATTCAGCTGCTTTTAACTAT
TCAGGCTACCTTTTATACTAAACCTTGAAAACTAGAATCTAATGTCTACCCCAAAAAAAGT
AAGTTCTTTGATATTTTATCTTATGTACCTTTGGCCCGGTCTAGAACTA
Sequence 2285

Sequence 2286

Sequence 2287

Table 1

AAGTATTTTAACATCTTCTAAACCTCAGTGAATTCATTTTCTTAAAAAGAAAAAAATCTT

Sequence 2288

Sequence 2289

0

Sequence 2290

CCGCGGTGGCGCCCCGGGCAGGTACTGCTAAAGAACTCTAGAACATACAGGGTGTAG ACGCAGTCTTCTTGGGGAAAAAGAGGCTTCAGGATTGCAAGATTTCAGCTACTGTCTCT CCTCGGAGCAGGATTCCATCTTTTCCATGGCTGGGGCCCTTGACACATGTCACTGTACAC TGCTCTTCTCGCTGGGATTTCCAAAAGACCTTGGCTCAAGGTGTCACTTTTGCAGAAAAG CATTTACTGACTGTTGACTTGGCCAAATCCCTTGTGCTGTGTTTCCTAGCACGGNGAGTT GCATTTTTCACATGAACTCATGCCTACCTTCTCTTGTTTTATAAGCTTCATGAAGGCAGG TACCT

Sequence 2291

CCGCGGTGGCGCCCCGGGCAGGTACCCGGGAGGCTCGCATGTGTGGGTGCATGCCGT GGCAGGAGAGGCTTCCGAAGAGCCATGCATGCGTCCTCTGGCTGCTCCAGGTGTAAAAA ATGCCAGGGAGGGACAATGATGAGTCCTAGGCAGGAAAGGTCCTCTGGAGAGAGGAAAT GGCACACGCGCAAGCACGGAGGCATGAGGGGCCAGGGTCCTGGAGGACACTGGGGCCGGG ACAGATCAGACTCCCCCCGCGTACCT

Sequence 2292

Sequence 2293

CCGCGGTGGCGCCCCGGGCAGGTACGCGGGGGGGAGATGCTGCCACCTAGGTTACTTG
TAGGACCCTATACGGCAACCTCCTTTGCCAGGAACTATTTATAAACATCCTGCAGGAAAA
TGAGTCTATATGTCAGAATACACATTTCCCACCTTGCCCAACAGTAGAAAAACATAAGAA
GAGAAAAACATTAAAAAATGACAAGGAAGTTAATGGAAGTCAGCAATGTGATGGGTGTTT

Table 1

GGAGGTGGAGCCTTCAGAAGGTAATTAATGCCCTTGTAAGAAGAGGCCAGAGAGCTTGCG CACCTTCTTCCTGCCATGTGAGGAGCCAAAGAAGCCGGCTGTCTGCAACCTGCAAGAGGA CCCTCACTAGAAGCTAGCCATACTGGCATCCTNATCTTGGCTTTCCAACTTCCAGAACTG TGAGAAGTATATTGTTTGTGGTTTAGTCAATGGGTCTATG

Sequence 2294

CCGCGGTGGCGGCCGAGGTACACTGATTTCCGATCAAAAGAATCATCATCTTTACCTTGA CTTTTCAGGGAATTACTGAACTTTCTTCTCAGAAGATAGGGCACAGCCATTGCCTTGGCC TCACTTGAAGGGTCTGCATTTGGGTCCTCTGGTCTCTTGCCAAGTTTCCCAGCCACTCGA GGGAGAAATATCGGGAGGTTTGACTTCCCCGCGTACTTTGGAGTCCCCTGGTTTCTCAAG AATTGCCGTTGACTCTTTCTTTGGCTTCTGCTGCACGGTAACCAGACTCCCTACAACTG CACTCTTTGTCTTTGTCATGGAAGCCGCGAGCCGTAGAGGTTCCGCGTGCTCTGCCGGAC TGTGAGCAGGNTCACTGGGTCCTTTACACTTGTGAATTCGAAGCTTGCCAGA Sequence 2295

Sequence 2297

Sequence 2298

Sequence 2299

GACTCCTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACGTAATAGTATCA

Table 1

Sequence 2300

GAGCTCCCCGCGGTGCCGCCCCGGGCAGGTACATGGAGGGCTGATTTATCACATACG
TGGGTTCTGTAGGGCCCACTGTGGGACTTGAGTATGCATTGGGTTTTTGTATACTCAGGC
GTTCTGGAACTATCCTCCATGTATACCAAAGGATGGTTATTTCTACAAAAGCAGGAGGTA
AAGCCCAATGCACAGCTTGCAGATTCCCCTCAGGCGAGAGACAGAGGTTAAGGGTAGATG
GCAGATGACCTAAGTGGCTTGTTTTAGGAGGCCACTCCCAGGGCCACAGCTTTCATGTGT
TTGCCACCAGGGTAGAAAGGTCTTGCTGACAAGGGCAATGACTACTAACAGCCCCAGCTTG
CATGGAAACAGAAAAGGGCATATTGCTTGTGGCCACCAGGGCTCAGGCTCTATCCCTCAG
CAAGCTTTGGGATC

Sequence 2301

Sequence 2302

TACGACTCCTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGGAAC
TTGTGTGCTTAGACCTGACGCTGGGAGGAGATGCTGCCACCTAGGTTACTTGTAGGACCC
TATACGGCAACCTCCTTTGCCAGGAACTATTTATAAACATCCTGCAGGAAAATGCAGTGA
AGTAGAAGAGACAGGGAATATCCCAGAAGGTTATGCAAAACATCAAGAAGAAGAAGAAGAAGAAGAACATTATGTCAGAATACACATTTCCCACCTTGCCCAACAGTAGAAAAACATAAGAAGA
GAAAAACATTAAAAAATGACAAGGAAGTTAATGGAAGTCAGCAATGTGATTGGTGTTTGG
GAGGTGGAGCCTTCAGNAAGGTAATTAATGCCCTTGTAAGAAGAGGCCAGAGAGCTTGCG
CACCTTCTTCCTGCCATGTGAGGAGCCAAGA

Sequence 2303

Sequence 2304

Table 1

TAAAATTATGAGTAATTAACTTTATGACAGGTAACACTAATAAAGTGCAGTGGCATGTTC
CTGAAATCCCAGCATTTTGGGGGGATGAGGTGGGGAAGGGATTACTTTGGAGGCCAGGGA
GTTTGGGACTAG

Seguence 2305

ACTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACACTGAGATGATTAT
TCCCTCTTTTTTTAAAATTTGAAGTTTCCTTTGATTCCCCTTTTCTTTTACAAAATGGAG
TCATGACACGATCCCCGTGTCCCGTGTTGAGAACTGAAAGGTTTCTGTAGCTTTCCTTTG
ACATGAAATTTCAAAAATATACTACTCTGTTTCACTCTGGCCTGTAATTGTTGCACTCTG
GCCTTTAATTGTTGCAACTGATTAGACATTTTTCCTTCCAGCATTATGGTAGACTCGATG
CCC

Seguence 2306

AGGTACTCTTGGTTTTTTAAGACAAAGAGCAAATCCTCCCCTGCCAGGATTGACTTTTGG
CTCTTTTTTTCAAACCTCACTGCTTTTTGGTTTAGTTGTCATAAAATGCCAAGCACCAT
GAACAGGGCTCCATGAAGGGGCTCAGAGGTAGGAGGGCTGTGATTAGGAGAAGGCTTGGA
CTGATGGGCAATTTGAGTGCTCAGAATTAGAGTGAGGGGTGGGGGTGCTGCAGGGACAG
ATGCTGGGGAAAGACACCCTGAAGGGCAAAGGGGAGCAACAAATGGGCTGCAAGTACCTT
GCCCCGGGCCGGCCGCTTCTTAGAAACTAGTGGGATCCCCCGGGCTTGCAAGGAAATTCG
ATATCAAGCTTATCGAATACCCGTCCGAACCTTCNGAGGGGGGGGGCNCCGGGTACCCAA
GCTTTTTTGTTTCCCTTT

Sequence 2308

CTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACNCGGGGATGCTGCCA CCTANGTTACTTGTAGGACCCTATACGGNAACCTCCTTTGCCAGGAACTATNTATAAACA TCCTGCAGGAAAATGAGTCAAGGAAGCTTTTNTTTTGAGCTATTTACAGCTTTTAGCAAT TGAGTAAAGTATACTCCTGTGAACAAAATTTGGAACATATTTGNTTCTNTCTAACTGATT TCTNCAGAATTTGGAACTAGTTCAGTGAAGTAGAAGAGACAGGGATATCCCAGAAGGTTA TGCAAAACATCAAGAGAAGATGAGAGGAGTCTATATGTCAGAATACACATTTCC Sequence 2309

GACTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACNCGGGGGCAGTGG
GAAGCTCGCNGCAGCTGGGAGGAGCCAAAGCCTCGCAGCTCACCTAANCCGCANGGAG
ATACACCCAACTGGGAGTGAGGAAACAGCNACCCAGAGAGGAGAACTAACCCACACAGG
ATCATTTNCCGAAGGAGCACGGCTGAAGAACCANACCTGGACTTTCTTAGGACAAACTTA
CTGCAGCTTGAANGANCCAACCATGGATTTGAGGCGTGTGAAGGAATATTTCTCCTGGCT
CTACTATCAATACCAAATCATTANCTGCTGTGCTGNTTTAGAGCCCTGGGAGCGATCTAT
GTTTAACACCATCTTACTAACCATTATTGCTATGGTGGTATACACTGCCTATGTCTTTAT
TCCAATCCACATTCGCCTGGCTTGGGAATTTTTCTCAAAAA

Sequence 2310

Table 1

AAATNNAANANAAAAANAAAAANNNNANGGTACCTGCCCGGGCGG Sequence 2311

Sequence 2312

Sequence 2313

Sequence 2314

Sequence 2316

Sequence 2317

Table 1

Sequence 2318

ATCATACTTAGGGCGAATTGGAGCTCCCCGCGGNGGCGGCCGCCCGGNCGGGTNCCCGGG
GGANATGCTGCCNCCTAGGTTACTTGTAGGACCCTATACGGCAACCTCCTTTGCCAGGAA
CTATTTATAAACATCCTGCAGGAAAATGTCAGAGATGGGAAGAAACAAGAACTTTGACAT
GCTTGGTGTTCTTGCCCAAGCTTTGAAGAAGATTTACAAAGTCTATATGTCAGAATACACA
TTTCCCACCTTGCCCAACAGTAGAAAAACATAAGAAGAGAAAAACATTAAAAAATGACAA
GGAAGTTAATGGAAGTCAGCAATGTGGTGGTGTTTTGGAGGTGGAGCCTTCAGAAGGTAAT
TAATGCCCTTGTAAGAAGAGGCCAGAGAGCTTGCGCACCTTCTTCCTGCCATGTGAGGAG
CCAAGAAGCCGGCTGTCTGCAACCTGCAAGAG

Sequence 2322

Sequence 2323

Table 1

Sequence 2326

Sequence 2324

Table 1

Sequence 2330

Sequence 2331

Sequence 2332

Sequence 2333

CCGCGGTGCCGCCGAGGTACAGTAGGAGTGCCCAGACTCGGGGAGAGGCAAGCTGGCGC
GTCTCCAAGGTGCTTGTCACTCACCACTAGAACGTGGTCCTTTACCACTAGACAAGATCT
CCTGGTTTGACAATGCAGGTGACACAGCTGAAACTTTATCTCAACACGGCCTGAAGAATA
CCACTGTCTAAATATGAGGTGCTAAAATACTATGACCTACTCTAATATTCTCTCCCAACT
CTGTCCATCCTCGTGACTGGCACCCATGCTGGCCCAAATGATGACAACCTCCTGTTCTAA
GTGCACAAGCCGCACATTTAATAAACCTTTCACCCAGTTCCTTCACTGGTGTTCATCTCT
CGGCTTCACTTACAACCACTCCCTGTGGCTTTTGCAGTGAAGCCTCTTAGCCCAAAACTC
TTCCACTCCCA

Sequence 2334

CTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACATGAAGGAGG GCACTAGGGGGAGTTAAGAATTTGTGAGTTAGGTAGCCAAGATTGTTGAGGTTGGAAGAA TGAGGAAAGAAAGGGGATCTGTGGCAAAAATATGCTATTGGATCCACAGTTCTAGTTTAA GGACATGTCTAGTCCCTTTTCCAGCCCCCAGTTAATTACAATCCCCTGCTGCCCAAATGG AGAGGGAGGTTGTTCACCAGTAGAGGGAGCCAGGGGCTGGGTGTCTCAATAGAAACTGAT CTGGTCCCAGAAGGGGCCTTTAGATTTAAGTTTTTCGGATCGAAGGCAGAGCAAAGTGTC

0

Table 1

CCTTACAACCAATGGCTAAAATGTATGCCATTGTAGTAGATCACATTGTTAGTTTTCTTT

Sequence 2335

Sequence 2336

Sequence 2337

Sequence 2338

GGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACGCGGGGGCCACCTAG
GTTACTTGTAGGACCCTATACGGCAACCTCCTTTGCCAGGAACTATTTATAAACATCCTG
CAGGAAAATGAGTCTATATGTCAGAATACACATTTCCCACCTTGCCCAACAGTAGAAAAA
CATAAGAAGAGAAAAACATTAAAAAATGACAAGGAAGTTAATGGAAGTCAGCAATGTGAT
GGTGTTTGGAGGTGGAGCCTTCAGAAGGTAATTAATGCCCTTGTAAGAAGAGGCCAGAGA
GCTTGCGCACCTTCTTCCTGCCATGTGAGGAGCCAAGAAGCCGGCTGTTCTGCAACCTGC
AAGAGGACCCTCACTAGAAGCTAGCCATACTGGCATCCTCATCTTGG
Sequence 2339

CCGCGTGGCGGCCGAGGTACCCTGCTGAAAGATTATTTCTAACAGGCTTGTAGAGAAAC
GTCGGTTCATGTAAATTAGAAATTATGGGGCCACTTTGCCATTCTTCACACCTGCAATGA
ACAGGTGTTTATCTGCAGTTCTGACTTATCTCTTGAACTCCATTTGCATGTTATAGTGGG
ATGCAGCTGATGCCCTGTCCAGATCTTCTTCAGGCCACTACATCTATATATGCATTCATA
TTCCAGTGGCTGTGAGTGTTGGCTGTTGGTTGACAGAGGAGCTGCATCCTTCTGGAGGAA
ACTGAACTCAGCTGATGAAAGCCACCCTGGTCCTGGGAGGTGAAGCATCTTCCAAATGAC
AGCCTGCAGTCAATGACTGATGAATATGACTTCATTGCCTCATGACAGGGA
Sequence 2340

Table 1

Sequence 2341

Sequence 2344

Sequence 2345

Sequence 2346

AGGTACGCGGGGAGTGTCCTCCAGGACCCTGGCCCCTCATGCCTCCGTGCTTGCGCGTGT GCCATTTCCTCTCCAGAGGACCTTTCCTGCCTAGGACTCATGATTGTCCCCTCCTGT GTTGCCTAGTTTCCTGGTATTAAGGAGAATCAACTCTCTGGATAAACGTGCCTTCTCCTG CCACGGCATGCACCCACACATACGAGCCTCCCGGGTACCTGCCCG Sequence 2347

CGCCCGGGCAGGTACCATGATTAGTTAAAATATAAGACTCCGTAATTTTTACAATTTTAAC AATAATTTTATTTCTTCAAGCTTGTTAGTTTGGGATTGTATTAAAACTACAGTGTGTGAC

Table 1

TTAGAAAATGATAATGCTGCTTTATGGAAAATGGATTATAGGTGGGTAAGACTTCATTGC
AAAAATTGTGTAATACCATCAGTGTTAGGAACCCAGTTGAAGTCTAGAAGACAGATGTTA
GTATCTTAGACTAGGTTGGTATTTGAATAGATATTGGTAATATCAGTAGAATTTAATAAT
ACATTAGAAAGAAAGAAATCAGAGAAGATTCTTTTATTTTCACTTGATACTTGTTGTT
ACTTTCAATGAGATAAGAAGGACAGGCAAAGGAAAGTTCAGGGGCAGGGGATGAGAAG
AAAACAAGAATTTTATGTTGGACATGCTAAAGTTAAACACCTGCTTAACTCAAATTGGCT
TCTGTGGAAGCAGAGGCTGCATGAGGTTGCTTATGAAAATGCTTTTTTGANGAAGCCATT
GCAGGAGGAATCTCTTANGAANCCAGGGAAGAAGGAAG
Sequence 2348

Sequence 2349

CGAGGTACCATGATTAGTTAAATATAAGACTCCGTAATTTTTACAATTTTAACAATAATT
TTATTTCTTCAAGCTTGTTAGTTTGGGATTGTATTAAAACTACAGTGTGTGACTTAGAAA
ATGATAATGCTGCTTTATGGAAAATGGATTATAGGTGGGTAAGACTTCATTGTAAAAATT
GTGTAATACCATCAGTGTTAGGAACCCAGTTGAAGTCTAGAAGACAGATGATAGTATCTT
AGACTAGGTTGGTATTTGAATAGATATTGGTAATATCAGTAGAATTTAATAATACATTAG
AAAGAAAGAAATCAGAGAAGATTCTTTTATTTTCACTTGATACTTGTGTTGTTACTTTCA
ATGAGATAAGAAAGACAGGCAAAGGAGAACGTTCAGGGGCAGGGGATGAGAAGAAACAA
GAATTTTATGTTGGACATGCTAAGTTAAACAGCTGCTTAACTCAGATTGGCTTCTGTGGA
AGCAGAGGCTGACATGAGGTTGCTTATGAAAATGCTTTTTTTGAGGAAGCCATTGCAGGAG
GAATCTCTAAAGGAAGCCAGGGAAGAANGAAAGAGAAAGGGAA
Sequence 2350

Sequence 2352

CCGGGCAGGTACCGCGGGGGCAGTGGGAAGCTCGCAGCAGCTGGGGAGGAGCCAAAGCCT

Table 1

Sequence 2353

Sequence 2354

Sequence 2355

Sequence 2356

Table 1

GGAAGGAGGACTTAAGATGAAAGTGAAGCAAGAGAAAAATAATTAAANAANANANNTNNN NNGTACCTGCCGGGC

Sequence 2357

GACTACTATAGGGCTTTTGGAGCTCCCCGCGGTGGCGGCCGAGGTACACAACCACCCCCA
TGCCTCCTACCCCCGAGGTTCCTAGAGCTAGGCTCTCCTGAGGCAATGCTTTCCTTCTCA
ATTCATATTCTTCCAGGAGGGGCACCAACGTTTTTTAAAATGATGTTGGCGACGAGGACG
GTAAATTTCTAGATGACTGAAGGCTGACTTTCCCCTTTCTGTGACTCTCTAGGCAACAC
CGTGACAGGAGAGACGACTCCCTTTCTCTCTTGTGACCACTTCTGAATCTGTGACCCG
AAATCACAGCCAGTAGCTTTGTGGTCTCCTGGGTCTCAGCTTCCGACACCGTGTCGGGAT
TCCGGGTGGAATATGAGCTGAGTGAGGAGGAGGAGATGAACCACAGTACCTGCCCG
Sequence 2358

CCGGGCAGGTACCATATAGGTCCAAACCCAAACTGATTTTTGTTTTATGAAGTAGAAAT GGTTGCATGGGCTCTTGGCTAGAACCATCTTTGGCCCCATTGAAAATCAAGTTTCTGAGAC TGAAAAGGAAACACACAGTGACACCATTTTGATGAGGAAGAAGAAGAATTCTGAAGGAGCC AGAATATATTTGCTGAATTTTGACACTGAAGAAGAAATAAACATTGAAAAAAACAAAGCAA AACAACAGCAACAACAAAAAACTAAACCCATTTAGGTTTCCACTACAGATGCAAGAAAAA AGTGCCCTTGCACGTTTTTTCTGTCTGAGTGTCAGCCAAGGTTGCATGGGGGAATTCA GGATGTATAAAAACATAGACAGAGAGAAGAAGATNATTTTGCACCTCAGAAATAACCTTG TGAACAGCTGAGTAGCCTGT

Sequence 2359

Sequence 2360

AGGCCGAATTGGAGCTCCCCGCGGNGGCGGCCGAGGTACAGATTGTGTCCACTGGAAAGG
TAAATGATTGCTTTTTTATATTGCATCAAACTTGGAACATCAAGGCATCCAAAACACTAA
GAATTCTATCATCACAAAAATAATTCGTCTTTCTAGGTTATGAAGAGAATAATTATTTGTC
TGGTAAGCATTTTTATAAACCCACTCATTTTATATTTAGAAAAAATCCTAAATGTGTGGTG
ACTGCTTTGTAAGTGAACTTTCATATACTATAAACTAGTTGTGAGAATAACATTCTGGTAG
CTCAGTTAATAAAACAATTTCAGAATTAAAGAAATTTTCTATGCAAGGTTTACTTCTCAA
GATGAACAGTANGACTTTGTAGTTTTATTTCCACTAAGTGAAAAAAGAACTGTGTTTTTA
AACTGTAGGAGAATTTAATAAATCAGCAAGGGTATTTTAGCTAATAGAATAAAAGTGCAA
CAGAAGAATTTGATTAGTCTATGAAAGGNTCTCTTAAAATTCTATCGGAAATAATCTTCA
TGCNAGAGATTTCANGGTTTGGATTAGCCAGTGGGAATAAAGAAATGGGCCATTGGTTCCC
TATAATTGGGCTGGTTTTATAACTTTTGTAATATTACCTTTTTTCTGGCTGNGGTTTTATA
CTTATCCCATATGCNTGGATGGGGAAAAAATTT

Sequence 2361

Table 1

Sequence 2362

Sequence 2363

Sequence 2364

Sequence 2366

Sequence 2367

Table 1

Sequence 2368

Sequence 2369

Sequence 2370

AGGTACCATGATTAGTTAAATATAAGACTCCGTAATTTTTACAATTTTAACAATAATTTT
ATTTCTTCAAGCTTGTTAGTTTGGGATTGTATTAAAACTACAGTGTGTGACTTAGAAAAT
GATAATGCTGCTTTATGGAAAATGGATTATAGGTGGGTAAGACTTCATTGCCAAAAAATT
GTGTAATACCATCAGTGTTAGGAACCCAGTTGAAGTCTAGAAGACAGATGATAGTATCTT

Table 1

AGACTAGGTTGGTATTTGAATAGATATTGGTAATATCAGTAGAATCTTAATAATACATTA GAAAGAAAGAAATCAGAGAAGATTCTTTTATTTTCACTTGATACTHGTGTTGTTACTTTC AATGAGATAAGAAAGACAGGCCAAAGGAGGAACGTTCAGGGGCAGGGGATGAGGAAA ACAAGGA

Sequence 2374

AGGTACGCGGGCATCCTTAGGAGACCTGAGTCCTCAAGAAAACCCTCTTCTGGAAGTAGT
TGCTCCTTCAGAACGTTTTACAGAAAACACTAATGTAAAAGACACAACTAATGTNAAAGA
CACAAAAGAGATGTTCAAAGACACATTTCTGAAAACACAAAANCTNACAAATTCAAT
CCTCCCTGGAGNGGCAAGTTTTCNGGCCTGGGGNAACCTTGGCAATTTCNAAAACTTNT
NANGAAACCCCATAACCTTGGTTTNAAAAACCAAAAAACCTTGGAAGGAACCAAATAATA
TTTGNGNGGAANATTAACCAAANCCAANAATTGGTTGGGGGGGCCCAATTTTGGAACCNT
TTTGNGTTCNCCCCCCTTGGGAAGNCCCCCCAAAAAANAGGGCCTTTTTCAANANTTTTA
ANCCCCCCCAATTTTGGGCCTTCNTTCCNGGTTTCCCCCCCCAAGGGGGTTTNGNAATTC
CAAGGNCCTTTTGGTAAAANAATTTTTCNAAGGNCCTTAAAACCCCGGAAGGNCAANGCC
TTAACCNGGGGTTCTCCCCCTTNNATTTCCCCCCCCNAAACCGGAAGGGGATTGGTTGG
AAGGAAAAAAGGGTTTNCAATTGGGTCCTTNCAATTGGGTTTAATTCCNTGGGGGAACCC
CTTTGGGAA

Sequence 2375

Sequence 2376

Sequence 2378

CCGCGGTGCCGCCCGGGCAGGTACTTCATCTCTCTGACCTCATTCGCATGGCATTC
ATGGCTGCAACTGATCATAGCAACCAGCTGCGAATGGCTGGGCTCCAGGCGCTTGAAGAC
ATTATCAAGAAGTTTGCGTCTGTGCCTGAGCCAGAATTTCCAGGTCATGCGATACTGGAG
CAGTATCAGGCTAATGTGGGAGCTGCTCTAAGACCAGCCTTTTCACAAGATACACCATCA
GATATAAATAGCGAAAGCTTGCCAGGTATGTAGTACCT

Sequence 2378

Table 1

CCGCGGTGGCGCCCCGGGCAGGTACTTCATCTCTCTGACCTCATTCGCATGGCATTC
ATGGCTGCAACTGATCATAGCAACCAGCTGCGAATGGCTGGGCTCCAGGCGCTTGAAGAC
ATTATCAAGAAGTTTGCGTCTGTGCCTGAGCCAGAATTTCCAGGTCATGCGATACTGGAG
CAGTATCAGGCTAATGTGGGAGCTGCTCTAAGACCAGCCTTTTCACAAGATACACCATCA
GATATAATAGCGAAAGCTTGCCAGGTATGTAGTACCT

Sequence 2379

Sequence 2380

Sequence 2381

CCGCGGTGGCGCCGAGGTACAACATGGGGCTGTTCATCCTTCGTCTTGCTGAAGATGGT CCTGCCACCAAAGATGGCAGAATTCATGTTGGTGACCAGATTGTTGAAATCAATGGGGAA CCTACACAAGGAATCACACATCTCGAGCAATTGAGCTCATTCAGGCTGGTGGAAATAAAG TTCTTCTTTTTGAGGCCAGGAACTGGCTTGATACCTGACCATGGTGATTGGGATATTA ATAATCCTTCGTCTTCAAATGTGATTTATGATGAACAGTCACCATTACCCCCATCTTCAC ATTTTGCTTCCATATTTGAAGAGTCTCACGTGCCAGTAATTGAAGAATCTTTGAGAGTTC AGATATGTGAAAAGGCAGAAGAATTAAAGGACATTGTGCCTGAAAAGAAAAGCACTTTAA ATGAAAATCAGCCTGAGATAAAGCATCAGTCTCTTCTCCAGAAAAATGTGAGTAAAGAGG GATCCACCCAGCAGTCATGGGCACAGTAACAAGAAAAATCTATTAAAANTAGAAAAATGG TGTTACACNAAGAGGTAGATCGGNTAGTCCCAAAAAGCCAGCCAGTCACATTCAGAGGGA ACATTTGGATAAGATTNCTAGTCCTNTNAAAAATAACCCCAAA

Sequence 2382

Table 1

TATTCAAGCTTATTCGATTCCGGTCNACCTTCGANGGG

Sequence 2383

CCGGGCAGGTACGCGGGGGGGGGGGGATTCTTGATCCATGCACAGCGATGTGAGCTGAGG TGCAGGCACCAGACCTAGGAATTCCTAGAAAAATAGTCAGGAAGCATTTAGACACATCAA ATGTTAAACGAGTCCTGATTATGATGATAATGATGATGATTTTGGTGGTTGCAATAGCAA AGCCTTAAGTATGAAGGAGACGTGCCAGCTGGAAATACAGGTAGACAATGAACAACTGAA TTTAGAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTGAGCCGTTTCATTGAGAT CAACAGCCTCCACATGGTGACAGAGTACCT

Sequence 2384

Sequence 2386

Sequence 2387

AGGTACGCGGGTTTCCTCAACATGGCTGCGCCCTTGTCAGTGGAGGTGGAGTTCGGGTGA GTCACAGAGCTGGGGCCCGTGGGGATGGATTGAAGTCGTCGGGCCCAGAATTCCTTTCT TTGCCGTGGGGCCTGACA

Sequence 2388

Sequence 2389

Table 1

CCAGACCCATGACCCATAAACTATTTCAGGTAGGAAGTAAGCAATACTATAACTTGGACT CGAGGGGGAGCAAAAGGGCACCCCTCAATGGTGATGGCTGCCCACTTGGTCTCAACACTG TAAAACTTGGGACTTGCT

Sequence 2390

Sequence 2391

Sequence 2392

Sequence 2393

CCGCGGTGCCGCCCGGGCAGGTACGCGGGGAGAACAGGCGATATCTTCACCATGCG
CACAATGAAATCAATACTCAGAGAAGGCAGATAATTCTCCACGAGGCCAGAAAACTAATA
AATGAACAACTTGGGTGAAATGTCCCACCAGACGGTGTGATATTTAGTAGCCCAGAAAGC
TGCCAAGGGGTTGAATGACACTATCTGAAGATATGAACCAGTTTGCTCTCCATAGGGAGG
ATTTCATCAACAGGAAACAGATGCCTGGAAGGCATTGGATTTGCTAAGTGTCTATGCCAT
ATGATTCTGCTGTTTGCGTTTGATTTAGAATGCTGAGCTGACTCAAAGTCAAACTATTTC
ATATGTTGAAATCCTGACTCCCAGCCTGAGGGCATTACGAGGGGCTCTGGGAGGTGATTA
GGTCATGAGGGTGGAGCCCTCATGAATGGGATTAGTGCCCTTATAAAAAGAGGCATCAGA
GAGATCGTTTGCTCCTTCTGCCATGTGAAGACCACANCAATGGATGACTATCANGGTATTA
AAGAAAGAACA

Sequence 2394

CGCGGTGGCGGCCCGGGCAGGTACGCGGGGGGGATGAGTCAGGGAGAGCTAGTGTG GTAGCAGTTTCTAGAGCTGTTTTCAAGGAATGGAAAGAGGAGTGGGGAAAGGATTTAGGA TCTATGGGGTTGGCTAGGTTTCCCTTTCTGAGTTTATATAATGGTTTCGAGAATAAATGT TGAAGGAGCANGAGGGTGTCTTGTTGAGAAGATTTAAAGGAGGGGGCTACAAAGTAGAAGG

Table 1

CCGCGGTGGCGCCCGGCCGGGCAGGTACTGTGATATCCACATATTTTTGAGAAAAATTC
CCAAGCCAGGCGAATGTGGATTGGAATAAAGACATAGGCAGTGTATACCACCATAGCAAT
AATGGTTAATAAGATGGCGTTAAACATAGATCGCTCCCAGGGCTCTAAAACAGCACAGCA
GCTAATGATTTGGTATTGATAGTAGAGCCAGGAGAAATATTCCTTCACACGCCTCAAATC
CATGGTTGGCTCCTTCAAGCTGCAGTAAGTTTGTCCTAAGAAAGTCCAGGTCTGGTTCTT
CAGCCTTGCTCCTTCGCGAAATGATCCTGTGTGGGTTAAGTTCTCCTCTCTGGGTTGCTG
TTTCCTCATCTCCCAGTTGGGTGATCTCCCTGCGGCTTAGGTGAGCGCCGAGGCTTTGG
CTCCTCCCCAGCTGCTGCGAGCTTCCCACTGCCCCGCGTACCT
Sequence 2396

TGGCGCCCCGGGCAGGTACTTTTTTTTTTGNTTTTTTNANTCNTTTTTANAACAAACA CAAAAAAGTTTTATTTAAAAAAAAAAGAGTTTGACATTTAAAAGTTTGAAATAATATTAAAGT GACACCCTGTTTCCTTGGAAACACAATGCANAACCACAAACTCTGAGACTTATTATAGCG AAAGTATTGTCATTCAGTTCAATCTAATGGTATGAGGTTAGCTTTGAAGGCCAAAAGAAA CTAGTTTCTAATTCTTCTCCCCACTAGACTTGTGGCCTAGGTAATTTTGTAATC TTTCTGAGTCTGTTTTCTCATCAGGAGCAGGATAATTCCTAAGTAATAGATCATATGTAG AAGTGAATATGATCTCATGGCAGAGGACATNAACCATAGTTAATTATTAAGAATATTTT ACATTGAGCTATCCTTTTATNTACTTTAAAAA

Sequence 2397

Sequence 2398

ATTACTNCTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACGCTGGCAGGGCCAGTGGCAGGAGGAGGAGGGACAAGTGGACAGTGGTGTGTCTGAATTGTAGAGTTCCAGGGAGGACAAGTGGACAGTGGTGTCTGAATTGTAGAGTTCCAGGGTCATTCCATCTAAGCCAGGAGGTCAAGCTGTCATCTAAGCCCAGGGAGTTCAAGGAACAGGCCACATCTGGTTCTTGGAAGTATATGCCCAGGCATTTAAGCCGGATCTTTCCTCTTTTGGGCCATGGGTGGATTTCCTGCTCAAGCAACCTTCATCTCTTAAGCTTGTTGTTGCTTGGAAATTCTGGGACT

Sequence 2399

AGCGGCCGCCGGGCAGGTACGCGGGGGTTGGAGACCATTGCTCTATAGCAAGACCAGAC TTTGCCCTTCCTCCTCAGCCTACTCAACGTGAATATAATGAGGATGAAGACCTTTGTA ATGACCTTTTCCCACATAATGAATAGCCATTGGGAGACACACTTCTGAACACCACCACTG

Table 1

GAAAATCACACATGCTGAAATGGGAGAGTTCCCTGACCCCCTTGCAGGATATGTGACAGG AGTGTGGCTCATCTGTTCAGCTGGAGTGCATACTCAAACCCCTTATGAGACAAGGAGTAT GCAGACAGGAAGGTGCAGGGAACTGGGGAAGCAAAATATAAACTAGTTAA Sequence 2400

Sequence 2401

Sequence 2403

Sequence 2404

Sequence 2405

TAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTATTATTCTTTCCTTT

Table 1

Sequence 2406

AATTGGAGCTCCCGCGGTGGCGGCCGAGGTACCCTGGACTCATACCTGAAAGCAGTGTT CAACCTTAGCAAAATCTCCAACCAGCGCATGAACAATTTTCTACATCACAACGACCTGGT TTTCAAATTCAGCTCTCAAGGCCAAATCTTTTCTAAATTTAACCAAGAACTTCATCAGTT CACAGAGAAAGTAATCCAGGACCGGAAGGAGTCTCTTAAGGATAAGCTAAAACAAGATAC TACTCAGAAAAGGCGCTGGGATTTTCTGGACATACTTTTGAGTGCCAAAAGCGAAAACAC CAAAGATTTCTCTGAAGCAGATCTCCAGGCTTGAAGTGAAAACGTTCATGTTTGCAGGGA CATGACACCCACATTCCAGTGCTATCTCCTG

Sequence 2407

CGCGGTGGCAGGCCGCCGGGCAGGTACCCGTTAACTTCCAATTAACTAGTTTTGACAAC
ATTCAAAAAAGAGTNATAAACTNNGGCTTAATTTTAATAATCAANACCCTNCTAGCCTTA
CTACTAATAATTATTACATTTTTGACTANCCACAACTTCAACCGGCCTACATAGGAAAAA
ATTCCACCCACTTAACGAGGTGCCGGCTTTTCGTACCCCTTATTATCNCCCNNGCCCNCG
GNCGGTNCCNCTTTTNCTTCCCAATAAAAAANTNTTCNTTTCTTTAANGGTAAGACCTTA
ATTTAANCCCTTTTCCTTTTAATTATANTTTTTNGGAATCCCTTAAGGNAAAAAATNTTG
GCNCCNCTTCCCCTTTTTTTTAACCCCNCCCTTTAACNNCNATTTGNAAGGNCNCNCTTT
NNCNAAAAAACCAAAATCTTTANAACCCCNTNGNCCCCAACCTTAANAATTAAGNGTTTT
NATTNGTGTCAAATTCCCCCTTTCCTTTTAATTTTTAAAAA
Sequence 2408

ACTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGGCTCTCACT GCTCCCAAAAATGGCGGACGCATTCGGAGATGAGCTGTTCAGCGTGTTCGAGGGCGACTC GACCACTGCGGCGGGAACCAAAAAGACAAGGAAAAGGACAAGGGGAAATGGAAGGGGCCT CCAGGGTCTGCAGACAAGGCAGGGTAAGGAAGAAGTTCCAGTTGTTGCTTTTATTTTTT TCTCGGTGGGGAGGAAGAAAACACTACTCTCTTAGGAAGAGCACCGAGAAAGTGAAGTGT ACCTGCCCG

Sequence 2409

GTTTACCCGNCCGGGGGGGGAAAACCATATNGTTGGTTGGTCCTNTTAGGGAACCCC
TTGGTACCCGNCTTGGGGGGAAAGGGAAAGGAATTGGCCATGGGCCCCAACGCCTTAA
GGGTGGTTTAACCATTGTNGGTGATGGGGGAACCCCCCTTTAATTANCCGGGGGCAAAAA
CACNTANACTTTTTTGTCTCNANGGNGCAAACCTTAAATTTTCTAAATTTAAANAACCA
ATTNCTCCTTGCCATGGGNANAAAAANTGGGAAGCTACCTTAAATNATTTGGTTCCANGG
CAAAANTAACCCAACCAATTNTTTTCCACCCCAACCCCTTTTTGNCCCCCCAAAAACCAA
GGTTAATGNAAAAAAAAACCAATTTANATNGGAAAAAGGNAAAGGAAAAANAACATANC
CACTTTTATAANAAANAANATTTGGNAACCCAAAANGGTGGGAAAAAGGATTTAAANAT
TTGGGGGGAAAAAGGCCCAAAAATTGNGTTGGAAATTGGGGGTTTGTTTTTTAAAA

Table 1

AATTGGCCCCNCCCTTTTNGGTTATAAAGGAAAAAGGGAAAGGGGGCCCCCAAGAAAAGN AAGGCCCTTTTGGGCCGGCCAACCCCCTTTTNCTTTTTCCCCTTGGGCCCCATTTNGTTT GGNAAGGGGAAAGGCCCCCAAAAAGGNAAAAAGNCCNCCGGGGGCCTTTGNNTTCCTTT GGCCCAAANCCCCTTTGGNCCNTAANGGAAGGGGGGACCCCC

Sequence 2411

CCGCGGTGCCGCCCCGGGCAGGTACTTTACTCACCCTTCCTCTGACAGAAAAGGATG
AAGTCAAGGGCCTGGTAGAGGCACCACTAAGAAAGGCATCTGAAAGGACCAAAGAGAGTG
ACCAGCAAGCATTTTTTGCAAGGCTGAGGAGCTGACAGCTTCCATGAAAGGCTGGACCAC
CCAGTGGTGAAAAGCATCATCTGGGTTACCTTGTGCTGCCATAAAACACACCACAGACTT
GGTGACTTAAACCACAGATATTTATCTTCTCACAATCCTGGAGGCTGGGAAGTCTGCAAT
CACCGGGTGCCCAGCCATGGGTCAGGTTCTGGGTGAGGCCCTCTTTCCTTCTCACCTGT
GTGCTCTT

Sequence 2412

Sequence 2413

TTTTTTTTTTTTTTTTCTTCTTCTTCTTCCTTTCAGGCATCTCCTCGTTTTA
TTTTCTGTAACTCACAGAGTGCTGCAAAATAATGTTAGGGCTTTGCAGTTTATTCCTTGC
GATTTAACTGCATAAATATAAAAAGTGCCTGAGCAATAATGCACGTTGGGTTATTCAATA
ACACAAGGAATGTAAAGCCGATTTCATATCTCCTTGAATCAGGAACNTTAATTAATCATA
TGATGAGAATGCNACGTTTTNTTTACCANGGNCAAGGAGGCTGCCAAGAANCTTTCTGAG
GTTTAATAATTGCACCCNCTNTGGAGGGGAAAAAAT

Sequence 2414

Sequence 2415

CGACTCCTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACATAGTTCACAT
TTTTTGGAAGAATTCCACAAAAGAAGAAGAAAAGGAAATCTAATCTAAAAATACTATTTT
GGAGGGGATAGCAGATTGAAAATGAGAATTTGAAAGTTTCAATACCAGTGGGGAAAGCA
TTTGCTAGAGTTTAGAAGGACAGCATATGGTACACCAGATCACGAGACATCGTTTCATAC
TTCCCAAATAGTTTTATATTTTAGCTTTGAAGGTCAGTTACCAGAGCCAAACTTGTTCTT
AACAAGCAGAATTTTATGTCCATTCAAAGAGTCTCTTTACACCTTTCTGGGCCTATTCACT
TGCAGAGAGAGTCGAAACTGTAACCAG

Sequence 2416

Table 1

TGGTCAAATGACCTTTTAAATAAAAGATGGTTCTTACCTTCTAATTTTCCACTTATTTTA

Sequence 2417

CCGCGGTGGCGGCCGAGGTACGCGGGGACGCTGGGAGGAGATGCTGCCACCTAGGTTACT
TGTAGGACCCTATACGGCAACCTCCTTTGCCAGGAACTATTTATAAACATCCTGCAGGAA
AATGAGTCTATATGTCAGAATACACATTTCCCACCTTGCCCAACAGTAGAAAAACATAAG
AAGAGAAAAACATTAAAAAATGACAAGGAAGTTAATGGAAGTCAGCAATGTGATGGTGTT
TGGAGGTGGAGCCTTCAGAAGGTAATTAATGCCCTTGTAAGAAGAGGCCAGAGAGCTTGC
GCACCTTCTTCCTGCCATGTGAGGAGCCAAGAAGCCGGCTGTCTGCAACCTGCAAGGAGG
ACCCTCACTAGAAGCTAAGCCCA

Sequence 2419

CCGCGGTGGCGCCCCGGGCAGGTACGCGGGGGCAGTGGGAAGCTCGCAGCAGCTGGG GAGGAGCCAAAGCCTCGGCGCTCACCTAAGCCGCAGGAGATACACCCAACTGGAGATG AGGAAACAGCAACCCAGAGAGGAGAACTAACCCACACAGGATCATTTCGCGAAGGAGCAA GGCTGAAGAACCAGACCTGGACTTTCTTAGGACAAACTTACTGCAGCTTGAAGGAGCCAA CCATGGATTTGAGGCGTGTGAAGGAATATTTCTCCTGGCTCTACTATCAATACCAAATCA TTAGCTGCTGTGGCTTGTTTTAGAAGCCCTGGGAGCCGATCTATGTTTAACACCCATCTT

Sequence 2420

TGGGGTAAGNCTTTCTCANCTCCGTCCGNGNTTGGGTCAGGGTCTCCGTCTCNCCGGGGG TCCANGGGTTTACCCGTCCGGGGGGGGGGNNACCNCTTGGTACCCGCCTTGGGGGGTAGGG GTAAGTAATGGCCTTGGTCNCCACCCCTTTAAGGGGTNTAACCTTNTGGGTTANGGGGAA CCNCCCCTTAATTACCCGGGGCNAAGGCTCCTTCNCCTTTTTGGGGCNCCAAGGGGNAAA ACCTTAAATTNTTTATTNANAAACCAATTTCCCCTGGGCCAAGGGGGAAAAAAATTTGG CCAAGGGTGGGANAAGGTTANGGTAAAAGGGAAGGTAACCAANGGGGGGGTAATNAATTC CTCCCAAAGNAANAAGGGGGTTNTTANTTTGGCCCAAAATANTACCCAAATTTCTAATAN GNGAAGNAAAAAGGNAATTTGGAAAGGGAAGGGGGNAAGGTTCCTTNAATTTAATTGGGT TTCCAAGGGAAAAATTAANCCAACCCAAATTTTTTTCNNCCCCAAACCCCCCTNTTTGG GCCCCCCAAAAACCCAAGGGTTGAANGNTAAAAANAANAAAAACCCCAATTTTNTNN NNNACNACAANNACNATATAATATCATNANAAGAATAANATNATTATCACATNANNACAA TNANGAGAANAATAATNANAANGANNGGGGNTTTNTCCCCCTTTNGGGGGNCCCCCCGGN CTTTTTCCNTTTAAANAGAAAAACCCTTTAAGGGGNGGTGGGGGGGAATTNNCCCCCC CCCCCCCNGGGGGGGCCCTTTGGTCCCAAAGGGGGGGNAAAAATTTTTTCCCGNNNA ATTTNNTTTCNAAAAAAGGGNCCTTTTTTATTTTCCGGGGAATNTAANCCCCCNGGTTTT NNGNGAAACCCCCCTTTCTTTAAAGGGGGGGGGGGGGGG Sequence 2421

TGGGGNCCGGGNGTCCGNCTTGCTTTTGCNCCGGCNTGTGCCCTTGCGGGGCTTGCAACC NTGGNNACATTCNGGCTTGGNCGTCTTTCNGGGGTNTCTGTTNTACNGAGACCTTGGGCN GTGGTCCGTAAGTCCGNGNTTATTNCAANGACATNCAAACCTNCAANATAGGGGGGCCGG GGGCTAANAATTAACCGGGGGGTTTTAATTTCTCCAACCAAAGGGAAAATTCCAAAGGGG GGGGGNAATTTAAAAACCCGGCCAAAGGGGNAAAAAAAAGGAAAANCCAATTGGGTTNGNA AAGGCCAANAANAAAAGGNGGCCCCCAAGGCCNANNATAANAANGNGGGCNCCAATGNN GTAAANANCCCCCGGGTTTANNAAAAAAAANAAAGNGGNCCCCCGCCNGGGTTTNTGGNCN

Table 1

Sequence 2422

Sequence 2423

ATTATTTTGATTTTATATCTGAGTATGTTTNTAGCCAGAAGAAGAAGAAAGAAGATTAA AAAGCAAAAACAGAATTTATAGATGCACGATATTCTTCTGAACAAGAAAAACAGAAACTGGT AGGAAAATTTATTTTAAAAAAGTGTTGAAGGAAAAGAATCAAGACCACAGATCCAGATCCG GAGATTATTTTGCTAAAGAATAGCAATTGTGAGGCATGAGGTGGGAGGGGGGAAGAAGCT ATGAACTTAATTTTGAGGTTTCTGAATAAGGAAACTTGAGTGAATTCACTTCAGATGCAT TTGGAATGTTNGCACTCCAGAAGATNANATTGTGTGTGTCTCTGGAGAGTATTGGAAGA Sequence 2425

Sequence 2426

CCGCGGTGGCGGCCGAGGTACGCGGGGGGATGTGGGAGGATTGCATTCAGTCTAGTTCCTG GTTGCCGGCTGAAATAACCTGAATTCAAGCCAGGAAGAAGCAGCAATCTGTCTTCTGGAT TAAAACTGAAGATCAACCTACTTTCAACTTACTAAGAAAGGTATTAAGCGCCTTTCTGAG

Table 1

AGCTCTCAGTGGGCTTCCTAAGCACGTTCACTCTGCCTCCTTTAAGTCTTATATTTATGA
TCAAGATGAAAGGGAGGGATGTATCACTGCACAGAGATTCTACAAGTGGATATATAAAGC
TAATAATGTTTTCAGTGAGCTCTTCTCTGGCAACTACTTTCCAAGTGCTTTCAGCATTCC
ACCTTGAAGCACAACGTTAATAATGCACAATTTCTTATGTTCAGCCACAGAATGTTCACG
TGTGATTTGGTTACAACATATTGCTCTATCCAGGCCTCTAACAAAACTGACCTCTTTCAA
ATGGACTTGCAGTTGCTGAATTCCAAATCAACACTTTATCTTAAAAACAGAAAANGAAGG
GAANGGTGGANGGAGGGGAACAAGAAANGGTCCTGNCCG

Sequence 2427

Sequence 2428

CGCGGTGGCGGCCGAGGTACGCGGGGGAGTCTGATCTGTCCCGGCCCAGTGTCCTCCAGG ACCCTGGCCCCTCATGCCTNCGTGCTTGCGCGTGTGCCATTTCCTCTCCAGAGGACCT TTCCTGCCTAGGACTCATCATTGTCCCCTCCCTGGCATTTTTTACACCTGGAGCAGCCAG AGGACGCATGCATGGCTCTTCNGAAGCCTTCTCCTGCCACGGCATGCACCCACACATGCG AGCCTCCCGGGTACCTGCCCG

Sequence 2429

Sequence 2430

Sequence 2431

Table 1

TTTAAAAACATATACAAATCTACTTTCATTCACGAATCTGTGGTTCCTCCTCTGTAGCCC GTATATTCTTTTTGTTGATTACAATGACTACTTCCTATAGTCAATCCGTTAGAATTGAAA TCTGAAAAGTCTGAAAATTAACATTATTTCATTAGAATGCACAAAAAATATAAATTTGACT AACTTCTATGAATTATTTCTTCACAAAGCAGTCACATACTCTTCTACTCTGAAACAAGGT ATATCCTATATTTCCTGTNCATTCANAAAACTTTAATTACCTACCATCTCTCATTTCTTT GGAAATTTTT

Sequence 2432

Sequence 2433

CTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACATTTCTTCTAATTGATC
ATATCTGCTTATTTTCCTCTGGATTAAGGATCAAGGAGATAGTATATTAGATGATTTGAT
AAATTTCCAATGCTTTGCAAAGTAGTTGAACAACTTTTCTTTGTGATGCTAGGTGGCAC
TACTAGTCAAGACTTGGTATTTCATAGCTGGCTTTCTTATTCTGAAGGTTGTAAAAAGAC
ATATGAAGTAATATTTAACATTGAAAACATGATAATCAATTTGATTATCTATGAATTGTC
CTAAACGTTCAGAGTAAAGTTTCCTTTAAAGTTAAAATCTTTCAAGTGAAGGAAATTATA
AAGTCACATGTAAACACCAAAATAAGAGGAATAGAGCAATAGGATATTTTTTGGCTTTATA
ATTCAATTTAAAAATTAAGGTGCATTTATTTTTTTTGGCNGCTGGCCATAAAGCTTCAATG
TCCAGTAAGCAGTTGCTATCTATGATTCATGAAGATCATGGGGGGGTTCCC
Sequence 2434

Sequence 2436

Table 1

Sequence 2437

Sequence 2439

CCCGGGCAGGTACGCGGNGGAGGAGATGCTGCCACCTAGGTTACTTGTAGGACCCTATAC
GGCAACCTCCTTTGCCAGGAACTATTTATAAACATCCTGCAGGAAAATGAGTCTATATGT
CAGAATACACATTTCCACCTTGCCCAACAGTAGAAAAACATAAGAAGAAGAAAAACATTAA
AAAATGACAAGGAAGTTAATGGAAGTCAGCAATGTGATGGTGTTTTGGAGGTGGAGCCTTC
AGAAGGTAATTAATGCCCTTGTAAGAAGAGGCCAGAGAGCTTGCGCACCTTCTTCCTGCC
ATGTGAGGAGCCAAGAAGCCGGCTGTCTGCAACCTGCAAGAGGACCCTCACTAGAAGCTA
GCCATACTGGCATCCTCATCTTGGCTTTCCAACTTCCAGAACTGTGAGAAGTATATGTTT
GTGGGTTAAGTCAATGGTCTATGGTAATTTTTTTATAGCAGTCCCAGCCAAGACACTGTCAA
ATAAAGAGATAAGGATACCATTTATATTATTATATAGGCTCCTTTCACTAGTTTTTAGTATACAAATA
TTGGAGAAATAGGTTGGTATTAACTATCTCATNCAAGAAATGCCANATTCATGGTGGTTC
TAATTTTTATATTAATTGACAAAATGAAAAAAAATTTTT
GCCCAAGGAATGAAAAGAATNAAAAAAAAATTTTT

Sequence 2440

Table 1

NGGGGACAAAACCAAGACCCCTTGTNTTAAAAGAAAAAAAAGAAAAAAAGCC Sequence 2441

Sequence 2442

CCGCGGTGGCGGCCCGAGGTACTTGCAAGAAACCTCAGGACTTGAGTAACAGCAACATGG
TTCTTCTGAGCTATGAAGGGGCCCAGATTTAAGGGCTATTTTTTGACACCCTAAATGTGCT
GAGACAAGTCATTAAGGTGGTCCTGCCAGGACCAGCCATCTAAAGCAGCAATCTGCTTC
TTGCCAGAAAATCTCGTGCCTCTGCAGAGCCTTTTCCAGAATGAACCACCACCATGCTGAG
GAAAGGAGAAAAGAGACCACCTACTGCATTTCTGTCACTCGCTGAAAAGGACACTCTGTCA
GAAAATCTTCTAGCAAACTTCAAAGGGCAAAATCACCCCTTGTTACTGATAAAGCCCAGA
GAGCTTCAGCAGCTAACATTCCCTGGACAGGGCACAGCAAGGATTTGAACCTAGGTCAAG
TCTGGCCAGAACACCCACAAGCTTTCCTTAACTCAGTGTGCTATCTCCCCACGACTAGGT
CACTACTGCTTTATAATCACCTTTGTAGCCACCAGTGGATTT

GGTACATATTCTTACTTCTTGTGTAGGAGGCAAAAGGTATCTGCAGGGCTCTGGGCTTGC
TAACCAAACCGTTAATCGCTTAGAAACAGCANGANNTNNACTAGTGAGATGTTTATCACA
TACCTGGACACGAGTTGACTTTCTGTGAGACATCATTCTGGAATGAAAGCCAAAATCTCT
CTGCTATTCAGTTGAGGCTGAAAAAACAATCACATCAGAATTAGTAAGGCCCATNACAAN
GAGAGGAAATGAAAACAAGCCAGTATTCAATGGGGCTAGGGGGAAAATTACCTGGGCTT
CAGGAATTCAGGAGGTTGGGGTTTTGAGAAAGGTAAAAAAGTGGGCCAAGTGCGGTGGCT
CAAGCTTGTAATCCCAGCACTTTGGAACGCCAAGGCAGGTGGATCACGAGCTCAAGAGAT
TGAGACCAGCCTGGCCAACATGGTGAAACCCTGTCTCTACTAAAAACACAAAAATTAGCC
CGGG

Sequence 2445

TAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTAAACAAAACTAAAAATAAA

Table 1

AAGTCAAAAATTGGAGATGAAATGTATGTTTTGAAACACATTATTTTGGATCTTAAAAGA
TTTCCATGATATTTTTTGAAGGTGTAATATTAAAATGATGTCTCTTTTTTCTGTCTCATT
CCAAAGAACCATAAAAAAAGCAAATTAAAACAGTGATGAAACAAAACGCTTACAGGTTTGT
ATCTCAGTGCATCTCTGTAGGATCCAAACAAAGCAGCCTGTGCTCTAAGAAAGGCCCCTAG
CTACTCCATCACCCGTAGCTGTAGACTGCTTCTTCAAGTTTATTTTTCAAGGCCCCCGCG
TACCTGCCCG

Sequence 2447

Sequence 2448

GGAGCTCCCGCGGTGGCGGCCGCCCGGGCAGGTACGCGGGGGCGGCTTCTTAGCTTTAC
GATGGCAACAAGTATGGCGGCTGCTAGTGGTAGATTTGAAAGTGCGAAGAGTATCNAAGA
GCGGAAAGAACAGACCCGGAATGCCAGGGCCGAGGTGTTGCGCCAGGCTAAAGCCAATTT
TGAAAAAANAAGAAAGGCGTAAAGAACTTAANCGACTTCGGGGTGAGGATACATGGATGC
TACCTGATGTGAATGANAGAATTGAACAGTTCTCACAGGAACACNTCTGTGAANAAANAA
GAAAGAAAAAAATGACCNAGCTTTTCNAAAAAAAAGCNATGGAAANGGAAAAA
Sequence 2449

Sequence 2450

Sequence 2451

Table 1

TTCTTAAGTGAATTAATAAATACTTTTTAGTATCTGTTTTAATTCTAACAGTATGAGTGT
TGGTAGTTATATTCCAAATAAACAAAAACTCTTAGAGTCCTCAGTAATTTTTAAGACTGT
AAAGGGGTCCTGAAAATGATTAAATGTTTGAGAATAACTGCCTCAGAACATTGTTCTTCA
ACCCTAATCAAACCCAGCACGGCATTTATATAAAAAATGATTTTATAATGCCCATTTGCT
AATCCTGAAATAAAAATACATAGGTAATAAGAATGACTTANCCAATTTCAAAAAATACAA
TGGAGGGAATACTAGTGTTTGGAGACCTAACTATACAGGAGAAATAAAAGGAAAGTCATT
TTTTATAACATTATGCATGCATGTATAAAGCACTCAGATCTGATGACATTGGGAGACACG
GTGGCATAGCCAGATCCTTACACCTGTTTGTGGACTCACCATGAATACAGCAAGTGGCCA
AAGCAAACCCCCNCGCTATAACTGATAGGAATTTCATTGGCTTNGGTGATGGTCATTTCT
ANAATGGTAAGAAAATCTTGGTAAGGTTAAATGAACCAA

Sequence 2453

Sequence 2455

TANGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGGGACACCCTAGATCC
CAAGATCTCCAAGGATTTGGTGGCATACCCACTCCAGCACACAGAAGCATGAGGTTCATG
ACTCTCCTNTTCCTGACAGCTCTGGCAGGAGCCCTTGTCTGTGCCTATGATCCAAAAGCC
CGCTTTTGCCCAAGATCGGGGAACCCCTTTGCCATTGAAGCATCATCCAGCTTAAAAAGG
AAA

Sequence 2457

Table 1

Sequence 2458

Sequence 2459

Sequence 2460

TCGACTCCTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGGAGAG CTCTTTGTGGCTTGGGTGGTCAGCAAGAATTTTTTAAGCAGAGATACTCTTGATTGGGTT GGATAAATAAAAGAGCAAGGAGGACATTGTAGGAGGGGGAATTGCTCCCAGCAGAGCCTAG AAGCAGAGAGTTTTCCAGGGTTCCCAGGAGAAGAGATTGAATAAGTGCAGTGGGCCATG TGGTGACACATCTTGAGTGTCCAGCTGGAGAACTGGAAGTGCATATCATAACAGGGGTGG AAAACTCAAGAGGTTGATAGGGAATGGTTGAGGTTGCAATGAGGGGACCCGGTGGGGGAC

Sequence 2461

Sequence 2462

Sequence 2463

TCCACCGCGATGGCTGGCCGCCCGGGCAGGTACTCTTTCCTGGATTTACCATTTATACA
AAGAAAATTCTTACCCAGCTGGAAGAGGAGGAGCAAAAACTTTTTACTATCAGGGCACAGG
CAAAAAATNCATTTGTGCAAGAGAGACATATAAGCAAACATGCATTTACAGTGTAGAGGA
ANNGGGGACCNCAGTATTTTTTTCTCCTGGGAANNCTTACATTTTAATTAAATNNCNC
CTTGNAAAATTTTGTAGNANTANTTAANANGCCTTCCNTTGATTTTCANATGCAATTCAA
NACCTCNNGCCAATGNAATATNCAAAACAACNTTTCANGGTATGTTGGGGGAATNGTCNCN
ACGATTATGTANAAGTAAAAAAAGTGGCTCCANGTAAAAAA

Sequence 2464

Table 1

CCGCCCGGCAGGTACCTTTCTTTGGAATGGTTTGGTTCGACCGTCATACTTNTTCAAGGTGATATANACGCTGCCCGACGTTNCGGCACTTTCTGGAAAAGTNTGGTCAGCTCCGTCAGGAACATGCTCNNTTCTNCAACAACACCCATNCNCGGNNNGACCCNNNGNNTACTCNTGGGCCGCTTTNTAGAAAACATACGNTGTGNATTNCCACCGGGGCCTGNCAAGGAAAATTACGTATNATTNTAAAGGCNTNTATTCNGNATTACCCCGATACGTAACNCTNCTGAAGNGNGNGGGGGGCCACACGNGGTATCTCCCAANACATTANTTNTGGATTTCNNCCCTNTTTAAGTTCGGAAGGGGGNTTTTAAAANTTTNGNCNGNCNGACNTTTTGNGACCGTTNAAAATNTCAATTGGGGGTTCNCAATNACGNCCTTTGNTATNTACNNCATCGGTGGGNTGGAAAAAAANTATTGNTTTAATNACACNGGNTTTCCNAACNAAAATTATTNCCCCAACTAACCAAAACNTATTTAACCCNTAAAGGCCTCNGGGGNGGGAAGGACNAATTAAAAAAAAGTTTG

Sequence 2466

CTNCTATAGGGCGAATTGAGCTCCCCGCGGTGGCGCCGAGGTACGCGGGATTGACCCA
AAACCTGGATGTCCTATCTGTGTTTCCAGTAGTGCCCTATTTTAAATGTGTCATGATAT
CTATTACTTTGTGTGAAAATTACCTGTTTGTTTTTTCAGGTTATATAATAGTATAACACT
GCCAAGGAGCGGATTATCTCATCTTCATCCTGTAATTCCAGTGTTTGTCACGTGGTTGTT
GAATAAATGAATAAAGAATGAGAAAACCAGAAGCTCTGATACATAATCATAATGATAATT
ATTTCAATGCACAACTACGGGTGGTGCTGAACTAGAATCTATATTTTCTGAAACTGGCTC
CTCTAGGATCTACTAATGATTTAAATCTAAAAGATGAAGTTAGTAAAGCATCAGNAAAAA
AAAGGTAAAACAAAATTGCTCC

Sequence 2467

CGCGGTGGCGGGGGGTACGCGGGGGGCAAACGCCGGGAGTAGCCGAAGGGGACTGCCGGGAACAGGAATTTCTTCACATGGCTCCTGGAGAAGTGACCATCA

Sequence 2468

CCGGGCAGGTACCCGGGCGTGTGAGGTGTNAGTCTGCCCCTACTTGGGGGTGCCTCCCAG
TTAGGCTACTNGAGGGTCTGGGACCCACTTGAGGAGGCAGTTCTGTCCGTTCTCAGATCT
CCAGCTTGCGTGCTGGGTGCNTGGGGGAGAAACCACTACTNTCCCCGCCGTTACCTNAGGC
CCGCTTCTTAAGAAACCTANTTGGNATTCCNCCTCGGGTCTTGTCATGGTAATTTCCNAT
TATTCAAAAGGCTATATTCNGTATAACNCCGTGCTGACNCTTNGNAGGGGNGGGGGGGNC
ACTCCGGGNTACCCCCAAGNCTTTTTNTGGTTTCCCACTTTTAANTTGNAGNGGGGTTTA
AAATTAGTCGACCGCCCTTTGGNCNGTTANAANTCAATTGGNGTTCAATAAAGGCCTGGA
TTTTCCNTTGTTGGTNGGAAAAAANNTNGTTNTATTNTCCGNCATTCAACCANANTTTTT
NTCAACCACCAAAACCNATTANCCGTAAGGCCTCCNGGNGNNAAGTCCAATTAAAAAAAAT
NNTTGGNTAAAANAAGGCCNCNTGGGGGG

Sequence 2469

GGCCGCCCGGGCAGGTACGCGGGGANTTNTCTACTGGCGAAACCTGTATCCGGGCCCAAC
CTGAAAACATCCCAGCCAAGAACTGGTATAGGAGCTCCAAGGACAAGAAACACGTCTGGC
TAGGAGAAACTATCAATGCTGGCAGCCAGGTTANGAATATAAATGTANNAAGGGGAGTAG
ACTTTCNCAAGGGGAAAAATGGCTTACNCCAAANCTTGCCTTNCATAGNCGCNCTGCTGG
GCCAACTTATGCCCTCNTCAGAAAACAATCAACNCTTACTCACATGCAAANGAANCGGGN
CATTNGGCAATTAACAATGNGGATTGGATGGTAGTACTTGGGCAAAACNCATGAAAAAAA
AAGGGCCTNGNACAAATATNCTTAACCAAGGGGGNCCTTCNCTTAAATAGGAATTGNTAT
NGGAAAACCATTNGGNTTGGCNTTGGAAGGGGGGCCAAAACCCCAAGGCNAAGTGGGNNTT
CCACCTTTTTANCCAACCCTNGGTGNTCCNTNTTGGGTAANGNNAAATGGGGGCNNTNGG
NCTTCCCTNNAAAAAA

Sequence 2470

AGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTAAAAGCAAGGNGATCTGTGATATTTT CGTCCTTTTGTATGATTCTCTACTTCTTATTCAAGACCTGTGATTAAGTTGNGTGTATAT TGTCTGTAAAATGAAACAAAAGTAGGTCCTAAACATTGTAAGAATATGGTATACTAAAAA GCTTTGAAACCAAAAGAAAATTTAAAAAAAACAACAACAACAACAATGTAGAGTACCTCAT

Table 1

ACCTAACAGACACTATAGAAAAGCTGATATTTTTTTCCGTTGAAGTTAGGACATTANATC ATTTTTCACAAAAATAGATTCCTTAAATAANACATGTTGTCTAACAGGTATTTACA Sequence 2471

AGGTACTTTTTTTTTTTTTTTTTTTTTTACATGTATCAATTTACTTTACTTTGGTT
TTGCTCATTTTTACTGAAAATATGATTATCTATGTGGTGCATTATTTTCATCTCAAAT
AACTTCATTTTTACATAGTGTAGTCCAGCTGGAAACGTTTATTTCATGTTTATCTTTTAA
ATGATATTTTCACTGGATACAGAAACCTGTCTTCTGCCTCGCTCACGCTGGGAGCTGTAN
ACTGGAGCTGTTCCTATTCGGCCATCTTGGCTCCTCCCCACTAATGCTGTTCTTCTAGAC
ATGTTTGAAATAGGGGCATTGCTATAATGAATGGCTAGCAAGTAGGACAA
Sequence 2473

ATTGGAGCTCCCCGCGGTGGCGGCCGNCNGGGCAGGTACTCTACATACCTGTATCTNATT
TCATCCTAACAATAGCCACAAAGCTAGACATAATTATCCCATTTTCCAGGAGAAACTGA
AGTTCANAGCATTTAGTAACTTCCTCAAATTTATACACCTNAATAAGTGGTAGAGCCAGA
ATTTG

Sequence 2474

Sequence 2476

ACTACTTAGGGCAATTGGAGCTCCCCGCGGTGGCGGCCGGGGGTAGGATGGGAAGCCGTG GGGCAAGGGAGGTTGCAGGAAGCCCATCCTTCCCCTCCTGCGGCAGGTACCT Sequence 2477

TACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACCCTGCAGGT
AGGCATTTAAATTGGTGCAACCGCTTTGGATTGCTGCTTTGTAGTATCTTGGTGCAACTGA
AGATGAACATGCCCTGTGACACAGCAACCGCACTTCTAGGTCAATACCCTAATTATATTC
TTACTGTGGTTCACAAGAAGGTATGTAAGAGGTCATTGCCTGAGCACTGTTTAGAATAGG
GGCAAACTGGAAATCCTCTAAATGTCTGTCAATGAAGGAATAGATAAATTGTAATATGTT
CATATAAAATACTGCATAAATAAGTGAAATTTATAAATGTACCTCGGCCGCTCTAGAACT
AGN

Sequence 2478

ATACGACTNCTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGGGCAGGTACT GCTGGTTCGGGCTGCCATAAAAAGCACCACAGACGACATGGCTTACACCACAGAAACTCA

Table 1

Sequence 2479

Sequence 2480

Sequence 2481

CCGCGGTGCCGCCGAGGTACATCCTGGATGGATGAGAATGGGCACCATATTTTTATGA
ATATATTTTTCTTTTTTTGTTTTCTACAGCACCAAAGAAATCAAATAGGAAAAGGA
GAGTTGAGAATTGGGAATCAAGAATCAGCCCTGTTTCCATCTTAGCCACCACCAACTTATA
TCTTTATGATTTTCAAAGCTTTTGCCATGTGATTCTGCCCCCACAAAGGCATCGGTATTT
CCTAAATGGTACCTGCCCGGGGCGCCCCTCGAAATACCGAGCCCGGGAGCATTAAAA
GTGTAAAAGCCCTGGGGGGTGCCCTTAATGGAGGTNGAGCCTAACCTCACATTTAAATTT
GGCGTTGCGGCTCACNTGCCCGCTTTTCCAAGTTCGGGGAAACCT

AGGTACGCGGGACTGTTATTCTCTCCAAAGCTTACCCAGCAATAGGAACTCCCATACCAT
TTGATAAAATTTTGTATAACAGGCAACAGCATTATGACCCAAGGACTGGAATCTTTACTT
GTCAGATACCAGGAATATACTATTTTTCATACCACGTGCATGTGAAAGGGACTCATGTTT
GGGTAGGCCTGTATAAGAATGGCACCCCTGTAATGTACACCTATGATGAATACACCAAAG
GCTACCTGGGATCAGGCCTTCAGGGGAGTGCCCATCATTCGATCTCACAGGAAAAATGAC
CCAGGGTGTGGGCTCCAGCTTTCCCAATGCCCGAGTCAAAATGGGCCTATTACTTCCTCT
TGGAGNTATGGTCCCACTTCCTC

Sequence 2483

CCCGNGGTGGCGGCCGCCCGGGCAGGTACCGTTCCTCCAGTGCCCAGAGATGCTCTCCGC ACCAAGCCACAGATGTGGAGGAGGCAGGTAGGGGGTCAAAGAGGGGTGGTNTCGGTTATT CAGGACTTTTTTTTTTCTTAAATATCCTGNGCTTNTTTCAATCATTTGAAGGTAAAACC AGGTCCTGNGANTGGTAAACTGATTTTTGGTTCT

Sequence 2484

Table 1

GGCCCCGGGTACCCCAAGCTTTTGTTCCCTTNTAGTGGAGGGGTTAAATTGGCGCCGCT TGGGCCGTA

Sequence 2485

GAGAGGCGGTTTGCCGTATTGGGGCCGCTCTTCCCGCTTCCTCGGCTCACTTGACTCGCT GCGCCTCGGTTCGNTTCGGCTGCCGGGCGAAGGCGGTAATTCAGCTCACACAAAGGGCG GGT

Sequence 2486

TAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCGAGGTACGCGGGATAATTAACAATTTG
TGGAAATTGAAAAAGCATAAACTGTGTTATTTGATTAGTAATATGTTCCCTTAAAATTCA
TTTTGAGGTGTATGTTATACACACAGTAAATTTTTGTTCAGGAATGACTTGCTCATTCTG
TGTTTTTAAAAATAGGAAATGAGGCATAGTGAGTCATCATTACATCAATTAACCAAAAAA
TATTTCATCCCCTCCGTCACTGAAATTATCTACTTCAGCCACCTTTCTTATTCTCCGTGT
TAGGGAGGGCCACGTTTATGGGACTTNTTTAATTTTCCATGTGCCCATTATTTTGTCCCAC
TTACCCGGGCAGTTAGCCCAAAAGGCTAGGCCTGTTTCAGTTCCCACAGGA
Sequence 2487

Sequence 2488

CCGCGGTGGCGGCCGAGGTACGAAAGAGAGACAAAAGGGTTCTCTTGGAAACAAGAAGAG TGACTCCAGATGTGGCCTGAATAATTGCCATGTTAAGTTAATGCAAAAGATCAGAACAGG GCTACATTTGCACAGGCAGTTTCTCTCCGGGCCGTAGTTTTCACTGATGATCACCTTTCA CAGCATTTTCCCCAACCAGCATTTCACTTAGTCTTCTCTATACCCAGCACCTCCCCCGGC ACCCCCGGCAAGCCCACTTATCACTTCCCGACTTTCCAACGTGGCATTCCCGTGGAGGAT CCTGTTCCACATTAGGGCGAAAGCAGGGAGAAACACCTGGNGNAGCCAGCCAGGGATGGG GTTTTGGGAAAGGAGCCATGCCCTCTGGG

Sequence 2489

CCGGGCAGGTACGCGGGAGCAGAAATGATTGCACTATTGATAAATTCCGAAGGAAAAATT GTCCATCTTGTCGTCTTCGGAAATGTTATGAAGCAGGGATGACTCTGGGAGCCCGGAAGC TGAAGAAACTTGGTAATCTGAAACTACAGGAGGAGGAGGAGGGCTTCCAGCACCACCAGCC CCACTGAGGAGACAACCCAGAAGCTGACAGTGTCACACATTGAAGGCTATGAATGTCAGC CCATCTTTCTGAAATGTCCTGGGAAAGCCCATTTGAAGCCAAGGTGTAAGATGTGNTGCC TGGACACCGACAANCAACCCAGGCCCCGACTTCCTTTGGCAGGCCTTTGGCTTCTCTAGC CCTCACTGGAACTGGGGGAGNAGAAGA

Sequence 2490

GCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTTTAATAGCTCAAACTCAGAGTCA TCGTGCTCCCAATTCCAAAGAGATTCCTAAAAGAGGCAACTT

Sequence 2492

Table 1

ACTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCGAGGTACAAGTGGATACCCCA GAATGACCTTCTAGGTCATCCAAAAACCAGAGCTTTTATAACTCATGGTGGAGCCAATGG CATCTATGAGGCAATCTACCATGGGATCCCTATGGTGGGCCATTCCATTGTTTTTTGATCA ACCTGATAACATTGCTCACATGAAGGCCAAGGGAGCAGCTGTTAGATTGGACTTCAACAC AATGTCGAGTACCTGCCCGGGCGGCGCGCTCTAGAACTAGTGGGGATCCCCCGGGCCTGC AGGAAATTCCGATATCAAGGCTTATCGATACCCGTCCGACCCTNCGAGGGGGGGGCCCCG GGTACCCCAGCTTTTTGTTTCCCTTTTAAGTGGAGGGGGTTTAAATTGCCGCCGCCTTGGC CGTTAAANCATGGGTCATT

Sequence 2493

Sequence 2494

Sequence 2495

TACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGTTTGAGAAGCCAGCGCTCACCC
ACCCGGGGTCTCTGTGCATTGACCTTTGGGTGCTGACTTGGAGAAAAGCACAAACACGAC
CAGTCCCATCCTGGCTCCCGTGGGGCTTCTTCTATCTACGCATTGTATCGACTGCATTAG
TTGGACTAAGATGATGACTCAGTTAAAGGAGAGACAAATGCTGACTGTCTAAGCAAGAA
TGGCCCAAGCTGGCAAGAAAAAGCACACTTGCATACATCCCGCGTACCTCGGCCCGCTCT
AGAACTAGTGGGATCCCCCGGGCCTGCAGGNAATTTCGATATCAAGNCTTATTCGGATTA
CCCGTCCGACCTCGNAGGGGGGGGCCCCGGTACCCCAAGCTTTTTGTTCCC
Sequence 2498

CCGGGCAGGTACTGAGTCAAGGACGTCTTTAACGTCATGGACGGCTCCTTTACCCACGCT TTCTAGATCTTCGACTGCATCTTTTCCTAGTTTTCCGAGTCCCCCACAGCTTTTTTTGC TCCGTCTAGGCCTTTTTCCAGAAGGCTGGATCTCTGCTTCCTTGGCTTTGGTGCCTGTCT

Table 1

GGCTAACCCTGGGTCTTCACCTGCATTTTCCTTTTGAGCTGCTGATGCTTCATGGCAAGG GTTCCCCCGATCCTGGGCAAGCCCCGCGTAACCCTCGGCNCGCTCTAGNAACCTAGGTG GGATTCCCCCGGGCCTGCAAGGGAATTTCGGATATCAAAGCTTATCGGATACCCGTCCGA CCTTCGGAGGGGGGGGCCCCCGGT.

Sequence 2499

Sequence 2500

Sequence 2501

ACTGTNNCCCGACCCTGCCCGCTTACCGGGATACCTGGTCNCGCCCTTTCTCCCTTCGGGGAAGGCGTGGGCGCCTTTCTTCATTAANCTCACCGCTGTAGGGTATTCTCAGTTCGSequence 2502

Sequence 2503

Sequence 2504

Table 1

Sequence 2505

Sequence 2506

0

(

Sequence 2507

Sequence 2508

Sequence 2509

Sequence 2511

Table 1

AAGACATAAGAAAGAGAAGGTGTGGTTTGCAGCAATCCGTAGTTGGTTTCTCACCATACC CTGCAGTTCTGTGAGCCAAAGGTCTTGCAGAAAGTTAAAATCACAAAGACTGCTTG TCATTATATTAATTGCTAGGAAAG

Sequence 2512

Sequence 2513

Sequence 2514

Sequence 2515

Sequence 2516

TCTGGGTTGGGGATTATTTCTGGGTTTCTACTTCCTGTTNGAAGAATGTTGGCATGGAAN AGTGGTAAGTTTGAAGAAGATGAGTGCCGGGGGCCTTCATCTAATCCCTNGGAAAATTGG TCTTTTTCCCCACCAATTCCCCTTGGACACCAAGAAATTANTGGAAGCCCANTACAAGGG AANTTCTTGNAAAGNAAAATNGGGGGTNCTTCTTTGGCCCACCCTTCCCCAAGTTAAAAA

Table 1

Sequence 2517

Sequence 2518

Sequence 2519

Sequence 2520

ATTGGAGCTCCCGCGGTGGCCGGCCGCCCGGGCAGGTACAGAAGGGCCATGCTGTTATT
ACTCTTACACAAGGAGGCAGCCCTCGAGCCACAGGGTCCAGCTGTTGGCTATAATAGCCT
ACCGGTCTCTGATGATCACCATGTTTCTGGAATTCAAGCCAGGAAGAAGCAGCAATCTGT
CTTCTGGATTAAAACTGAAGATCAACCTACTTTCAACTTACTAAGAAAGGGGATCATGGA
CATTGAAGCATATCTTGAAAGAATTGGCTATAAGAAGTCTAGGAACAAATTGGACTTGGA
AACATTAACTGACATTCTTCAACACCAGATCCGAGCTGTTCCCTTTGAGAACCTTAACAT
CCATTGTGGGGATGCCATGGACTTAGGGCTATATGAGCCATTTTTGATCAAGTTGTGAGAAC
AAA

Sequence 2521

Sequence 2522

CTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCTGTGAATTGGACATCTG

Table 1

TTGTTTGCAGATGTAATTAAGATGGGTCATACTTAAGTAGTGGGGCCTCTAATCCAATG
TGACTGGAGTCCTACTAAGGGAGCAGGGTCAGAGGCAGACATGGGAGAATGCCATGTGAT
GACGGAGGCTGAGATTGAAGTGTTGCAACTGCAATCCAAGGAATGCCAACATTTGGTGGC
CACCATGACAAGGTAGAAGGAGGCAAGGAAGGCTCCAACCAGTGTCTCAGAGGAAGCATG
GCCCTGGTGACATGCTGAGTTTACGCTTCCAGCCTCCAGAGCTATAAGAAGGTNAAATTG
TCTGTTTTCTNTNGGTTCCCTGTTACAGCAGCCTTAAAAAAAAT
Sequence 2523

AGGTACCGCATTCCTACTTCATTGCCCCTGATGTAACTGGACTCCCAACAATACCCGAGA GTAGAAATCTTACAGAATATTTTGTTGCCGTGGATGTGAACAACATGCTGCAGCTGTATG CCAGTATGCTGCATGAAAGGCGCATCGTGATTATCTCGAGCAAATTAAGCACTTTAACTG CCTGTATCCATGGATCAGCTGCTCTTCTATACCCAATGTATTGGCAACACATATACATCC CAGTGCTTCCTCCACACCTGCTGGACTACTGCTGTGCCCCAATGCCATACCTGATTGGAA TACACTCCAGCCTCATAGAGAGAGAGTGAAAAACAAATCATTGGAAGATGT Sequence 2524

Sequence 2526

Table 1

CTTTCAATCCAAAGACTTACTGGAATTGNGTCAAGCTTCTTGTGGTCAGAAATGAGGNCT TCTCTTTATTTTTGGC

Sequence 2527

GCGTTANACGACTCACTNTNAGGGCGAATTGGAANCTCCACCGCGGTGGCGGCCGCCCGG GCAGGTACGCGGGCACTGTAATGCTNACTTANCATTAACCTTTTAAGTTAAAGATTAAGA GAACCAACACCTNTTTACAGTAGAAATGCCCCAACTAAATACTACACGTATGGCCCACCA TTAATTACCCCCATACTNCTTACACTANTCCTGATCACCCAA

Sequence 2528

CGAGGTACGCGGGGGGGTGCTGTGGTCCAAAGGACAGGCTGGATGGCGGGTGCATCGGCG TGGGCGTGGTCAGCATGTCTCGCAATGCCTGTGGGCTCTACTACAAGCTTCACAATATT AACAGACCCCTGACTATGAAGAAGGAAGGCATCCATACCATAAACCGAAAAATGTCTAGC AAATCCAAAAAGTGCAAAAAAAGTGCATGACTCACTGGAGGACTTCCCCAAGAACAGCTC GTTTAACC

Sequence 2530

AGGTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAGAGACCTTTATTAAATTACAGTGTATT
ACAGATTATACATAATAATAAGCCTTTCATCTTTAGGCTAATATGATACAAAAACCTAC
TTGGCCACATTACTTCTTGAGTTTCTTTTTGGGCAGCTTTCTTNTTTGACCATNTGTAAT
CCGCTTCATAGCATTGANCCCGTGATTCTTTTGTGAAAGTTTGGGGCCCTTTAAGGGATGC
TGAGGGAGAGCTGCTGGATTCTGAAANNAATTTTGCTNGGTAAGAACCTGCCCGGGCCGG
CCGCTCTTAGAACTTAGTTGGGATCCCCCNGGNGCTGCAGGGAATTCNATATCNAAGCTT
ATCGAAACCCGCCGACCNTCNAAGGGGGGG

Sequence 2532

AGGTACAGCTGCTATCTTATTGGACTACAGTAAATATTTTTTAAAAGGACACCAATGAGG

Table 1

Sequence 2534

Sequence 2535

Table 1

Sequence 2539

Sequence 2540

Sequence 2541

CTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCCTGCTGAAAGATTATTT
CTAACAGGCTTGTAGAGAAACGTCGGTTCATGTNAATTANAAATTATGGGGCCACTTTGC
CATTCTCACACCTGCAATGAACAGGTGTTTATCTGNNGNNCTGACTTATCTCTTGAACT
CCATTTGCATGGTATNGTGGGATGCAAGCTGATGCCCTGTCCAGATCT

Sequence 2542

TCGACTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGTCACACTCATTTACCCG GGGACAGGGAGAGGCTCTTCTGCGTGTAGTGGTTGTGCAGAGCCTCATGCATCACGGAGC ATGAGAAGCCCGCGTACCT

Sequence 2543

Sequence 2544

TTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACNATATACAAAGACTNTGAGCTGNNTGCCTCCGATGGTTTCCAGTATTGGCCCGTTGTAAAGCTCATTAAGGCCAACTTTNACTTNANTATGTGATTCTGCAGAATTAANTTAAGGAGGCGCTGATCCATGCTGAGAGTATCATNAGAAAANGGCATTAATCCACAAGGTGCCAANCAAAAGTTGTAATTTNNTTNCATCNTGGCTCTCANGAAGCAANATGCCAANGCNTTAATNTGGGGNACACCAAAGAATCCGTTGAAAGGGNAGGTTTGCTTG

Sequence 2545

Sequence 2546

Table 1

Sequence 2547

Sequence 2549

Sequence 2550

Sequence 2551

ACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCCCCGGGTAAATGAGT

Sequence 2552

CCGCGGTGGCGCCCCGGGCAGGTACGATGTCTAGTGATGAGTTTGCTAATACAATGC CAGTCAGGCCACCTACGGTGAAAAGAAAGATGAATCCTAGGGCTCANAGCACTGCAGCAG ATCATTTCACCCGCGTACAGTTTAGGGGATCCTTTCTAATGACAGGAAGGCACTGCTTTC CTCAACACTGTGATCTGACCTGTGACAAGTCTGTACCT

Sequence 2553

Table 1

AACATGAATCTGCATTTCTTGGATGAGATAGTTAATAACAAACTATTTCTCAATATTTGT
NTACTAAAAAACTAGTGAAGGTGTTATGTGTTTCAGTATCTTATTTGAACATG
GGTTTCTGAAAGGAGCCTATNTAATAATATAAATGGTATGTAGTAAATGAGGCACTGTCT
TGGCTGGGACTGCTATAAAAAAAATTACCATAGACCATTGACTAAACCACAAACATATGCT
TNTCACAGTTCTGGGAAGTTGGAAAGCCAAGATNAGGATGCCAGTATGGCTAGCTTCTAG
TGAGGGTCCTC

Sequence 2554

NTTTTTTTTTTTTNTNNNNNNNNGNGNNCATATTAATATANGGCGAATGNAGCTCCACC
GCGGTGGCAGNGGCCGCCCGGGCAGGTNCAGAGGACACACATTGTANACAGGCCTGTGTC
ATGTTTCCTTACAGTCGTTTTTTACAGAGAAAAGGGGCATTGTTTTTTCACTGCTTTCTC
AACANTTCCTTGTGAATAAATGAAACATTTCGGAACTCCCTNGNTGNGCAAANAGCCCTT
CNACTTTTGNTTNNTTTGCCGGGNTAGCCCNGGGGAACCCATTGTTGGTTTGGGTGGAAA
TTCGNTGNTTTNNCCTTGGTCGNGGGGGGGCCCCAACNTTTNNACNTTTCAAAAAAATNN
GNACNAANCACCNTGGGGAANGGGGGCACTTAGNTNTTTCGCTTATCCCCCTTTTAANNC
CAACCTTTCNNCTCTTTTCNACACCNCAAGTCTCCCTCGGNACCTTNTCCNTTATNGNNN
CCCNTTCCACCTNNNGCGCCCCNAAAACTCCAAGGNNANCCAACCGCCTTGCAAAAA
Sequence 2556

Sequence 2557

ATACTTAGGGCGAATTGGAGCTCNCCGCGGTGGCGGCCGAGGTACGCGGGGTAGATGGAA GGAAGAACTTGTGTGCTTAGACCTGACGCTGGGAGGAGATGCTGCCACCTAGGTTACTTG TAGGACCCTATACGGCAACCTCCCTTGCCAGGAACTATTTATAAACATCCTGCAGGAAAA TGCAGTGAAGTAAAAAGAAGACAGGGACATCCCAGAAGGTTATGCAAAACATCAAGAGAA GATGAGAGGAGTCTATATGTCAGAATACACATTTCCCACCTTGCCCAACAGTNGAAAAAA

Sequence 2558

Sequence 2559

TAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACTGGCCCTGGGCCAATGCGTC
CTCGCTGGAGCCTTTGCCTCCTTCTACTGGGCCTTCCACAAGCCCCAGGACATCCCTACC
TTCCCCTTAATCTCTGCCTTCATCCGCACACTCCGTTACCACACTGGGTCATTGGCATTT

Table 1

GGAGCCCTTATCCTGACCCTTGTGCAGATAGCCCGGGTCATCTTGGAGTATATTGACCAC
AAGCTCAGAGGAGTGCAGAACCCTGTAGCCCGCTGCATCATGTGCTGTTTCAAGTGCTGC
CTCTGGTGTCTGGAAAAATTTATCAAGTTCCTAAACCGCAATGCATACATCATGATCGCC
ATCTA

Sequence 2560

Sequence 2561

CTCCTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGCCGAGGTACGATATATAACAATGAGGTGCTCCATCAACCACTTTCTGAAGCTCAAAGGAAATCCAAAAGCCTAAAAATTAATCTCAATTATGCAGGAGATGCTCTAAGAGAAAATACATTGGTTTCAGAACATGCACAAAAGAGACCAACGTGAACACCAGTGGCCAAATNGAAGGGAAGCTGGAACACACTGGTNTCAAAACCGAACAAGATAATGTGAACAAACACACTGAACAGCAGGAGTCTCTAGATCAGAAATTATTTCAACTACAAAGCAAAAATATGTGGCTTCAACAGCAATTAGTTCATGCACATAAGAAAGCTGGCCACNAAAAGNCAGGATTACCATTGGTATTTCATTTTTCTTGGGAGAGGGAAAATGCCAACATCATCTTCCTAAAAAGGAGAGAAAATGAGGAGGAGAAAATGCCATTTAAAA

Sequence 2563

ATTGGAGCTCCCGCGGTGGCGGCCGAGGTACGCGGGCTTTCCCCCAGTGCAAAAGACTG
TTACTTATTATTGTATTCAAAATTCATTGTGTATATTACTACAAAGACAACCCCAAACC
AATTTTTTCCTGCGAAGTTTAATGATCCACAAGTGTATATATGAAATTCTCCTCCTTNC
TTGNCCCCCCTTTCTTTCTTCCCTCTTTCCCCTCCAGACATTCTAGTTTGTGGAGGGTTA
TTTAAAAAAAAACAAAAAAGGAAGATGGTCAAGTTTGTAAAATATTTGTTTTGTGCTTTTTC
CCCCTCCTTACCTGACCCCCTACGAGTTTACAGGTCTGTGGCAATACTCTTAACCATAAG
AATTGAAATGGTGAAGAAACAAGTATACACTAGAGGCTCTTAAAAGTATTGAAAGACAAT
ACTGCTGTTATATAGCAAGACATAAACA

Sequence 2564

Table 1

CCAAACCCNAAAA

Sequence 2565

ACTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACATATTCATTGTANG ACTTCCTGTGGATGAGCATGAGCTATCATGACCTCTTCTTCTCCAAGACTGCAGGCTGC TGAGAATCAAAGTGGGAGGGCTCTTGTGAGTCTGCTCGTAAATAGCCTTCAGTTCGATCA TCTGTATCTACTTTCTCCTCNTTTTGTTGGAAGNTTGAGGATTCATACTTTTGGACAACTG CTTCTTAATCTCCACATCATCATCATTTTCAGGTTTCTTCTGATTCTTTTTCTTCTTATC TTTAAATTGTTTGATCAATGTGAAGGACATGTTTCAACAAGGAAACCATNAAATACAGGC CTCCTAGAGCTGGTTAGACCCTTCCACGTGGGAANTCAAAATAGGCACTTTTCTTCTATG TTTTNGAGAAGACAGAATGACTGNAAAAAAGGTGGGTCCTCTTTTTTCAT Sequence 2567

Sequence 2568

Sequence 2569

GCGGCCGCCGGGCAGGTACGCGGGACAGCGGCTTCCTTGATCCTTGCCACCGCGACTG
AACACCGACAGCAGCAGCCTCACCATGAAGTTGCTGATGGTCCTCATGCTGGCGGCCCTC
TCCCAGCACTGCTACGCAGGCTCTGGCTGCCCCTTANTGGAAGAAATGGTGATTTCCCAA
NGACGANTTCATATTCCCACAATNTTGGNTCTTAANGACCTTGGAAATTAACCAAAAAGG
AAAC

Sequence 2570

CTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGNCAGGTACACAACAAGCN NNGTCTNNCATAACTGAAACAGANGATTCTGNTTTAGAANAANGCCCATCTGAGCTTANG AGCNTAGAAGGAAAAGAAGAAAATATNAGGAGCTTTGTGCATCTTCTACAATGCCTGCAA TTTCANAGCTTTCATCATNGCTTTANGGGAGGANTCTCATANTGAATNACNTTAAACCTT TCTCGTCCCAAGATCATCAGNCTANAGTCGGAAAAGAACCACCTGCCTCTGTAGCTGGAA

` . . .

Sequence 2571

CATCTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCGAGCATGAACATCT GCAGCCTCTTGCAGAATCACCCCAGAAGGGGACTGAATCATGGTCCTCTTGATAGGTATG

Table 1

TTCAGCAGAGTTTCCAGTCCTGAGGTGTATGAGGCCAGCTGGAGCTCATAATCCTTAATT CCCGCGTACCTGCCCG

Sequence 2572

TCTTAGGGCGAATTGGAGCTCCCGCGGTGGCGGCCGTGGCCACCGTGCAAAGCTTCCA CTTGGTGCCTGCGTGGGAACGCACCACCTGCCGTGGAACTTCCTCCTGCGGGGCAGAGGA GGGGTCCCCGCGTACCT

Sequence 2573

Sequence 2575

CTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGGAGGATTTCGGC CTGAGAGCGGCCGAGGAGATTGGCGACGGTGTCGCCCGTGTTTTCGTTGGCGGGTGCCT GGGCTGGTGGGAACAGCCGCCCGAAGGAAGCACCATGATTT Sequence 2576

Sequence 2578

Sequence 2579

Table 1

Sequence 2580

Sequence 2581

AAAGNCCCCGGGGGAAAGNCCANTTAAAAAAAGGGTTGGTTTAAAAAAAGGCCCCTTGGG

GGGGGGTTGG Sequence 2582

Sequence 2583

GCCGAATTGGAAGCTCCACCGCGGTGGCGGCCGANGGACTCTGGCGTTGGTAACAATGG
TTTCCNGGANCTTNGGNTNGTAACNACTGCTTCCNGGGAACTTCTGCGTTGTAACCACTG
GCTTCCCGGGACTCTGCGTTGTTACCACTGCTTTCCCGGGACTCTGCGTTGTTACCACTGC
TCCCGGGACTCTGCGTTGTTAACCACTGCTTTCCCGGGGACTCTGCGTTGTTACCACTGC
TCCCGGGACTCTTGCGTTGTTACCACTGCTTTCCCGCGGACTCTGCGTTGTTACCACTGC
TTCCCGGGACTCTGCGTTTGTTACCACTGCTTTCCCGCGTACTCTGCGTTGGTTACCACT
GCTTTCCCGCGGTAACCTCTGGCGNTTGTTAACCATTTGCTTCCCGCGTTACCTGCCCG
GGCGGCCGGCTCTAAGAAACTAGTGGGAATCCCCCGGGGCTTGCAGGGAATTTCGATAT
Sequence 2584

Table 1

 ${\tt CTTCAGCTTGCAGTGTGAAAGGGGCAGGGAAGACTGGCCAGCT}{\tt GTCAAAAACTGGAACAGTC}$

Sequence 2585

Sequence 2587

GGCGAATCGGACTCCACCTTNGGTGGCGGCCGAGGTACATTTCCTTGTAGACTCTGTTAA
TCTCCTGCAGCTCCTGNTTTGGTTTCTGGAGCANATGAATCTCAATGAGGAGAGTCCTCG
TCGGTTCCCAGCCCCTTTATGGAAGCTTTANNCTCAGAANCGTCATACTGAAACAGGCNT
TTTTCAANAAGGNCCCNAAAAAANCACCCGGTTTTTCCAAGGGTAGGGCCNANAAAAAAA
GGGCCCNAACTTTNCAANATGCCTTGAAATGCCNAANNGTNTTCCCNTTTTTNAGGGGTC
CCCCTTCTNCCTNGGGGNTAANNGGCCNAAAAAGGCCAAATTAANTCCCCTGGNACTTCT
TGGNNGGCCAATTNNGGCCCCCCCNGGCNGGTAANCCCNGGCCCCCGNGGGCCNAAGGNC
CAGCNTNCNTAANAAAACCNAAAGTNGGGNAATCCCCCCCCGGGGGCCCNTGGCAAGNGN
AAAATTTATCCNAATTATTCAAAAGGNCNTTTAAANCCNGAATACCCCCGNCCCNAAACC
CCTTNNGAAGGGGGGG

Sequence 2588

ACTNCTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACACTCCT CATCATCACTGTTGCTTGAGCACCGAAGAAGAGAGGGCCCAGCCTTTTGGGTGCAGCTGTA AGGACGTGATGCAGTTCCGTGGTCACTCTCACCAAGAACTTCAGGGGTTACGACTTCAA GACTATTTCGTGGTGAAACTCCTGAACTTTGAAGTAGTTCTTCTTGCTCTTAAAATGGGA TAGCTGCCTACTTCTAAAGACTTAGTTAAGTCAAGGTCATGCAAAATTAAGAGATATCCA GAGGACGTTGAAATCAACATTTTGGAACAATCTGGTGTTAACCTCATTCGCATGAGAAAA CGTGTGTGAAAGAATTTCTTATGTGGACACCCCATCTTCTGTATACCTGTTAGTGTCCCAA ATAATGACATTTCCATCAAATCCTGATGTTACTAAGAGTCTTGTATTAAGTATCA Sequence 2589

Sequence 2590

CNGGCGAATTTTCTCCTNGCNGCGGCGGCCGAGGTACGAACTTTTCTCCANAGGATANT

Table 1

TAGGTTGCACCNTTGTATTTGTAAAACAGGAGCAAATTTGGACCTTGCCGGGCCAAAGTC
GTGTCACGTGGAACCTCTTAATCTCAGCATCCGGAGCTCCAGGAAGGGAAAATTTCAAGT
CAGATAGAATTCTATATATACCATTTCTTTGGAACCTTCAGCCCTCAAGATTCCAACATC
ATGACCTCAGTTTCAACACAGTTGTCCTTAGTCCTCATGTCACTGCTTTTTGGTGCTGCCT
GTTGTGGAAGCAGTAGAAGCCGGTGATGCAATCGCCCTTTTGTTAGGTGTGGTTCTCAGC
ATTACAGGCATTTGTGCCTGCTTGGGGGGTATATGCACGAAAA

Sequence 2592

Sequence 2591

Sequence 2593

Sequence 2595

Table 1

CACCATACAGGGAGACAGCTGTGTGAATACAGGCTGTATGGACACTTGCTTCCATCCCAT
TTTCCTGCTTCTTTGGGTTGGCAATCAAGAGTATCCTCAAAACGACTTGACTTTAATTTT
CT

Sequence 2597

CGCGCAGTCCGCCTGACTATACTACCTTTAGTAAATAAACCNCCCTTTCNGGATGCCACT ATCTCCGATGGCACTATACCCTCTCTACCTTCTATACCACTAAATTAAACCAACTCCCCT CCTCCCCCAAGCNATAAAAATAAAAATATACAAACCCTGGGCCAAAATGANNAAAATCTG TCNTTATTATTGCCCCACAATCCTAGCCTCNCGCCGAGACCTCGGCGNTCNAAACTAAGT GATNCCCGGCTGAGNATCGTATAAGCTNATCGATCCGCGCCTCGANGGGGNCCGNACCC Sequence 2598

Sequence 2600

CAGGTACAGTGGATTTTTCATTTGCAAAGACGTTAAGCCCTCCAAATGTGCAAATCATGA
AGTCAGTNGTTGTTCCAGCAAGGTTTGCCCAGCGGTAAAAAACAAGATAAAACTAATGCA
CTAGCTGAAACCAGGTGGGGAGACCATGTGTGGTAGTGCTTGGGGGTGGAGGGAAACTAT
TTCTGAAATGAGGACTTAAAGTATAATACCAGCTTCACTGCCTGTTCACATGAGAAACCA
AAGCTTCAATTTAACTGCANGCAATAGGAGTTTCACACTGTCAGCACCAACTGTCTAANA
TNCAAAACTAGTATCTAAATGTGTAGGATCAAAACCAAAAATCTGGAGGGATCTAGTTAA
ACTTCAATATGCATGACCCCAGATTCCCN

Sequence 2601

Sequence 2602

Table 1

Sequence 2603

CTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCGAGGTACGCGGAACAATCAACAGTT
TCTGATGTTCCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAGC
TGGGATGCTCCTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGGA
AATTNGCCCTGGNCAAGGNANTTTANNTTGGGNCCCNGGGAGCAAAGTTCTTACAGCTTN
CCCANTNAAGCTGGGNCCTTTANNACCTTGGGAGNTTTGAATTTATTACC
Sequence 2606

Sequence 2608

CGGCCGCCCGGGCAGGTACACTTATNGTTGAGAGCCANGTCTCCCTTATCATTGGTGAAT
GAGAATGAGCTACTGAAAACAAAAAGAGGGTCTTCTACTTCAGCCTGTACCCCTAANATT
TTATTATCAGNAAAGCAGNAGATTNACCNGTCCTTTACTTNTTTTACCNCCCTTTTAATN
NGGGTAAAAANAAAAANGGTAAATGTTTTCCCCTTATNTAAAANAANATTTCCCTTTCCC
CNGGTTTTCCTAACCCCCTTGGNNAAAAAACNTTTTTTAATGGGCCTTTTTNTTCCCTNG
GTTTTNACCCANTAAAANTCCAATGGGGCCAATGGGGGGGGCCTNAATGNAAACNCCTT
AAAAACCNTCAATTTTTNTTTGCAAAAATTTCGNGGGCAGGGNNTTGGTTTTCTGAAAG
NGGGGCCTTANTAAAATNTTTTCANTNCNNTGNGCCNTTAATTTTTTGGGAACCANNNCAA
NANTTTTGGANTAAAATAATTGGGNTTGGGNNTTCNCANATTTTTTCTCCATGNAAGGAT
CANNNACNNNTTGGNANTAAACNCATAACANTATCTTCTNTGGGGTANTCCCCCACNANT
NTTATTTCCAAAAATTGG

Sequence 2609

Table 1

Sequence 2610

Sequence 2611

Sequence 2612

Sequence 2614

GAGCTCACCGCGGTGGCATGCGGCCGCCCGGGCATGGTACTCCTGCCAAGGCANGCTCCC ACCGCTATGGGCACAAGGAAGTTGTCGTCATCTGCACTGCANNCTTGAGCTGTAGAATNC T

Sequence 2615

CTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACCATTGGTGGCCAATT GATTTGATGGTAAGGGAGGGATCGNTNACCTGATNTGTTATATNAANGANTCAACGGGCT GAACAAGGAACATCAGCATCCTTTATGAAATGGATCCCCAACAATNNCAAGACANCCGTC TGTTACATNNCACCTNNNTNGGCCTNAAAAATGGCAGTCACCTTCATTGGCAATAGCACA GCCATCCATGAGCTNTTNAAGCGCATCTCGGATCANTTCACTGCCATGTTCCNCCGGAAG GCCTTCCTCCACTGGTACCT

Sequence 2616

CGACTACTTAGGGCGAATTGGAGCTCNCCGCGGTGGCCCGGGCCAGGTACGCGGGGT CCCAACCAAGCCTCCAGCAAGGATTCAGAGTGCCCCTCCGGCCTCGCCATGAGGCTCTT CCCGTCGCTCCCGGTCCTGGTGGTGGTTCTGTCGATCGTCTTGGAAGGGAGTGGTTTTCA NAGACATTTCAGAAAGTGAAGGAGAAACTCAAGATTGACTCATGAGGACCTGAAGGGTGA

Table 1

Sequence 2617

Sequence 2618

Sequence 2620

Sequence 2621

Sequence 2622

AGGTACGCGGGAGAGTTCTGCCTCGCTTCCCGGCGCGGTCGCAGCCCTCAGCCCACTTAG GATAATGGCGACAGCTGAGGTACATTGTGATACAACTTCTTCACAGATGAAGGCCAGCAG AGACAGCAACAGCTGCAAGCCCTTGAGAACGCGCCGGAGCAATGGGAGCCGGCCCATGAA

Table 1

AAAGTAGGCAGCGAGGCCGCTCCGGGGGCCCTCTGGCGGGCCCGGGTCCTCCGTAGT

Sequence 2623

Sequence 2624

Sequence 2626

CCGCGGTGGCGCCGAGGTACTGTTCCCTTCTGATTTGGTCTAGATACCAGAATCCATTC
TCTTCCGTCAAACGGAAGACACAAGGCACCTGAGGCTGATCCTTCCCAGAAATTAACTCC
AGAGGCTGCCACATCTGGTATGAGCGTCCAAACCCAGCATCGACAATGTAGTTCCTGCCA
TCAATGGTCACCTGCAGGAGAAGGTGAATCATGCCAGTGCTGTATTTTTTGGCTGGAGTG
CTGTAAACATACCCTCCCAACATCGTGGTCTCAAAACCAATAGTGGTCAGAGCCCAGTAC
AGAAGATGATTGACCTGGAGACACCATCCACCCCGATTTCTTCTCACAACTTGATCAAAA
ATGGCCTCTAAGCCTAAGTCCATGGCATCCCCCACAATGGGATGTTAAGGTTCTCAAAGGG
AACAGCTTCGGATCTGGTGTTGAAGAATGTCAGTTTAATGTT

Sequence 2627

Sequence 2628

CCGCGGTGGCGGCCGAGGTACTCCGAAACAAGTAGAAAAGTGCTGTTTGAGGGATTTTAT
TAAATCTTTTTTTAATGGAATGTGGTACAGTTAGCTGTCACTCAGCTGACACCATGATGT
GGCAGCAGAGAGGGAAACCTACAAGTGGTTTGCCTCATTGCCTTTTGCCACATCTGAAGTT
CTCAGCAGCACTACCTTAGACTTCATGAGCTAATAGGAAACTTTTTATGGTGTAAATGCT
GTAAGACTTTGTACCTGCCCG

Sequence 2629

Table 1

CCGCGGTGGCGGCCGAGGTACTTCCTCACAGTTCTCACATATGGAAAGGATACACACTTT
GTAGAAACAAGAACTTTATGTTATCCAAGTTCTAGGATAGCCATGAGCTCCAATTATCTC
AGAGCTCTGAGTCCTCTACTCAATACCCATTGAGATTTATGTGTTCTGAGGCTTTTGTCT
TCTAGCTACTTCATTCTCCATGGGTAACGGTCATTCATCCACATTAACTAATTTCC
TCACTCCAAGCTCTTTTCTAGAGATAATCTCCAGTCCCTGTGCAGAAACTGTCATTGCAC
TTTCTGCTGAAATGGCAGTTTCTTCTCAGCAAGGTGAGATTATGGAATCCAGAATCTTTT
TTCAGGGGGTCACATGCCCATTTCCCCACTTGCATGAATGTCGACACTGCAGCCACAGTTT
TGGCCGTAAATGTGAATTTGGCAAGTAACCA

Sequence 2631

Sequence 2632

CTTAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACACTTCAGTCTCAATTCTG GAACTCTAAGAAAAACGTTCCAGACTTCTACGCAGCTGCCACCTCGGAGGACGGGAGAG CGGGGGACGAGGAAAGATCAGGATAAGACCCTAACTCCCACAAATGACTCCAGGAAAGGG AGACCACCACTCCCGAGCTTTGGAGCGCCGCGGGACCCGCGTACCTGCCCG Sequence 2633

CCGCGGTGGCGCCCCGGGCAGGTACGCGGGGAAAACGGAGTCCCTGAAATAACAGAT GCAGCCACAGATCAGGGCCCTGCAGAAAGCCCACCCACTTCCCCTTCATCAGCCTCTCGG GGTATGCTGTCTGCCATCACCAATGTGGTTCAAAACACAGGTAAAAGTGTCTTAACTGGA GGCCTTGATGCGTTGGAATTCATCGGCAAGAAAACCATGAATGTCCTTGCAGAAAGTGAC CCGGGCTTTAAGCGGACCAAGACGCTCATGGAGAGAACTGTTTCCTTGTCTCAGATGTTA AGGGAAGCTAAGGAGAAGGAGAAGCAGAGACTGGCACAGCTCACGATGGAGAGACC GCGCACTACGGGATGCTGTTTGATGAATATCAAGGCTTGTCACACCTGGAAGCCCTGGAA ATTCTGTCCAATGAAAGCCGAAAGCAAGGT

Table 1

Sequence 2635

Sequence 2636

Sequence 2638

TAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGCCCGGGCAGGTACGCGGGAGGTATG
AGCGCCGGGACCTGTGACAGGGCTGGTAGCAGCGCAGAGGAAAGGCGGCTTTTAGCCAGG
TATTTCAGTGTCTGTAGACAAGATGGAATCATCTCCATTTAATAGACGGCAATGGACCTC
ACTATCATTGAGGGTAACAAGCCAAAAAAACTTTNTCTTGTCAACANGAACAAGTCATCG
GCTATTGTGGAAATATTCTCCAAGTACCT

Sequence 2639

GGCGAATTGGANCTCCCCGCGGTGGCGGCCGAGGTACANAGTGCTTTTCTGTTTAGTTTT
TACTTTTTTTGTTTTTTTAAAGATGAAATAAAGACCCAGGGGAGAATGGGTGTT
GTATGGGAGGCAAGTGTGGGGGGGTCCTTCTCCACACCCACTTTGTCCATTTGCAAATAT
ATTTTGGAAAACNGCTCNTTTTAATTCTGATTGATCAGCCAAAACNGTCCCTGCCCGGGC
GGCCGCTCTANAACTA

Sequence 2640

CGAATTGGTTTTCCCCGNGGTGGCGGCCGGCCCGGGCAGGTACCAAAGGTGCAATTTATGA CTCCAGAAGGANTTCAAAACACATCGGAATCATGACAGCAAGATAACCCCAAGACAGTCT

Table 1

Sequence 2642

Sequence 2644

AACACTTTTTAGGGCGAATTGGAGCTTACCGCGGTGGCGGCCGAGGTACGCGGGGACACC CTAGATCCCAAGATCTCCAAGGATTTGGTGGCATACCCACTCCAGCACACAGAAGCATGA GGTTCATGACTCTCCTCTT

Sequence 2645

Sequence 2646

Sequence 2647

Table 1

CACCGCGGTGGCCGCCCCGGGCAGGTACGCGGGGGCCTCACAGATGACTTTCTT CATCTTCTTGCTCTTTTTCCCATCCTTCACCGGGGTCTTGTGCACCCTGGCCATCACCAT CTGGAGATTGAAGCCTTCANCTGACTGTGGCCCTTTTCGAGGTCTGCCTCTTCATTCA CTCCATCTACAGCTGGATCGACACCCTAAGTACCTNGGCCCGCTCTAGAACTA Sequence 2648

CGCCCGGCAGGTACACATGGGGTTTCACCATGTTGGTCAGGATGGTCTCGAACTTCAGA
CCTCAGGTGATCCGCCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACC
NNACCCAGCCAGTTAATTTTTCTATTAACTACAGACCTANTTAANATTGAGGCAAAANAA
ATGGGTCCTTGGGATTTGAAAATTACTATNCANTTTGGAAGTTNAATTTGCAACATANAT
TGTCTGTTATTAAATTACTAGATATAATATCNCATAGGTGGAAAGAAAGGTTGCTTAATT
AAAGATCTAAGTTACTAGTCATGGTGTCAGATATNGANAATGATTGAANGTTATNAAGAN
TCNCACACCAGATGAGTAAATTGNTGTTTTCNNGAAGAAGTTACATNAANGTNACCGGAG
TATATTTCAGCATTTTTTGNTANATTAAAAAATTTGTNAAGCTATTTTCAATTTCACATG
TTAACACCCTCCTTGAGCCCCTTTATTTTTTTAAAGCTCTTNAATNTATTTTGGNCCTGA
AATTAACCNTTTCTTTTAAGGAAGAATTTNAAAAATTTTTTTTGAAAAAAAGTTGGAAAATT
CNTGGAANAGGCCCCTGGTTATNTTTTCAAATT

Sequence 2649

Sequence 2651

Sequence 2652

CGACTNCTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGATGTTT GCCACTTTGCAAAGGAGCTCACTGTGGTGTCTGTGTTCCAACCACTGAATCTGGACCCCA TCTGCGAATAAGCCATTCTGACTCATATCCCCTATTTAACAGGGTCTCTAGTGCTGTGAA AAAAAAAATGCTGAACATTGCATATAACTTATATTTGTAAGAAAATACTGTACCTGCCCG

Sequence 2653

TATAGGGCGAATTGGAGCTCCCCGCGGTGGCGCCCGAGGTACTTCCGAAGATGGGCTTGT
ATCTGGTTTCGGACGGACTGTTAATGACAATTTGATCGACGGGAATTGCACACCCCANAA
TCCACCACAAAAGAAAAAGGTTACAAATTTAACAATTTATAGTCCTTTTAATAGTTTTTT
TTTTTTCATAATACTACTGAGGGGAATTGGTNAGAATGTATNNATGTAAGGCNTTCTTA
ATTTAAGTTATTAAAGTTTACAGTTTTAATATTTTTAAACCTTTTGTAAATGCTTGGCTT
AATTAGAAAATGTTTACAGAAAAGTAAAAAAATTCTAGTAATATTGGGAAATCCTTGTAAG
CAGCATGGTTTCAGAAAAAATCTCAAGATGATTTATTTCACCAAATTGAGTNTTTTTTTAA

Table 1

AACTAGGNAACTTCCCCAACCAAAAACACANGACNTTGAATAATATTTTTGTGTTATT Sequence 2654

CCGGGCAGGTACTCTNTTTTTTTTTTTTTTTTTTTTTAGGCAGNTNAAATCTAGGATGGTGTT
AACCTTGTCTTCATTTNGCCAATNATATNTNAAAAATNANAAACNACATTGAATCTGCAT
TTCTTGGANNAGANNGTNNATAACAAACTATTTCTCAATATTNNGATACTANAAACTAGN
GAAGGNGNCATGGGNTCCAGCNTCTTATCTNTNATNTGAACATGGGTTTCTGAANGGAGC
CTATATNATAATATAAATGGTNTGNNNAAAATGAGGCACTAGCNTTGNCTGNNACTGCTA
TAAAAAAAATNACCA

Sequence 2656

Sequence 2657

Sequence 2658

Sequence 2659

Sequence 2660

Table 1

Sequence 2661

Sequence 2662

Sequence 2663

Sequence 2664

Sequence 2665

CTACTTAGGGCGAATTGGAGCTCCCCGCGGTGGCCGCCCGGGCAGGTACCAATGTGT GGCAGTCCAAAATTACGAGGAAAATGAGTTCCCTTCATGGGTCACATCAGCAATTTTTTT

Table 1

CGACTCACTATAGGGGCGAATTGGGAGCTCCCCGCGGTGGCCCGGCCCGGCCCGGGCAGGT
ACAATCTCTGGCCCTACATTTTCTAAATGTTATGCCACCCCGACCAAGGGGCAACTCCTA
CAAAGCCAGGCAAAATAATAAAAATCATATTTGTCTCTAGTGGAATGGATAACTATGCCTA
AAACTGTGCCCTTTGAAAAGCAACTAGAGAGATAATTTCTGAAGTGTTTGTCCCTACCTG
AATGTGTGGCAAAATTCTAAACTCCCTGAAGTGTGAAAGTGGTTTCCAAGCCACATGCAC
ATCCAGTAGTGGTAAAGGGGTGAAAATCTAACTGGCTAAGAGGGCTTCATAGCAACATTAA
CCAAAAAGTGGTTTATGTAGTCTTTGCCTGCTTCATAATTCCCTANGCATTCTATGCTAT
TCTGCACCT

Sequence 2668

Sequence 2670

Table 1

Sequence 2671

Sequence 2672

Sequence 2674

CCGCGGTGGCGCCGAGGTACAGGAGACTTTCTGATTTCCAATCTTGGCTCAGGTCAGAA
GAAAAAGGGGAAAGGTTACATTCCTGGAAAGAAAATACAGCCTATTTGAGGGCATGCCTG
ACTTTCAGTCCATGCACTAGTCCTCTTGGCTCGTAGAGTTTTCAGTGCCCTGAAACCATG
ATCCCTCTGCCTCCATGGTCCTCTGAGTGTAGTTATTATGTCTGCAAACCAGTAATGTCA
CAAGTCAAAGGGTCTGGGGCTTCCCAGGGAACCACTATGACTGAGTATATTCTGATTTGA
GAAACCTGTGACAAGTCTTCTCAGCACTCGCCTTCTAATTTTTGGAGCCGATGCCTGGGT
TCCCAGCATCCAGGTCACAGTAGCTGGAAATCATGCAGGAAGGGCAAAAAGCCAGCAGCC
CAGAATGGACTGTCTCTGCAGCTCTGGCACATTCTCTACACATCGCCACACCACTCAAAT
GTCCTATAAAATATCAAAACCAATAACCTGGACATGACCCGGTTAATCTGTACCTGCCCG
GGCCGGCCCGCTCTAGAACTAGTGGGATCCCCCGGGGCTGCAGGAAATTCGATAT
Sequence 2675

CCGCGGTGGCGGCCGAGGTACTTCAGTTTCTCTAGATTACCATGTAAGACAGCTCTGTGG ATCCTCTTCAGATGATACGGTTTAATGGGGTATTGGGGAAATGCGAAGCCATCCGAGCAC AAGCGCTCCATGAGGGTGGGCCACCTCTCCCGCTTGCCGTCTTCCATAATCGTCGGCTGC AAATTGTAGCCTGCAGCCGTATTTCAGCTCGCCTTCGGGGATCGCCGCCTCCGAAGAGCA ACAACGAGCAAAGCAGTCTGTCCACGGACCTCCGCACAGACTCTCAGCGCCTCCCGCCTC

Table 1

TCAGCAGAAACGCCCAACAGAAGGGTTAGAACCAGCGAGCACGCGCACCTTAGCCGGCCC
TCCCCGCGTACCTGCCCGGGCGG

Sequence 2676

CCTGACGCTGGGAGGAGATGCTGCCACCTAGGTTACTNACTCGGTCCNNNTACGGCAACC TCCTTTGCCAGGAACTATTTATAAACATCCTGCAGGAAAATGAGTCTTATATGTCAAAAT ACACATTTCCCACCTTTGCCCANCNGTNNNAAAACCNTAGGAAGGANGAAAANCATTTA AAAAATGACACNGGAATGTTAATGGAAGCAATGTGATGGTCGTTTTTGGAGGTGGAACCCT TTCAANAAAGGTAATTAAATGCCCTTGGTTAAGAAGAAGACCAAAAGAAGCTTGCGCACC TTTTTTCCTGCCATGTGAGGAAGCCAAANAAGCCGGCTGTCTGCAACCTGCAAGAGGACC CTCACTAGAAAGCTAGCCATACTGGCATCCTCATCTTGGCTTTCCAA

Sequence 2677

CCGCGGTGGCGGCCGAAGGTAATCGGGGGCCAGTCTTTATACTGCTGACAGTAATAAATT CCAAAATCTTCAGACTGCAGTCCACTGACGACGAGGGTGAAGTCTGTCCCAGACCCAGAG CCAATGAATCTGGCTGGGACACCAGTGGCCCTGGTGGATGCAGCAAAGACGAGGAGCCTG GGAGCCTGGCCAGACTTCTGGTGGTACCTGCCCG

Sequence 2678

Sequence 2680

Sequence 2681

CCCGGCCGGGCAGGTACCATGGTTGGAATGATAAANGATATTGTCATTTTTGTTAGCANT GAAGTGAGTGGCATCTATGTATTTTTTAAGGTATAATGAAATTGTGCCTAGGGGAGTN ATAATNCACTCTATGTA

Sequence 2682

CGCGGGATGGAAAGAATGAAGACANTTTTAGACNTGCTAGACTNATGGTTGACTATACA NCAACCATCTCAGAAAGAGTTATTCAGATATAGCTTCANACTGATANNTAAATCATATAA

Table 1

ANTAATGTGGTANTCAAAATANGAGTTANGTAACTACTGACANATATAAGGAAAGTCGTA CCANTTCNGAACTAAAAACAATGGTCTATGTTGCTGGANGAACAATGTGGGGAGGGT Sequence 2683

CTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCCCCGGGCAGGTACGCGGGAAATG
AAATTGGAGCTGGACCATTTAGTCAGTTCATTAAAGCAAAAACTCGGCCATTACCACCCT
TGCCTCCTAGGCTAGAATGTGCTGCTGCTGGTCCTCAGAGCCTGAAGCTAAAATGGGGAG
ACAGTAACTCCAAGACACATGCTGCTGAGGACATTGTGTACCT
Sequence 2684

Sequence 2688

Sequence 2687

AGGTACTTTGGCCTCTCTGGGATAGAAGTTATTCAGCAGGCACACAACAGAGGCAGTTCC
AGATTTCAACTGCTCATCAGATGGCGGGAAGATGAAGACAGATGGTGCANCCACAGTTCG
TGTGATCTCCAGCCTGGTCCCCTGGCCAAAAGTCCGAGGGATACTGCTACTCTGTTGACA
GTAGTAAGTTTNCAAAATCTTTCAGGTTGCAGAACTGCTTGATGGNGAAGAAGTGAAATC
TGTCCCAGATNCACTGCCACTTAAACCTTTGATGGGGACCCNACTTTTGCAAACTGGGAT
TGCANCNTAAGAATGAGGGAGTTTAGGGGGGCCCTTTCCCTGGTTTCTTGCTGATNCCAAT
TTTAAATAGATATTAATGGACTTGACTTGCCCC

Sequence 2689

CTATAGGGCGAATTGGAGCTCCCCGCGGTGGCGGCCGAGGTACGCGGGGGTTGTATCNGG ACTTATGGTGGCCACCAAATATGAAGTGAGTGTCTATGCTCTTAAGGACACTTNGACAAG CACACCAGCTNATGGAGNTGNCNCCANTCTGGNNAANGCNNGNCCACCAAGAAGGGCTNG TGTGACAGATGCTACTGNNACCACCATCACCATTAGNTGGAGAACCAACACTGAGACCAT